Sk Page 1

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OM nucleic - nucleic search, using sw model

November Run on:

2006, 10:38:34 ; Search time 93 Seconds (without alignments) 2.906 Million cell updates/sec

Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 0.5 Scoring table:

1733 seqs, 49269 residues Searched:

Total number of hits satisfying chosen parameters:

3466

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Match 0% Match 100% first 1733 summaries Minimum N Maximum N Listing f Post-processing:

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES DB Query Match Length Result No.

ACCESSION: CF305383 ACCESSION: CV732719 ACCESSION: CF329026 ACCESSION: CF298283 ACCESSION: CV733592 ACCESSION: CF317896 ACCESSION: CV724890 ACCESSION: CV733486 ACCESSION: CV734501 ACCESSION: DY231327 ACCESSION: AJ659250 :ON:CV730946 ACCESSION: CF302212 ACCESSION: CV725460 ACCESSION: CF331239 :ON:CV732463 ACCESSION: CF332233 AA587192 AA079243 AU103749 AU103750 AU103751 AU103772 T92783 CF298283 BG610636 CV733592 CF317896 CV732463 CV725460 CV732719 CF329026 AL046183 CF332388

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CF295807 CF299639 CF302447 CF312493 CF312013 CF319075 CF278251 CF278251 CF278251 CF298134 CF298134 CF298134 CF298134 CF298134 CF298134 CF309536 CF309536 CF309536 CF309536 CF309536	LIIG BO BO BO BO BO BO BO BO BO BO	Score 78.4; Score 78.4; Pred. No. 0.5 Mismatches GTGATCGAGATCTC A 948 A 80
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In Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: GapDs-rémail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1006 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
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// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Mol Type="mRNa"
// Ab xref="taxon:9606"
// Libsue type="colon tumor RER+"
// Lab hog="tablu0b"
// Loone lib="NCI CGAP Co9"
// Clone lib="NCI CGAP Co9"
// Note="Organ: colon; Vector: pT7T3D-PacI; lst strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (Soares4). "
                                        61 bp mRNA linear EST 23-DEC-1997 zm70b11.s1 Stratagene neuroepithelium (#93721) Homo sapiene cDNA clone IMAGE:530973 3' similar to gb:S38729 LUPUS KU AUTOANTIGEN PROTEIN P70 (HUMAN);, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 78)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2633 CCATGGTGATGGTGTAGCCCTCCCACTTTGCTGTTTTACTTTACTTGCTGAATAAAGA
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Best Local Similarity 97.4%; Pred. No. 1;
Matches 75; Conservative 0; Mismatches
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AA079243.1 GI:1618135
EST.
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RESULT 2
AA587192/c
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SOURCE
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SOURCE ORGANISM

AUTHORS REFERENCE

TITLE JOURNAL PUBMED COMMENT

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Fax.: yerzuki@yac.jp
Swzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                            Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU103750 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
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1 (bases 1 to 50)
Suzuki, Y., Taira, H., Taunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Bakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
FIND Rep. 2 (5), 388-393 (2001)
                          Hominidae, Homo.

1 (bases 1 to 50)

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T. Isogal,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 AGACTCGAGACCACGCTCCTTCCTCGGGAGGAGGAGGCGCCCCCCGCGTTT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP06290"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                       Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Far: 81-3-5449-5343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yutaka Suzuki
Department of Virologa
Institue of Medical Science, University of Tokyo
1-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                    mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
11375929
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AU103750.1 GI:13553271
EST.
                                                                                                                                                                                                                                                        Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                          Email: ysuzuki@hgc.jp
Suzuki,Y., Yoshitomo-N
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Fax: 81-3-5449-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149-156 (1997)
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Best Local Similarity
Matches 50; Conserv
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AUTHORS
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AU103750
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AUI03749 GI:13553270
                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2647 TAGCCCTCCCACTTTGCTGTTCTTTACTTGCCTGAATAAGAGCCCTAAGTTTGTA 2706
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                                                                                                   Hominidae, Homo.

I (bases 1 to 61).

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chiasoe, S., Dietrich, M., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hulfman, M., Kucaba, T., Lacy, M., Le, M., Le, N.)
Mardis, E., Moore, B., Morris, M., Passons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                                                                                                                                                                                                                   Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 2176 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 1. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3920485"
       sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
                                                                                                                                                                                                                                                                                                            and Marra, M.
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FEATURES

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JOURNAL
PUBMED
                                                          REFERENCE
                                                                            AUTHORS
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T92783/c
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                                                                                                                                                                                                                                                                      50 bp mRNA linear EST 28-JAN-2004 AU103751 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HEP06548, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ysuzuki@hgc.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Hominidae; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 50)

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Toda,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                               /mol_type="mRNA"
/db_xref="texaon:9606"
/dlone="HEP06361"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /moi_type="mRNA"
/db_xref="texaon:9606"
/dbone="HEP06548"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGTATCGAGACCACGCTCCTTCCTCGGGAAGGAGGCGCGCACCTCGCGTTT
                                                                                       DB 1; Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.7%; Score 46.8; DB 1; Length 50; Best Local Similarity 96.0%; Pred. No. 40; Matches 48; Conservative 0; Mismatches 2; Indels
                                                                                                                           1; Indels
                                                                                                                           0; Mismatches
                                                                                       Score 48.4; 1
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .50
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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AU103772.1 GI:13553293
                                                                                       1.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 81-3-5449-5343
Fax: 81-3-5449-5416
                                                                                                                           Conservative
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                                                                                                        Best Local Similarity
Matches 49; Conserv
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                                                                                       Query Match
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KEYWORDS
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792783 122-MAR-1995 ye27h02.81 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118995 3' similar to gb:S38729 LUPUS KU AUTOANTIGEN PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: yguzuki@hgc.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a S'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)
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I (bases 1 to 52)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, W., Parsons, J., Prange, C., Rikin, L.,
Rohliing, T., Schellenberg, K., Soares, M.B., Tan, P., Thierry-Meg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                  Hominidae, Homo.

I (bases 1 to 50)

Suzuki, Y., Tairat, Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                         Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Far: 81-3-5449-5343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGGTTATCCATTTGTGTTGTTCGTCAGTTAGGCCTGGCCTCGTCCCGCTT
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/organism="Homo sapiens"
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High quality sequence starts: 1
High quality sequence stops: 1
Source: INAGE Consortium, LIND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP13405"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P70 (HUMAN);, mRNA sequence.
T92783
                                                                                                                                                                                                                                                                                                                    Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
Homo sapiens
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Best Local Similarity
Matches 48; Conserv
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Gape

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Indels

FEATURES

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BG610636 46 bp mRNA linear EST 18-APR-2001
602611813F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4737482 5',
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM665 row: i column: 03
High quality sequence stop: 43.
                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae, Homo.

1 (bases 1 to 46)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.4%; Score 38.6; DB 1; Length 46; 91.1%; Pred. No. 1.3e+02; tive 0; Mismatches 4; Indels
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0; Mismatches 2;
                                                                                                                                                                                                                                                                                                         BG610636.1 GI:13662007
  l Similarity 95.3%;
41; Conservative
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    Local Similarity
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CV733592/c
LOCUS
DEFINITION
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COMMENT
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/cultivar="ManA"
/cultivar="ManA"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                /dev gragge="72 years"
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/lab host="SOLR cells (kanamycin resistant)"
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/note="Organ: lung; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. PrImer:
Oligo dT. normal lung. Average insert size: 1.0 kb;
UNi_ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF298283
7LEAF--01-J16.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-J16, mRNA
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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(Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kin, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
(Dnublished (2003)

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considerated overall poor quality Seq primer: -21ml3 High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .46
'organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.5%; Score 41.8; D
82.7%; Pred. No. 85;
ive 0; Mismatches
                                                                                                                                                    /organism="Homo sapiens"
| mol type="mRNA"
| db_xref="GDB:487284"
| db_xref="taxon:9606"
| /clone="IMAGE:118995"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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RESULT 9 CF298283/c DEFINITION

Matches

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

CV/33592 43 bp mRNA linear EST 05-NOV-2004 FLO--08-J04.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-J04, mRNA sequence.

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Gaps .

Bource

FEATURES

JOURNAL COMMENT

TITLE

REFERENCE AUTHORS

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40;
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Best Local Si
Matches 39;
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref=reacon:39947"
/db_xref=reacon:39947"
/clone="FLO--08-J04"
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XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5:
end with EcoRI and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 bp mRNA linear EST 15-AUG-2003

HD--07-M03.gl OsHDACl-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

HD--07-M03, mRNA sequence.
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                                                         Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantas, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnolitophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                              Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yoogin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 47)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa (japonica cultivar-group)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.4%; Score 38.4; DB 1; Length 43; 77.5%; Pred. No. 1.2e+02; ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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    Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
                      CV733592.1 GI:55440563
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Conservative
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Best Local Similarity
Matches 39; Conserv
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CLDI--01-124.b1 Rice cold treated leaf plasmid cDNA library (CLD1) CVPyza sativa (japonica cultivar-group) cDNA clone CLD1--01-124, mRNA sequence.
                                            /tissue type="callus" /dev stage="proliferated callus on 2N6 media for 2 weeks" /dev stage="proliferated callus on 2N6 media for 2 weeks" /da_nost="E.coli DH10B" /clone lib="colloAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiphantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhatroideae; Oryzeae; Oryza.

I (bases 1 to 44)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Nahm B.H.
Gontact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Yongin, Kyeonggi, Korea
Far: 82 31 33 130 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/lab_host="E.coli DH10B"
/clone_lib="Rice cold treated leaf plasmid cDNA library
(r.n))"
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                                                                                                                                                                                      /note="Vector: pCR4-TOPO, Site_1: EcoRI, Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was
                                                                                                                                                                                                                                           reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
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Pred. No. 1.5e+02;
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cultivar="Nackdong"
db_xref="taxon:39947"
/clone="CLD1-01-124"
tissue_type="leaf"
/db_xref="taxon:39947"
/clone="HD--07-M03"
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RESULT 16
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Oryza sativa (japonica cultivar-group)
Bukaryota; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Enrharcoideae; Oryza.

E 1 (bases 1 to 46)
S Kim,J.S., Jun,K.M., K.M., Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Lupublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin; Kyeongi, Korea
Tel: 82 31 330 6193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Oryza sativa (japonica cultivar-group)"
/organism="Ncryza sativa (japonica cultivar-group)"
/wol_type="mRNA"
/cultivar="Nackdong"
/db xref="taxor.39347"
/clone="FLO--07-F03"
//iabue_type="flower"
/lab host="E.col; SOLR"
/lab host="E.col; SOLR"
/nore="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/nore="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/norl; cDNA was inserted into lamda Uni-Zap XR vector at 5,
end with EcoRI and 3' end with XhoI site."
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NACL--04-D06.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-D06, mRNA
                                        CV732719
46 bp mRNA linear EST 05-NOV-2004 FLO--07-F03.gl Rice flower lambda phage cDNA library (FLO) Oryza Bativa (japonica cultivar-group) cDNA clone FLO--07-F03, mRNA
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza,
(fim.J.S., Jun.K.M., Cheong, P.J., Kim.M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
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Location/Qualifiers
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CF329026.1 GI:33806289
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CV732719.1 GI:55438841
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Best Local Similarity 92.9
Matches 39; Conservative
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RESULT 14
CV732719/c
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42 bp mRNA linear EST 06-JUL-2004 DKF2p434C127 s1 434 (synonym: hte83) Homo sapiens cDNA clone AL046183
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                                                                                                                                                                                                                                                                        /mol Lype="mrNA"
/mol Lype="mrNA"
/mol Lype="mrNA"
/mol Lype="naxon:39947"
/db xref="taxon:39947"
/clone="NACL-04-D06"
/tissue_Lype="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_nost="R.coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib=Rice callus plasmid cDNA library (NACL)" /note="Vector: pCR4-TOP0; Site_1: EcoR1; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 42)

Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)

Unpublished (1999)
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/db xref="taxon:9666"
/db xref="taxon:9666"
/clone="Dype="testis"
/dev stage="adult"
/db ref="best="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bhost="bho
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                                                                                                    bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL046183.1 GI:49682657
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Homo sapiens
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Query Match
Best Local Similarity
Matches 38; Conserv
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Best Local Similarity
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CF332152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mana"
/cultivar="Nackdong"
/duxref="taxon:39947"
/clone="NACL-08-002"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
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/note="Vector: pCR4-TOPO; Site 1: EcoR1; mRNA was capped with oligoribonucleotides and then used as templates for
                                                      Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                        1 (bases 1 to 44)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
YongIn, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Contact: Nahm B.H.

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Yorgin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongJi.ac.kr.

Location/Qualifiers
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FLO--04-L22.gl Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--04-L22, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                    Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Stage-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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1.5e+02;
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100.0%; Pred. No. 1.5
ative 0; Mismatches
                     CF332388.1 GI:33812996
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Matches 37; Conservative
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CV730946/c
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CF302212 44 bp mRNA linear EST 15-AUG-2003 7LEAF--07-I14.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-I14, mRNA
                                                                   /db xref="taxon:39947"
/db xref="taxon:39947"
/clone="FLO--04-L22"
/tissue_Lrype="flower"
/lab host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5,
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Nahm B.H. GreenGene Biotech Inc.; Division of Bioscience and Bacinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="leaf"
/dev stage="leaf"
/dev stage="Tays after germination"
/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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/organism="Oryza sativa (japonica cultivar-group)"
|mol_type="mRNA"
|cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                 Length 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lv.
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
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1.6e+02;
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95.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 2;
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; Pred. No. 1.6e+
0; Mismatches
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/clone="7LEAF--07-114"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/cultivar="Nackdong"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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CF302212.1 GI:33673973
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                                                                                                                                                                                                                                                                                                                                                               38; Conservative
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bhnahm@bio.myongji.ac.kr.

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Email: bhnahm@ggbio.com,
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Matches 38; Conserv
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S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Lupublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
CF332152 A6 bp mRNA linear EST 18-AUG-2003 NACL--08-I20.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--08-I20, mRNA
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with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                            Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTB

Unpublished (2003)

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Tel: 82 31 330 6193

Pax: 82 31 321 6355
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/mol_type="mRNA"
/cultivar="Nackdong"
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Location/Qualifiers
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Best Local Similarity 95.0%;
Matches 38; Conservative
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145alt--02-123.gl Salt treated rice leaf lambda phage cDNA library (145alt) Oryza sativa (japonica cultivar-group) cDNA clone 145alt--02-123, mRNA sequence. ö ö 'n Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Enrhartoideae; Oryzeae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTE /mol type="month" | Jupone of the property | Mol type="month" | Mol type="month" | Mol type="month" | Mol type="month" | Mol type="filower" | Mol type="weetor: pBluescript SK(+); Site 1: BCORI; Site 2: XhoI; CDNA was inserted into lamda Uni-ZAP XR vector at 5 end with BCORI and 3' end with XhoI site." Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Of Discience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers /note="vector: pBluescript SK(+); Site_1: BcoRI; Site_2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for Zhra. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site." /db_xref="taxon.39947"
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RESULT 23 CF331239/c DEFINITION

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VERSION KEYWORDS

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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CV729880 45 bp mRNA linear EST 05-NOV-2004 FLO--03-C10.bl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--03-C10, mRNA
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/note="vector: Splueserript SK(+); Site 2: EcoRI; Site 2: Shoi; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 45)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University YongJi, KyeongJi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of the contact and Bioinformatics, MyongJi University

YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 31 21 6355
Email: bhnahm@gdpio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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90.7%; Pred. No. 1.6e+02;
iive 0; Mismatches 4;
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza,
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Sukaryota, Viridiplantes; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahn,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Location/Qualifiers
Oryza sativa (japonica cultivar-group)
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Matches 39; Conservative
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VERSION KEYWORDS SOURCE ORGANISM

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Query Match

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LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT

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AUTHORS

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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryzae;

I (bases 1 to 44)

S Kim,J.S., Jun,K.M., C.K., Kim,Y.F.K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

VIDPUblished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

Yongin, Kyeonggi, Korea

Tel: 82 31 331 6193

Fax: 82 31 321 6355

Fax: 82 31 221 6355

Fax: 82 31 221 6355
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_nost="E.coli DH10B"
/clone lib="colabAcl-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                                                                                                                                                                                                                                                                                                                                                                        /organism="Noryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="NacKong"
/db xref="taxox:3947"
/clone="FLO-08-G21"
/tissue_type="flower"
/lab host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Yector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/note="Yector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/note="Cond and all state and all site and all site."
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeongqi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HD--05-K08.gl OSHDACl-overexpressing transgenic rice plasmid CDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--05-K08, mRNA sequence.
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Location/Qualifiers
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Location/Qualifiers
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza ...
El (bases 1 to 38)
S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTS
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                          145alt--01-L07.gl Salt treated rice leaf lambda phage cDNA library (145alt) Oryza sativa (japonica cultivar-group) cDNA clone 145alt--01-L07, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 43)
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/dev_stage="14 tays after gernimation"
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library (148alt)"
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/mol type="mRNA"
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                                         Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/db_xref="taxon:39947"
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Location/Qualifiers
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CV734501/c
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14-AUG-2003
14ROOT--02-M10.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-M10, mRNA
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopaida; Poales; Poaceae; BEP
clade; Enthatroideae; Oryzeae; Oryza.

1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bio. Genetics and Broinformatics, MyongJi University
YongJi, KyeongGi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                Gaps
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larity 97.4%; Pred. No. 1.7e+02;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.3%; Score 36.2; DB 1; Length 42; 92.7%; Pred. No. 1.7e+02; ive 0; Mismatches 3; Indels
                                                                                                            1; Indels
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CV734468.1 (
EST.
                                                                                             Best Local Similarity
Matches 37; Conserv
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Matches 38; Conserv
                                                                                                                                                                                                                                                                                                          seguence.
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CV734468/c
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LOCUS

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/tissue type="flower"
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/lab_host="E.coli SOLR"
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XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5, end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplanica cultivar-group)

Eukaryota; Viridiplanica; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP calde; Ehrhartoideae; Oryzae; Oryza.

Clade; Ehrhartoideae; Oryzeae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yogin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; BEP
clade, Ehrhartoideae; Oryzea, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CV734501 42 bp mRNA linear EST 05-NOV-20
FLO--09-011.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--09-011, mRNA
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Kim, U.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa (japonica cultivar-group)"
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EST 28-JUN-2004 mRNA sequence.

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Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Sitel: EcoRI
R. Site2: NotI 5' Seq Primer MiJF Normalised library constructed
from pooled early embryos, from 8- cell stage to blastocysts.
Clones available from UK Centre for Functional Genomics in Farm
Animals, Roslin Institite, Roslin, Midlothian, UK, EH25 9PS,
www.arkgenomics.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Compublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Wizidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 37)
Song, S. L., Kim, Y. K., Kim, Y. K., and Nahm, B. H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (1203)
Contact: Nahm B. H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="embryo"
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/note="Vector: pBluescript11(SK+); Site_l: EcoRI; Site_2:
Not1; Single pass sequencing. Normalised library
constructed from pooled early embryos, from 8-cell stage
                                                                                      AJ659250 MR277 Sus scrofa cDNA clone C0005215_D15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2708 ТАААААААААААААААААААААААААААААААААА
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00.0%; Pred. No. 1.6e+0.
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/organism="Sus scrofa"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to blastocysts."
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CF328866.1 GI:33805974
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                                                                                                                                                                                                                                                         Sus scrofa (pig)
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Best Local Similarity
Matches 36; Conserv
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CF328866/c
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//mol_type="mRNA"
//mol_type="mRNA"
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//db_xref="taxon:7091"
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//dow_grage="mrtaphase
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EST02078 BmP Bombyx mori cDNA clone BmpG_G114_2005-10-17_WD-051017
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                             /lab_hogt="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note=""vector: pBluescript SK(+); Site_l: EcoRI; Site_2:
Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with XhoI site."
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                                                                                                                                                                                                                                                                                                                                                   Tel: 86 571 86843194
Fax: 86 571 86843198
Email: yaczhou@chinagene.com
Seq primer: M13 Forward
High quality sequence stop: 44
POLYA-YES.
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/organism="Bombyx mori"
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tissue_type="flower"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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ACCESSION VERSION KEYWORDS SOURCE

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Length 37; 0; Indels

1.6e+02;

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CV730040/c
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CF300591/c
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                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
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/culTivar="Nackdong"
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/dev_stage="proliferated callus on 2N6 media for 30 days"
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/clone=lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: Ecoli, mRNA was capped with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CV731657 37 bp mRNA linear EST 05-NOV-2004 FLO--05-M14.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--05-M14, mRNA
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/tissue_type="fLO-06"
/tissue_type="fLOwer"
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_2:
Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with Xhol site."
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|mol_type="mRNA"
|cultivar="Nackdong"
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of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 31 21 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1.3%; Score 36; DB 1; Le
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
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Best Local Similarity
Matches 36; Conserv
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CV731657/c
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CV730040 38 bp mRNA linear EST 05-NOV-2004 FLO--03-G05.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--03-G05, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:39947"
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/lab_host="E.coli SOLR"
/lab_host="Taxoe flower"
/lab_host="Weach Taxoe flower lambda phage cDNA library (FLO)"
/note="Weach Taxoe flower lambda Uni SK(+); Site 1: BcoRI; Site 2: XhoI; cDNA was inserted into lamda Uni ZAP XR vector at 5'
                                                                                                                                                                                                                                                                                                                                                                          Orgina sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP
clade; Enrhartoideae; Oryzeae; Oryza.

(bases 1 to 39)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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    .38
    Organism="Oryza sativa (japonica cultivar-group)" /mol type="mRNA" /cultivar="Nackdong" /cultivar="Nackdong"

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2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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1.3%; Score 36; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 36; Conservative 0; Mismatches 0;
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CV730040.1 GI:55433852
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Query Match
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Matches 36; Conservative
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CV727347/c
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                                                                                                                                                                                               /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--05-C03"
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/lab_host="E.coli DH10B"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Yongin, KyeongJi, Korea
13130 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Genetics Institute, MyongJi University
Yorgin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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/lab.host="8.coli SOLR"
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library (145alt)"
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                                                                                                                                     Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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CV726948.1 GI:55414572
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Best Local Similarity 100.0
Matches 36; Conservative
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CV726948/c
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Oryza sativa (japonica cultivar-group)

Sparacota, Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Bukaryota, Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryzea; Oryzea; Oryzeae; Oryzea; Clade; Ehrhartoideae; Oryzeae; Oryzea; Clade; Ehrhartoideae; Oryzeae; Oryzea; Oryzea; Clade; Ehrhartoideae; Oryzeae; Oryzea; Clade; Ehrhartoideae; Oryzeae; Oryzea; Oryzea; Clade; Ehrhartoideae; Oryzeae; Oryzea; Oryzea
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/clone_lib=="salt_treated_rice leaf_lambda_phage_cDNA
library_(145alt)
/note="Vector: pBluescript_SK(+); Site_1: EcoRI; Site_2:
Xhol; Leaf_was incented_nt q C(360uM/m-2sec-1) for 2hrs.
CDNA was inserted_into_lamda_Uni_ZAP_KR_vector_at_S' end
with EcoRI and 3' end with Xhol site."
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/mol_type="mRNA"
/cultivar="Nackdong"
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         Length 39;
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100.0%; Pred. No. 1.7e+02;
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                                                    1.7e+02
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100.0%; Pred. No. 1.7e+05
iive 0; Mismatches C
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Oryza sativa (japonica cultivar-group)
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Best Local Similarity 100.0%; Pred. No. 1.7.
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TITLE JOURNAL COMMENT

FEATURES

AUTHORS

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Gaps

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EST 04-NOV-2004

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/tissue_type="flower"
/tab_nost="E.coli SOLR"
/clone_lib="Rice_flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: BcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vv/zbi08
14Salt--03-J05.bl Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-J05, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyra; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Nahm B.H. Genemics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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/clone="148alt--03-J05"
/tissue_type="leaf"
/dev_stage="14 days after gernimation"
/lab_host="E.coli SOLR"
/lab_nost="E.coli sols"
/lab_ary [45alt] treated rice leaf lambda phage cDNA
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                                                                                                                                                                                                                                                                 Length 41;
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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1.3%; Score 36; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 36; Conservative 0; Mismatches 0;
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              'db xref="taxon:39947"
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/organism="Oryza sativa (japonica cultivar-group)"
/oultivar="Nackdong"
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/clone="ABP--03-N04"
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/tissue_type="leaf"
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/clone lib="ABB7-overexpressing transgenic rice plasmid cDNA library (ABF).
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
1 (bases 1 to 40)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Sang,S.I., Kim,Y.-K., Min,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantaa, Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnollophyta; Liliopaida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                         Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yorgin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6555
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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(Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
(Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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/mol_type="mRNA"
/cultivar="Nackdong"
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100.0%; Pred. No. 1.7e+02;
tive 0; Mismatches 0; Indels
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Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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CV733657.1 GI:55440691
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RESULT 41 CV733657/c LOCUS

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VERSION KEYWORDS SOURCE ORGANISM ACCESSION.

TITLE JOURNAL COMMENT

FEATURES

AUTHORS REFERENCE

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Gaps

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EST 05-NOV-2004

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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
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Oryza sativa (japonica cultivar-group)
Cryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
   14Salt--06-L11.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--06-L11, mRNA sequence.
                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/\overline{m}-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yorgin, KyeongJi Korea
Tel: 82 31 310 6193
Fax: 82 31 31 21 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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FLO--09-102.gl Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--09-102, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                    Lee, T.H., Shin, Y.C.,
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/tissue type="leaf"
/dev_stage="14 days after gernimation"
/lab_host="s..coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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1.7e+02;
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100.0%; Pred. No. 1.7
tive 0; Mismatches
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/cultivar="Nackdong"
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Matches 36,
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44 bp mRNA linear EST 04-NOV-2004 (14Salt--04-J20.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--04-J20, mRNA sequence.
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                                                                                                                                                                      /db_xref="rackoon:39947"
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Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5, end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Estematophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Enrhartoideae; Oryzaae; Oryza.

1 (bases 1 to 44)
Kim, Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S. I., Kim, Y. K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Yongin, KyeongGi, Korea
Yongin, KyeongGi, Korea
Far: 82 31 33 16 155
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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/mol type="mRNA"
/culTivar="Nackdong"

    .44
/organism="Oryza sativa (japonica cultivar-group)"

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1.3%; Score 36; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 36; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 43;
bhnahm@bio.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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100.0%; Pred. No. 1.7e+02;
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7 10:41:28 2006

Tue Nov

RESULT 46 CF331757/c

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DEFINITION

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

FEATURES

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CV729079 37 bp mRNA linear EST 05-NOV-2004 FLO--01-L18.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-L18, mRNA
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Xhof; cDNA was inserted into lamda Uni-ZAP XR vector at 5:
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoidae; Oryzeae; Oryza.

1 (bases 1 to 37)
Kim, Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="flower"
/lab_hosf="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with XhoI site."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yogin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 45;
                                                                                                                                                                   Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Conservative 0; Mismatches
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CV729079
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                                                                                                                                                                   CF331757 45 bp mRNA linear EST 18-AUG-2003 NACL--08-A04.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--08-A04, mRNA
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantes, Streptcophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade, Ehrhartoideae, Oryzae, Oryzae, Oryza, 1 (bases 1 to 45)
I (bases 1 to 45)
Song, S. I., Vim, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzae, Oryza,
(hases 1 to 45)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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FLO--09-101.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--09-101, mRNA
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100.0%; Pred. No. 1.8e+02;
Live 0; Mismatches 0; Indels
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Oryza sativa (japonica cultivar-group)
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CF331757.1 GI:33811741
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Best Local Similarity 100.0
Marches 36; Conservative
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RESULT 47 CV734230/c LOCUS DEFINITION

ò 쉱 ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

ACCESSION VERSION KEYWORDS SOURCE

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Gaps

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Gaps

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL COMMENT

FEATURES

AUTHORS

REFERENCE

CV730711/c DEFINITION

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Oryza sativa (japonica cultivar-group)

ISM Oryza sativa (japonica cultivar-group)

Eukaryota, (lindiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota, Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryzea

(lobase 1 to 38)

Skim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 bp mRNA linear EST 15-AUG-2003
HD--04-A04.gl OsHDAC1-overexpressing transgenic rice plasmid CDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--04-A04, mRNA sequence.
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Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
                     Contact: Nahm B.H.
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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                    'organism="Oryza sativa (japonica cultivar-group)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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CF315184/c
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Fax: 82 31 321 6555
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Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with XhoI site."
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FLO--04-G10.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--04-G10, mRNA
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                              2707 CTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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SOURCE

REFERENCE AUTHORS

TITLE

ACCESSION VERSION KEYWORDS

CV734007/c DEFINITION

RESULT 50

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RESULT 52 CV727074/c LOCUS DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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E 1 (bases 1 to 38)

S Kim, J. S., Jun, K.M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,

Kim, J. S., Jun, K.M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,

Long, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H.

Large-scale Sequencing Analysis of Rice ESTs

Longublished (2003)

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  Oryza sativa (japonica cultivar-group)
bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridolplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 39)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
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/organism="Oryza sativa (japonica cultivar-group)"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Best Local Similarity 97.31
Matches 36; Conservative
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Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 38)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,S.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yogin, KyeongJi, Korea
Tel: 82 31 330 6193
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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                   Query Match 1.3%; Score 35.4; DB 1; Length 38; Best Local Similarity 97.3%; Pred. No. 1.8e+02; Matches 36; Conservative 0; Mismatches 1; Indels
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/clone="14Salt--05-A17"
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CV727074.1 GI:55414698
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Matches 36; Conserv
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TITLE JOURNAL COMMENT

AUTHORS REFERENCE

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ACCESSION VERSION KEYWORDS SOURCE

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Gaps

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/mol_type="mRNA"
/cultivar="Nackdong"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
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                                      GI:33673598
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Matches 36; Conserv
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7LEAF--06-N13.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--06-N13, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                           CV732133 39 bp mRNA linear EST 05-NOV-2004 FLO--06-H15.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--06-H15, mRNA
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhatcoideae; Oryzeae; Oryza.

1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-Goale Sequencing Analysis of Rice ESTs
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/clone="RtD0-o6-HIS"
/tissue type="flower"
/lab_host="E.coli SOLR"
/lab_host="E.coli SOLR"
/clone lib=-Rtoe flower lambda phage cDNA library (FLO)"
/note="Vector PBlueserript SK(+); Site 1: EccRI; Site 2:
/hote--Vector at 5:
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of the properties and Bloinformatics, MyongJi University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@pio.myongji.ac.kr.

Location/Qualifiers
/db_xref="taxon:39947"
/clone="14ROOT--02-K03"
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/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: BcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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/mol_type="mRNA"
cultivar="Nackdong"
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                                                                                                                                                                                           1.3%; Score 35.4; DB 1; Length 39; 97.3%; Pred. No. 1.8e+02; tive 0; Mismatches 1; Indels
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41 bp mRNA linear EST 04-NOV-2004 [14Salt--02-D04.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--02-D04, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bloinformatics, MyongJi University
YongJi, KyeongGi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/clone="7LEAF--06-N13"
/clone="TLEAF--06-N13"
/dev stage="leaf"
/dev stage="r days after germination"
/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoR1; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                     Contact: Nahm B.H. Genemics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                     Lee, T.H., Shin, Y.C.,
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                                                                                                                                                           Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Le Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Targe-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
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CF302691
7LEAF--08-H12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--08-H12, mRNA
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                                                                                                                                                                                                                                                                                                     /db.xref="taxon:39947"
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/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division Genomics and Boinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 31 21 6555
Email: bhahm@pbio.com, bhnahm@bio.myongji.ac.kr.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Pred. No. 1.9e+02;
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/cultivar="Nackdong"
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1 Similarity 97.3%;
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CV725096/c
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae, BEP clade; Ehrhartoideae; Oryzae; Li (bases 1 to 41)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice BSTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/db_xref="taxon:39947"
/clone="145alt--02-D04"
/tissue_type="leaf"
/tab_host="E.coli_SOLR"
/clone=lib="Salt treated rice leaf lambda phage cDNA
library (145alt)"
/note="Wector: pBluescript SK(+); Site 1: EcoRI; Site 2:
Xhof; Leaf was incubated at 4 C(36ouM/m-2sec-1) for 2hrs.
CDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
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FLO--06-G18.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--06-G18, mRNA
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    Location/Qualifiers
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Best Local Similarity
Matches 36; Conserv
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

JOURNAL COMMENT

TITLE

FEATURES

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AUTHORS REFERENCE

DEFINITION RESULT 58 CV732097/c

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Query Match
Best Local Similarity
Matches 36; Conserv
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Best Local Similarity
Matches 36; Conserv
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Taeniopygia guttata

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Ratchosauria; Avea

Restrildinae; Taeniopygia.

Butchosauria; Avea

Restrildinae; Taeniopygia.

Buda,K., Howard,J.T., McConnell,P., Lints,T., Rivas,M.V.,

Whitney,O., Horite,H., Patterson,M.A., White,S., Zhao,S.,

Sakaguchi,H., Hagiwara,M., Shiraki,T., Hirozane-Kishikawa,T.,

Skene,P., Hayashizaki,Y., Carninci,P. and Jarvis,E.D.

A molecular neuroethological approach for identifying and

characterizing a melody of behaviorally regulated genes

L Unpublished (2005)

Other ESTs: 0050800422.x0 Bll

Contact: Kazuhiro Wada and Erich Jarvis

Erich D. Jarvis Lab

Duke University Medical Center - Department of Neurobiology

Box 3209 Bryan Research Building, Durham, NC 27710, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hre. cDNA was inserted into landa Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
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/dev stage="adult and juvenile"
/clone_lib=-library 58 - normalized (50 mix pooled
juveniles + adults) - male"
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Plate: 0058P0042 row: B column: 11
Tel: 82 31 310 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/organism="Taeniopygia guttata"
/mol_type="mRNA"
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LOCUS

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Tenniopygia guttata

Taeniopygia guttata

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Ave; Neognathae; Passeriformes; Estrildidae;

Estrildinae; Taeniopygia.

Nada, K., Howard, J.T., McConnell, P., Lints, T., Rivas, M.V.,

Whitney, O., Horita, H., Patterson, M.A., White, S., Zhao, S.,

Sakaguchi, H., Hadjwarara, M., Shiraki, T., Hirozanae-Kishikawa, T.,

Sakaguchi, H., Hadjwarara, M., Shiraki, T., Hirozanae-Kishikawa, T.,

Sakaguchi, H., Hadjwarara, W., Shiraki, T., Hirozane-Kishikawa, T.,

Sakaguchi, H., Hadjwarara, W., Shiraki, T., Hirozane-Kishikawa, T.,

Sakaguchi, H., Hadjwara, W., Shiraki, T., Hirozane-Kishikawa, T.,

Sakaguchi, H., Hadjwara, M., Shiraki, Y., Hirozane-Kishikawa, T.,

Sakaguchi, H., Padiwara, M., Shiraki, Y., Hirozane-Kishikawa, T.,

Sakaguchi, H., Padiwara, M., Shiraki, Y., Hada, M., Willia, M., Milain, M., Mi
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/dev stage="adult and juvenile"
/clone_lib="library $8 - normalized (50 mix pooled
juveniles + adults) - male"
/note="Organ: brain; Vector: pFLC-1; Site_1: EcoR1;
Site_2: BamHI; The library was constructed as described by
Carninci, P. (2003) in DNA Microarrays: A Molecular
Cloning Manual, eds. Bowtell, D. & Sambrook, J. (Cold
Spiring Harbor, NY), pp. 647-670.
TAG_TISSUE=whole brain
TAG_SEQ-tcgagctctacacaggtgacacactagaacca"
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0058P0042B11 5' library 58 - normalized (50 mix pooled juveniles + adults) - male Taeniopygia guttata cDNA clone 0058P0042B11 5' similar to prohibitin, mRNA sequence.
Carninci, P. (2003) in DNA Microarrays: A Molecular Cloning Manual, eds. Bowtell, D. & Sambrook, J. (Cold Spring Harbor, NY), pp. 647-670.
TAG_TISSUE=whole brain"
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/organism="Taeniopygia guttata"
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                                                                                                                                                                                                                                       1.3%;
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                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/dultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="BalSCBOREMO04H05"
/dev stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_l: Sfila; Site_l: Sfila; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CF334384

44 bp mRNA linear EST 18-AUG-2003

JMT--03-K14.b1 AtJMT-overexpressing transgenic rice plasmid cDNA

Library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bioinformatics, MyongJi University
YongJn, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli bH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee, T.H., Shin, Y.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 44)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lv.
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3%; Score 35.2; DB 1;
92.5%; Pred. No. 2e+02;
live 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35.2; DB 1;
Pred. No. 2e+02;
                                                                                                                                                                                                                  /organism="Vitis vinifera"
                                                                        Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: a.hamdi@bordeaux.inra.fr
Seq primer: 77.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--03-K14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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cDNA library (JMT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CF334384.1 GI:33817097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Conservative
                                                                                                                                                                                             .43
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Best Local Similarity
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Best Local Similarity
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                                                          France
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
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                                                                                                                                                                       FEATURES
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                                                CF298596
7LEAF--02-A24.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A24, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CN545689

43 bp mRNA linear EST 30-APR-2004
EST 17633 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL004405 3', mRNA sequence.
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                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Europhyta;
Clade; Ehrhartoideae; Oryzaae; Oryza,

1 (bases 1 to 44)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vitis vinifera
Mkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons;
rosids; Vitaceae, Vitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bloinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 313 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"

cultivar="NackGong"

db xref="racxcon:3994"

clone="7LEAF-02-A24"

/tissue_type="lasaf"

/dow_stage="7 days after germination"

/lab_host="E.coli DH10B"

/lab_host="E.coli DH10B"

/lab_host="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO's Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases lto.,)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa (japonica cultivar-group)"
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.3%; Score 35.4; DB 1; Length 44; 97.3%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                  CF298596.1 GI:33670357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CN545689.1 GI:46910314
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nes 36; Conserv
                                                                                                                      sequence.
CF298596
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                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
RESULT 63
CF298596/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                LOCUS
DEFINITION
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Matches
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JOURNAL
COMMENT
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KEYWORDS
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36

Matches

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RESULT 66

CF315871

ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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/note="Wector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF335633

JMT--05-G03.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--05-G03, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:19947"
/clone="JMT--03-G09"
/tissue_type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli D#10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Embryophyta; Tracheophyta;
                                                                                                                                                                                  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 33 0 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 35)
Xim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTB
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 35)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="txxxon:39947"
/cloine="JMT--05-G03"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2709 АВАВАВАВАВАВАВАВАВАВАВАВАВАВАВАВА 2743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.3%; Score 35; DB 1; Le
100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF335633.1 GI:33819628
                                                                                                                                                                     Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35;
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Matches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 68
CF335633/c
LOCUS
DEFINITION
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                                                                                                                   TITLE
JOURNAL
COMMENT
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AUTHORS
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JOURNAL
                                         REFERENCE
AUTHORS
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzea.

E 1 (bases 1 to 35)

S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Lonpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplanes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; BEP
                                                                                                                                                                                                                                                                   HD--04-P06.bl OsHDACI-overexpressing transgenic rice plasmid CDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--04-P06, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Wettor: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                    Gaps
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1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                    3; Indels
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                                                                                                 mRNA
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                    0; Mismatches
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/clone="HD--04-P06"
                                                                                                                                                                                                                                                 35 bp
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                                                                                                                                                                                                                                                                                                                                                  CF315871
CF315871.1 GI:33687632
                    37; Conservative
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DEFINITION

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Gaps

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CV725518
14Salt--02-K09.bl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-K09, mRNA sequence.
                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group)

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

Kim, J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Gontact: Nahm B.H.

Genemics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
        14Salt--02-II5.bl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--02-II5, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: ANOI; Leaf was incubated at 4 C(360uM/m-2sec-1) for Zhrs. CDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="t=axon:39947"
/clone="14Salt--02-115"
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library (14Salt)"
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/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhrahm@ggbio.com, bhrahm@bio.myongji.ac.kr.
Location/Qualifiers
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                                                                                                                         CV725444.1 GI:55413,068
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Tel: 82 31 330 6193
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                                                                                               CV725444
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CV725518/c
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae, Oryza.

(bases 1 to 35)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Xim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRN
was reverse transcribed and then used for PCR. mRNA was
pepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 333 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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// clone=lib="Salt treated rice leaf lambda phage cDNA
library (14salt)"
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1.8e+02;
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CV725312.1 GI:55412936
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Best Local Similarity 100.0
Matches 35; Conservative
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TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

LOCUS DEFINITION

CV725312/c

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

EST 04-NOV-2004

linear

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RESULT 70 CV725444/c LOCUS

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Gaps

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14Salt.-04-D02.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone L4Salt.-04-D02, mENA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiphantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhattoideae; Oryzeae; Oryza.

1 (bases 1 to 35)
Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-Gcale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Bukaryota, Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University Yorgin, Kyongqi, Kyongqi, Kyongqi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="leaf"
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100.0%; Pred. No. 1.8e+02;
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Mismatches
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/cultivar="Nackdong"
/db xref="taxon:39947"
/clone="14Salt--04-D02"
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Location/Qualifiers
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CV726506/c
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Milopsida; Poales; Poacea; BEP clade; Ehrhartoideae; Oryzae.

Lades Ehrhartoideae; Oryzae.

El (Bases I to 35)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Tel: 82 31 321 6355
Bmail: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 bp mRNA linear EST 04-NOV-2004 [14Salt--03-B16.bl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone [14Salt--03-B16, mRNA sequence.
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                                                                                                                                                                       /db_xref="taxon:39947"
/clone="148alt--02-K09"
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/dev_stage="14 days after gernimation"
/lab_host=== coli SOLR"
/clone_lib="salt treated rice leaf lambda phage cDNA
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/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
                                                                                           Organism="Oryza sativa (japonica cultivar-group)"
mol type="mRNA"
cultivar="Nackdong"
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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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|clone="148alt--03-B16"
|tissue_type="leaf"
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/cultivar="Nackdong"
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Best Local Similarity 100.
Matches 35; Conservative
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Best Local Similarity
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SOURCE ORGANISM

TITLE JOURNAL COMMENT

FEATURES

AUTHORS REFERENCE

LOCUS CV725797/c

ઠ 요 ACCESSION VERSION KEYWORDS ö

Gaps

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/lab host="E.coli SOLR"
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Best Local Similarity
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E 1 (bases 1 to 35)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahn,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                         /db xref="taxon:3944"
/clone="14Salt--05-A23"
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/tlssue type="leaf"
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/lab_host="E.col; SOLR"
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library (14Salt)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xho1; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
CDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantaa, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Nagnoliophyta, Liliopaida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Nahm B.H.
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yorgin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="14Salt--05-G17"
/tissue_type="leaf"
/dev_stage="14 days after gernimation"
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Matches 35; Conservative
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Oryza sativa (japonica cultivar-group)

Cryza sativa (japonica cultivar-group)

Eukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

Clade; Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 35)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-escale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bhnahm@ggblo.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CV728725 35 bp mRNA linear EST 05-NOV-2004 FLO--01-D10.bl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-D10, mRNA
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/cullivar="Nackdong"
/db.xref=taxcn:39947"
/clone="FLO-01-D10"
/tissue_type="flower"
/lab_host="B.coli SOLR"
/lab_host="B.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: BcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni_ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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/clone lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360um/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
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/organism="Oryza sativa (japonica cultivar-group)"

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Pred. No. 1.8e+02;
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CV730547/c
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Large-scale Sequencing Analysis of Rice ESTs
L Unpublished (2003)
Conteact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/clone="FLO--01-J11"
/tlssue_type="flower"
/lab host="E.oli Solm"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/clone_lib="Rice"
/clone_lib="Ric
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Oryza sativa (japonica cultivar-group)
Bukaryota, viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza
                                                       Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantas Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopaida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bloinformatics, MyongJi University
Yorgin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Xim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/cultivar="Nackdong"
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CV/30547
FLO--04-C08.gl Rice flower lambda phage cDNA library (FLO) Oryza astiva (japonica cultivar-group) cDNA clone FLO--04-C08, mRNA sequence.
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/lab host="E.coli Solk"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/clone incerrup Enluserzipt SK(+); Site_1: EcoRI; Site_2: Ahol; cDNA was inserted into lamda Uni-ZAP KR vector at 5' end with EcoRI and 3' end with XhoI site."
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Xhoī; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza
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Yongin, Kyeonggi, Korea
Yongin, Kyeonggi, Korea
Far: 82 31 332 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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    35
    Organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/culTivar="Nackdong"

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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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/organism="Nackdong"
/cultivar="Nackdong"
/cultivar="Nackdong"
/db xref="taxon:3947"
/clone="FLO--04-C08"
/tissue_type="flower"
/tissue_type="flower"
/lab host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
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                                                                            Oryza sativa (japonica cultivar-group)

Euryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptcophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; Lilioppida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae. Oryza.

(Dases 1 to 35)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza
                                                                                                                                                                                                                                                                                                                                                   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bloscience and Bioinformatics, MyongJi University
of Rioscience and Bioinformatics, MyongJi University
of Songli, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Kim, J.S., Jun, K.M., Cheong P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, Y.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/mol_type="mRNA"
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Location/Qualifiers
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.00.0%; Pred. No. 1.8e+0;
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                            CV730547.1 GI:55434844
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Best Local Similarity
Matches 35; Conserv
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Bukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaae; Oryza.

1 (bases 1 to 35)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
/db_xref="taxon:39947"
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site=1:
Khol; cDNA was inserted into lamda Uni-ZAP XR vector at send with EcoRI and 3' end with Xhol site."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongln, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/lab_host="E.coli SOLR"
/lab_host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with XhoI site."
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35 bp mRNA linear EST 05-NOV-20 FLO--07-M22.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-M22, mRNA
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FLO--08-B08.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--08-B08, mRNA
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/mol_type="mRNA"
/cultivar="Nackdong"
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Location/Qualifiers
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at 5, end with EcoRI and 3' end with Xhol site."
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Oryza sativa (japonica cultivar-group)
Cryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
                                                          Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Fax: 82 31 221 6355
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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|mol_type="mRNA"
|cultivar="Nackdong"

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/organism="Oryza sativa (japonica cultivar-group)"

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1.8e+02;
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100.0%; Pred. No. 1.8e
tive 0; Mismatches
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/clone="PLO--08-B08"
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/organism="Oryza sativa (japonica cultivar-group)"
/organism="Norkdong"
/ollivar="Nackdong"
/ollone="FLO--08-D14"
/lab weet="Record Flower"
/lab host="E.col; SOLR"
/lab host="E.col; SOLR"
/nore="Vector: pBluesript SK(+); Site_1: BcoRI; Site_2: XhoI; cDNA was inserted into lamda Unizarp Kreez: XhoI; cDNA was inserted into lamda Unizarp KR vector at 5' end with EcoRI and 3' end with XhoI site."
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LOCUS CV733739 35 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--08-M15.g1 Rice flower lambda phage cDNA library (FLO) Oryza
/mol_type="mRNA"
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/db_xref="taxckdong"
/db_xref="taxckdong"
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/lab_host="E.-Coli SOLR"
/clone=lib="Rice flower lambda phage cDNA library (FLO)"
/clone=lib-"Rice flower lambda phage cDNA library (FLO)"
/clone=lib-"Rice fl
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyra; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Tyonglu, Kyeongqi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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100.0%; Pred. No. 1.8e+02;
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100.0%; Pred. No. 1.8e+05
ative 0; Mismatches C
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Location/Qualifiers
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Query Match
Best Local Similarity
Matches 35; Conserval
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SOURCE
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/mol trype="maker"
/cultivar="Nackdong"
/db xref="taxon:39947"
/clone="Fic.or 180km15"
/lab host="Fic.or 180km"
/clone="lib="Rice flower"
/clone="Vector: pBluescript SK(+); Site 1: EcoR1; Site 2:
Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5; end with EcoR1 and 3' end with Xho1 site."
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Wagnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae, Oryza.

1 (bases 1 to 35)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP
Clade; Ehrhattoideae; Oryzeae; Oryza.

I (bases I to 35)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yoogin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Boinformatics, MyongJi University
Yorglin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ptio.com, bhnahm@btio.myongJi.ac.kr.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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1.8e+02;
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                                                            CV733739.1 GI:55440852
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                                                                                                                                                                                                                                                                                                            Contact: Nahm B.H.
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Best Local Similarity
Matches 35; Conserv
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mummalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Mus.

E. (Dasses I to 35)

E. (Dasses I to 35)

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

##112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ623128 35 bp DNA linear GSS 13-DEC-2000 1M0460D02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0460D02 R, genomic survey sequence.
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                                                                                 /db_xref="taxon:39947"
/clone="FLO--09-G11"
/tissue_type="FLO-:09-G11"
/lab_host="R.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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'organism="Oryza sativa (japonica cultivar-group)"
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                                                                                                                                                                                                                                                                                                                                                                           Length 35;
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                                                                                                                                                                                                                                                                                                                                                                       1.3%; Score 35; DB 1; Le
100.0%; Pred. No. 1.8e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .35
/organism="Mus musculus"
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/strain="C57BL/6J"
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Location/Qualifiers
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                      /mol_type="mRNA"
/cultivar="Nackdong"
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AZ623128.1 GI:11745318
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Fax: 801 585 7177
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ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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                                                                                                                                                                                                                                                                      chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0063C15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0063C15 R, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Dusse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0063 row: C column: 15
Seg primer: CACACAGGAAACAGCTATGACC
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/strain="C57BL/6J"
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/clone="UUGC2M0063C15"
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Location/Qualifiers
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Best Local Similarity 100.
Matches 35; Conservative
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Fax: 801 585 7177
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ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored to the completent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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ALS97891 BP Chicken Brain Library Gallus gallus cDNA clone
ROS064403, mRNA sequence.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiids, Lamiales, Plantaginaceae, Antirrhineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (Dases I to 36)
Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
Saedler,H. and Zachgo,S.
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
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/tissue type="whole plant"
/clone lib="Antirrhinum majus whole plant"
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Pred. No. 1.8e+02;
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Pred. No. 1.8e+02;
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MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:4151"
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100.0%; Pred. No. 1...
0; Mismatches
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Antirrhinum majus
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EST.
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Best Local Similarity 100.0
Matches 35; Conservative
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Best Local Similarity
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AL587891/c
LOCUS
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AJ791385/c
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Oryza sativa (japonica cultivar-group)
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Best Local Similarity 100.
Matches 35; Conservative
                                                                                                                                                                                                                                                                                       mRNA sequence.
CF279874
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LOCUS
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CF279874/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="BP Chicken Brain Library"
/clone lib="BP Chicken Brain Library"
/note="Wetcor: pSPORT1; Site 1: Not1; Site 2: Sal1; Cloned undirectionally. Primer: Olfgo dr. 5' adaptor sequence: 5' TCGACCTCGAG 3'; 3' adaptor sequence: 5' GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
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Schistosoma mansoni
Schistosoma mansoni
Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 36)
Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S.,
Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C.
Mucroarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 36)
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AM046410 Schistosoma mansoni lung schistosomulum Schistosoma mansoni coma senistosomu cone SmlC13d11.q1k, mRNA sequence.
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Pred. No. 1.8e+02;
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/mol_type="mRNA"
/mol_tref="taxon:6183"
/clone="Sml013d11.q1k"
/dev_stage="lung schistosomulum"
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                                                                                                                                                                                                                                                                                                                                                    /organism="Callus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS064H03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trust Sanger Institute CB10 1SA, UNITED KINGDOM. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clonetech (*6854-1)"
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .36
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Pathogen Microarrays Group
                                                                                            Murray, F.
BP Chicken Brain Library
Gallus gallus (chicken)
Gallus gallus
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                                                                                                                                                  Contact: Frazer Murray
                                                                                                                                 Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                     Seq primer: M13F
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Matches 35; Conserv
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36 bp mRNA linear EST 15-AUG-2003
HD--06-J02.gl OsHDACl-overexpressing transgenic rice plaemid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--06-J02, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clada; Enthartoidaes, Oryzeae; Oryza.

1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Songs,S.L., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                           CF279874 linear EST 14-AUG-20. 14ETL--06-F10.b1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--06-F10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/lab host="B.coli DH10B"
/clone lib="Rice etiolated leaf plasmid cDNA library
[418TL]"
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/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"
                                                                                                                                             Gaps
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/mol type="mRNA"
/cultivar="Nackdong"
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                                                                                              1.8e+02;
0; Indels
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                                                                                     Length 36;
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Location/Qualifiers
                                                                                                                                                                                            2709 ААААААААААААААААААААААААААААААААА
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                                                                                     DB 1;
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1.3%; Score 35; DB
Best Local Similarity 100.0%; Pred. No. 1.8
Matches 35; Conservative 0; Mismatches
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'cultivar="Nackdong"
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Matches 35;
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CF333863/c
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Espermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae.

Es (Wassen to 36)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongGi, Korea

Tel: 82 31 320 6193

Email: bhaahm@gGbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
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clone lib="OsHDACI-overexpressing transgenic rice plasmid
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR: mRNA was derived from rice Histone Deacetylase overexpression line."
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    Location/Qualifiers
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CF331913/c
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzeae; Oryza
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/lab_nost="E.coli DH108"
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 31 21 655
Exar: 82 31 321 655
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF311983 36 bp mRNA linear EST 18-AUG-NACL--08-F01.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--08-F01, mRNA
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100.0%; Pred. No. 1.8e+02;
ative 0; Mismatches 0;
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Gaps

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Length 36;

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL

COMMENT

FEATURES

AUTHORS

REFERENCE

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CV724782
145alt--01-I19.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--01-I19, mRNA sequence.
                                                                                                                                                                  /organism="Homo sapiens"
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
/average insert size 1.1 kb. Library constructed by Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
Genomics and Bioinformatics, MyongJi University
YongJn, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/clone_lib="Solt treated rice leaf lambda phage cDNA
library (14Salt)"
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/mol type="mRNA"
/cultivar="Nackdong"
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Location/Qualifiers
        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9667 row: f column: 16
High quality sequence stop: 36.
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|clone="14Salt--01-119"
|tissue_type="leaf"
                                                                                                                       Location/Qualifiers
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E 1 (bases 1 to 36)

S NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Nammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Ggapbs remail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The TH. M. AG. E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza,
I (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Rim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bloinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggblo.com, bhnahm@bio.myongji.ac.kr.
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/dev stage="14 days after germination"
/lab_nost="E.coli DH10B"
/clone lib="AtUMT-overexpressing transgenic rice plasmid
cDNa library (JMT)"
JMT--02-022.b1 AtJWT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--02-022, mRNA sequence.
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="JMT--02-022"
                                                                                                              CF333863.1 GI:33816032
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Homo sapiens
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/db_xref="taxon:39947"
/dlone="148alt--02-M04"
/tissue_type="laaf"
/dev stage="14 days after gernimation"
/lab_host="E.coli SOLR"
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/cultivar="Nackdong"
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CV725592/c
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Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

El (bases 1 to 36)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

S Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTS

L. Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Fax: 82 31 331 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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| Organism="Uncation/Qualifiers" | Location/Qualifiers |
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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36 bp mRNA linear EST 04-NOV-2004 [14Salt.-02-M04.gl Salt treated rice leaf lambda phage cDNA library [14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 11Salt.-02-M04, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University
Yongji, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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|cloin=="146alt--02-E21"
|cloin=="146alt--02-E21"
|dev_stage="14 days after gernimation"
|deb_host="15 Solk"
|cloin=_lib==Salt treated rice leaf lambda phage cDNA
|ibrary (145alt)"
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/mol_type="mRNA"
/cultivar="Nackdong"
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Genomics and Genetics Institute, GreenGene Biotech Ir
of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6433
Fax: 82 31 321 6355
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Location/Qualifiers
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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
          14Salt--03-008, mRNA sequence.
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Best Local Similarity
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantas, Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnollophyta; Liliopsida; Poales; Poaceae; BEP
clade; Enthartoideae; Oryzeae; Oryza
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DEFINITION 14Salt.-03-008.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
                                                            /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/\overline{m}-2sec-1) for 2\overline{h}rs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
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/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
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/clone_lib="Salt_treated rice leaf lambda phage cDNA
library (14Salt)"
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/ tissue_type="leaf"
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Location/Qualifiers
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ilarity 100.0%; Pred. No. 1.8e+02;
Conservative 0; Mismatches 0;
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1.3*; Score 35; DB 1; Le
Best Local Similarity 100.0*; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0;
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Matches 35; Conserv
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CV726321/c
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/lone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xhol; Leaf was incubaced at 4 C(360uM/m-2sec-1) for 2hrs.
CDNA was inserted into lamda Uni-ZAP KR vector at 5, end
with EcoRI and 3' end with Xhol site."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhattoideae; Oryzaa.

1 (baess 1 to 36)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.T., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yogin, KyeongJi, Korea
Tel: 82 31 330 6193
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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/cultivar="Nackdong"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
CV726321.1 GI:55413945
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CV727111.1 GI:55414735
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bloinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SK(+); Site_1: EcoR1; Site_2: Xhol; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hre. CDNA was inserted into landa Uni-ZAP XR vector at 5' end with EcoR1 and 3' end with Xhol site."
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/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at end with EcoRI and 3' end with Xhol site."
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/dev stage="14 days after gernimation"
/lab.host="scol! SOLR"
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library (14Salt)"
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Organism="Oryza sativa (japonica cultivar-group)"
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iive 0; Mismatches 0;
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/cultivar="Nackdong"
.ocation/Qualifiers
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CV728870 36 bp mRNA linear EST 05-NOV-2004 FLO--01-G18.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-G18, mRNA
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhattoideae; Oryzae,
1 (bases I to 36)
Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTE
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//clone_lib="Rice flower lambda pkage cDNA library (FLO)"
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Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at 5
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bioinformatics, MyongJi University
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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
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FEATURES

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Xho!; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
                                                                                                              CV730921 36 bp mRNA linear EST 05-NOV-2004 FLO--04-L09.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--04-L09, mRNA
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida; Poales, Poaceae; BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJu, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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1 (Dases 1 to 36)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
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Pred. No. 1.8e+02;
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      36 ААААААААААААААААААААААААААААА
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                                                                                                                                                                                                                               CV730921.1 GI:55435583
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                                                                       RESULT 110
                                                                                            CV730921/c
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                                                                                                       Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae.
El (bases 1 to 36)
SKim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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S6 bp mRNA linear EST 05-NOV-20 FLO--03-K22.bl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--03-K22, mRNA
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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1.8e+02;
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Pred. No.
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Best Local Similarity
Matches 35; Conserv
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Best Local Similarity
Matches 35; Conserv
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EST.

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL COMMENT

FEATURES

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REFERENCE AUTHORS

CV730235/c LOCUS DEFINITION

RESULT 109

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FEATURES

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CV732659
36 bp mRNA linear EST 05-NOV-2004 FLO--07-D18.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-D18, mRNA
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FLO--08-J07.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-J07, mRNA
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/clone_lib="Rice flower lambda bluel" construction in the construc
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Wagnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoidae; Oryzeae; Oryzaa.

I (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTE
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Yongin, KyeongJi, Korea
Tel: 82 31 33 0 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Large-scale Sequencing Analysis of Rice ESTB
Uppublished (2003)
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/mol type="mRNA"
/cultivar="Nackdong"
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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/tlssue_type="flower"
/lab host="E.coli SoLR"
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/clone_ctor: pBluescript SK(+); Site_l: EcoRI; Site_2:
/hote="Wector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/hol; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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/hol; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryzeae; Oryzea,
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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FLO--07-B22.g1 Rice flower lambda phage cDNA library (FLO) Ory Bativa (japonica cultivar-group) cDNA clone FLO--07-B22, mRNA
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/mol_type="mRNA"
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   of Bioscience and Bioinformatics, MyongJi University
Yongln, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6555
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Pred. No. 1.8e+02;
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Location/Qualifiers
                                                                                                                                              Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
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/cultivar="Nackdong"
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CV732578.1 GI:55438562
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Best Local Similarity 100.
Matches 35; Conservative
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EST

ACCESSION VERSION KEYWORDS

RESULT 112 CV732578/c DEFINITION

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AUTHORS REFERENCE

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/organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nackdong"
/cultivar="Nackdong"
/cultivar="13947"
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/lab host="E.col; SOLR"
/lone lib="Rice flower lambda phage cDNA library (FLO)"
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XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 36)
Kim, Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University Yongin, KyeongJi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, MyongJi University
Yogin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6195
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0; Indels
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CV734403.1 GI:55442165
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JOURNAL
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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated mare and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|473214|qb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Really, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Diamid inserts

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

L Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT 84112, USA

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT Bmail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00

Plate: 0285 row: E column: 23
Seq primer: CGTYGTAAAACGACGCCAGT

Class: plasmid ends
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                                                                                                                                                                                         AC4.V916 1000 16 bp DNA linear GSS 04-OCT-200 1M0285E23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0285E23 F, genomic survey sequence. AZ470916
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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    .36
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/mol_type="genomic DNA"
/strain="C57BL/6J"

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High quality sequence stop: 36.
Location/Qualifiers
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/clone="UUGC1M0285E23"
                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
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Best Local Similarity 100.0
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AZ470916/c
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adappored vector DNA, and transformed into
chemically-competent E. coli Xii0-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

E 1 (bases 1 to 36)

S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

L Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                        AZ628484 13-DEC-2000 1M0480B08R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0480B08 R, genomic survey sequence.
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/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G78L/6J (male) was obtained from the Jackson
2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0480 row: B column: 08
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 36.
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0480B08"
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with TA DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pmyo2 (gilly192/14/194)AP12072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. ooli XLL0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                 GSS 16-FEB-2001
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2M0046G15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0046G15 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus. 1 (Basea 1 to 36)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid innerts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse lokb plasmid UNGCN library"
/note="Vector: PWD47ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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1.3%; Score 35; DB 1; Le
100.0%; Pred. No. 1.8e+02;
trive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0046 row: G column: 15
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/mol_type="genomic DNA"
farrain="C57BL/67"
/db xref="taxon:10090"
/clone="UUGC2M0046G15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: 0046 row: G column: 15
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                          AZ793484.1 GI:12938483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
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Best Local Similarity 100.
Matches 35; Conservative
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Fax: 801 585 7177
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Query Match 1.3%; Score 35; DB 1; Length 36; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 35; Conservative 0; Mismatches 0; Indels

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RESULT 120
AZ957867/c
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//lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
//lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
//clone_lib="Mouse l0kb plasmid UUGCZM library"
//note="Wector: PWD4Znv; Purified genomic DNA from M.
musculus G57BL/6/ (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gil 4772114[gb]AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                         AZ949866 10kb plasmid UUGC2M linear GSS 27-APR-2001 2M0213H10R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0213H10 R, genomic survey sequence.
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Barchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinne, Mus
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Std Error: 0.00
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.C
Plate: 0213 row: H column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Location/Qualifiers
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Mus musculus (house mouse)
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/gex="Female"
//lab host="E. coli strain XL10-Gold, T1-resistant, F-"
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//clone_lib="Whouse lOkb plasmid UVGC2M library"
//note="Wector: PWD42nv; Purified genomic DNA from
musculus C57BL/6J (female) was obtained from the Jackson
Labozatory Mouse DNA Resource
(http://www.jax.org/resources/ocuments/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil fly12114|gb]AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mus musculus (house mouse)

Mus musculus (house mouse)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Sciurognathi; Butheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murcidea; Muridae; Muschae; Muschae;

Thasmall; Murcidea; Muridae; Muschae; Muschae;

Sciurognathi; Murcidea; Muridae; Muschae; Muschae; Peachsuser., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

University of Utah Genome Center
University of Utah Genome Center
University of Utah Genome Center
University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0224 row: G column: 19

Class: plannid ends

Class: plannid ends

Class: plannid ends
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1. .36
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
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Ouery Match 1.3%; Score 35; DB 1; Length 36; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 35; Conservative 0; Mismatches 0; Indels

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RESULT 121

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CZ914006

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Example a rape subsp. perinents a beta subsp. perinents a cosids; eurosids II, Brassicales; Brassicaceae; Brassica.

I (bases 1 to 36)

St Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.; Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J. H. and Park, B.S. and Sau3AI (KBrS) BAC clone (Drublished (2005) Contact: Beom-Seok Park Brassica arapa Sau3AI (KBrS) BAC clone (Drublished (2005) Contact: Beom-Seok Park (All Total) Suwon, 441-707, Korea (25 Seodun-Dong, Suwon, 441-707, Korea (25 Seodun-Dong
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Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Core endicotyledons;

Spermatophyta; Magnoliophyta; endicotyledons; core endicotyledons;

rosids; eurosids II; Brassicales; Brassicacea; Brassica.

Tosids; eurosids II; Rrassicales; Brassicacea; Brassica.

Nan, J. H. and Park, B.S.

End Sequence of Brassica rapa BamHI (KBrB) BAC clone

Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

Tel: +82-31-299-1670

Fax: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@rda.go.kr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. coli DH10B"
/clone lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBACI; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
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/organism="Brassica rapa subsp. pekinensis"
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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/db_xref="taxon:51351"
/clone="KBrS013L23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/cultivar="Chiifu"
                                pekinensis
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DX046307.1 GI:84740604
                                   Brassica rapa subsp.
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Class: BAC ends.
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Matches 35; Conserv
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/organism="Zea mays"
/mol type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="texon:4577"
/tisuue type="loaf"
/dev_stage="adult"
/dev_stage="adult"
/lab host="Dhata" 10af; Vector: RescueMu (engineered from plauescript backbone); Site 1: BamH1; Site 2: BglII;
RescueMu is a 4.9 kb, modifide maize Mu transposon plauescript backbone) plaemid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the Wab site 'http://www.mutransposon.org/project/RescueMu/. Grid O was grown at Stanford in 2001. DNA was extracted from leaf stripp, double digested using BamH1 and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DU834235 36 bp DNA linear GSS 22-DEC-2005 KBrS013L23F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS013L23, genomic survey sequence.
DU834235 GI:83870831
                                                                                                                                                                                                  CZ914006 36 bp DNA linear GSS 08-AUG-2005
4013055908.2EL x1 4013 - RescueMu Grid O Zea mays genomic, genomic
CZ914006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University Balo, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
1 (base 1 to 36)
Walbot,V.
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Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013005 row: B column: 08
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                                                                       36 ААААААААААААААААААААААААААААА
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Location/Qualifiers
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Best Local Similarity 100.
Matches 35; Conservative
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PEATURES

RESULT 122 DU834235/c

ઠે 셤 LOCUS DEFINITION

ACCESSION VERSION

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Gaps

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RESULT 125
CF291818/c
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/mol_t
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602301748F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4403554 5',
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I (bases I to 37)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Notional Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CLONA Library Preparation: Library Librar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="Indace:1403554"
/tissue_type="mammary adenocarcinoma, cell line"
/tasue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NHH MGC 87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
of Brassica rapa ssp. pekinensis BamHI BAC clone
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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100.0%; Pred. No. 1.8e+02;
Live 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.8e+02;
iive 0; Mismatches 0; Indels
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/mol_type="mRNA"
/db xref="taxon:9606"
                                                                                                                                                   Location/Qualifiers
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Homo sapiens
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Matches 35; Conservative
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BAC end sequence
KBrB047024
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                                                                              Seg primer: T7
Class: BAC end
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CF291818

14-AUG-2003
14ROOT--02-G14.b1 Rice root plasmid cDNA library (14ROOT) Oryza
Bativa (japonica cultivar-group) cDNA clone 14ROOT--02-G14, mRNA
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantaa, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliophyida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="root" / dev stage=""4 days after germination" /lab_host="E.coli DH10B" / clone lib="Rice root plasmid cDNA library (14ROOT)" / note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Location/Qualifiers
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                                                       1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35
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100.0%; Pred. No. 1.8e+02
iive 0; Mismatches 0
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2709 ААААААААААААААААААААААААААААА
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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-G14"
                                                                                                                                                                                                                                                                                                                     CF291818
CF291818.1 GI:33660851
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KEYWORDS
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Eukaryota; Viridiplantea; Strebtcoup)

Eukaryota; Viridiplantea; Streptcophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

Clade; Ehrbartoideae; Oryzae, Oryza.

(Dases I to 37)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Large-scale Sequencing Analysis of Rice ESTs
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Gonomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bio. Genetics and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 655
Email: bhnahm@bio.myongji.ac.kr.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      /tissue type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:39947"
/clone="7LEAF--04-K23"
/tissue_type="laga after germination"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO' Site 1: ECORI; mRNA was capped
with_oligoribonucleotides and then used as templates for
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mol type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                       'organism="Oryza sativa (japonica cultivar-group)"
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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/clone="7LEAF--04-D21"
                                                                                                                                                                                                                                                      /mol_type="mRNA"
/cultivar="Nackdong"
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Matches 35, Conservative
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      TITLE
JOURNAL
COMMENT
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JOURNAL
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KEYWORDS
SOURCE
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Oryza sativa (japonica cultivar-group)

Cryza sativa (japonica cultivar-group)

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryzea

I (bases 1 to 37)

SK Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6155

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                    CF301560
37 bp mRNA linear EST 15-AUG-2003
7LEAF--06-H14.gl Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-H14, mRNA
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7LEAF--06-003.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--06-003, mRNA
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
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/clone="7LERF-06-H14"
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/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and Then used as templates for
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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100.0%; Pred. No. 1.8e+02
tive 0; Mismatches (
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/cultivar="Nackdong"
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CF301560.1 GI:33673321
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   Query Match
Best Local Similarity 100.0
Matches 35; Conservative
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HD--05-E13.gl OsHDAC1-overexpressing transgenic rice plasmid CDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--05-E13, mRNA sequence.
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/dab host="E.coll DH10B"
/clone_lib="0sHDACI-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
/reated with ABA(10um) for lhr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantaa, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida; Poales, Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
         /clone_lib="ABF3-overexpressing transgenic rice plasmid delballary (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoR1; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bioinformatics, MyongJi University
Yongln, Worea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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                                                                                                                                                                                                 Length 37;
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Location/Qualifiers
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                                                                                                                                                                                                                                               0; Indels
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.8
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/cultivar="Nackdong"
/db_xref="taxon:39947"
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Matches 35; Conservative
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CF321294
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae.

Str. (bases) 1co 37)
SKim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song, S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
L Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
clade; Ehrhartoideae; Oryzeae; Oryzaa.

El (Dases I to 37)

S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University
Yonglin, KyeonggJi, Korea
Tel: 82 31 321 6155
Email: bhaahm@ggDio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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/db_xaref="taxon:3994"
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/lab_host="E.col] DH108"
/clone=lib="Rice leaf plasmid cDNA library II (7LEAF)"
/noce="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABF--01-116.bl ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--01-016, mRNA sequence. (F307971.1 G1:33679732
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/mol type="mRNA"
/cultivar="Nackdong"
/b xref="taxon:39947"
/clone="ABF--01-J16"
/fissue_type="lad"
/dev stagge="14 days after germination"
/lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                                                                                    1. .37
/organism="Oryza sativa (japonica cultivar-group)"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.3%; Score 35; DB 1; Le
100.0%; Pred. No. 1.8e+02;
ative 0; Mismatches 0;
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Best Local Similarity
Matches 35; Conserv
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                                                     AUTHORS
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Gaps

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EST 18-AUG-2003

linear

mRNA

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                    /mol_type="mRNA"
/mol_type="mRNA"
/db xref="taxon 39947"
/db xref="taxon 39947"
/clone="NACL-01-E08"
/tissue type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_nost="E_coli DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JMT--02-J14.bl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--02-J14, mRNA sequence.

    .37
/organism="Oryza sativa (japonica cultivar-group)"

                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3%; Score 35; DB 1; Length 3/;
100.0%; Pred. No. 1.8e+02; "
Tel: 82 31 330 6193
Fax: 82 31 321 6555
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 1.8
Matches 35; Conservative 0; Mismatches
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/cultivar="Nackdong"
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                                                                                                                                                    Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyra; Embryophyra; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.

El (bases 1 to 37)
Si Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
L Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/dav stage="proliferated callus on 2N6 media for 2 weeks"
/dab_nost="E.coli DH10B"
/clone lib="OsHDAC1-overexpressing transgenic rice plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF326975 37 bp mRNA linear EST 18-AUG-2003 NACL--01-E08.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-E08, mRNA
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Bukaryota, Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae, Oryzeae, Oryza.
1 (bases i to 37)
1 (klamatoideae, Oryzeae, Oryza.
2 (klamatoideae, Oryzeae, Oryza.
3 (klamatoideae, Oryzeae, Oryza.
4 (klamatoideae, Oryzeae, Oryza.
5 Song, S. I., Kim, J. K., Kim, Y. K., and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
HD--12-101.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--12-101, mRNA sequence. CF321294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
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mol type="mRNA"
cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
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'clone="HD--12-I01"
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CF326975/c
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Orgin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           |db_xref="taxon:39947"
| clone="NMT-02-314"
| tissue_type="leaf"
| dev_stage="14 days after germination"
| lab_hoste="E.coli DH108"
| clone lib="AtUMT-overexpressing transgenic rice plasmid
| colne lib=aty (JMT)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.3%; Score 35; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0;
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Conservative
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AUTHORS
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CV724637 CY724637 GI:55412261
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 37)
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(Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)

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YongJin, KyeongJi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
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/mol type="mRNA"
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/lab_host="E.cli blubs"
/clone lib="AtJMT-overexpressing transgenic rice plasmid
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Location/Qualifiers
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Enthartoideae; Oryzeae; Oryza.

E i (bases 1 to 37)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTS

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.cm, bhnahm@bio.myongji.ac.kr.
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14Salt.-03-D12.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt-03-D12, mRNA sequence.
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library (14Salt)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xhoi; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was incerted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
                                                                                                                           Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongln, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/mol type="mRNA"
/mol tyne="mRNA"
/cultivar="wackdong"
/db xarca:39947"
/clone="14Salt--01-F06"
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Location/Qualifiers
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Spermatophyta; Viifiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
I (bases 1 to 37)
Kim,J.S. Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                        /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhO1; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. CDNA was inserted into landa Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhOI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University Yoogju, Koreaa Tel: 82 31 330 6193 Fax: 82 31 321 6355
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/organism="Oryza sativa (japonica cultivar-group)"
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/oulTivar="Nackdong"
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library (145alt)"
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clone lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
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Pred. No. 1.8e+02;
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100.0%; Pred. No. 1.8e+02;
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Oryza sativa (japonica cultivar-group)

ISM Oryza sativa (japonica cultivar-group)

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryzae; Oryzae;

Exim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.F., and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

M. Unpublished (2003)

Contact: Nahm B.H.

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Tel: 82 31 330 6193

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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/organism="Oryza sativa (japonica cultivar-group)"
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library (148alt)"
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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1.8e+02;
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14Salt--04-E15, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                   CV726571.1 GI:55414195
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EST 04-NOV-2004

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Oryza sativa (japonica cultivar-group)

Swaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryz
                                                                                                                                                                                          v,z/>o,
14Salt--05-M08.gl Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
LySalt--05-M08, mRNA sequence.
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14Salt--06-C16.bl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone laysalt--06-C16, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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/dev stage="14 days after gernimation"
/lab_host="E.coli SOLR"
/lone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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      2709 АААААААААААААААААААААААААААААААААА
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                                         CV727567.1 GI:55415191
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Best Local Similarity
Matches 35; Conserv
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LOCUS
DEFINITION
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CV727567/c
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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JOURNAL
COMMENT
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library (14Salt)"
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XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
CDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14Salt--05-J14.g1 Salt treated rice leaf lambda phage CDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--05-J14, mRNA sequence.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division Genomics and Genetics Institute, GreenGene Biotech Inc.; Division Of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gDio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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   Location/Qualifiers
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CV727448.1 GI:55415072
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Best Local Similarity 100.C
Matches 35; Conservative
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Best Local Similarity 100.0
Matches 35; Conservative
                                   source
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CV727448/c
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SOURCE
ORGANISM
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FEATURES
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CV730003/c
LOCUS
DEFINITION
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CV728197/c
LOCUS
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SM Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

E 1 (bases 1 to 37)

S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song, S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Lunpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeongqi, Korea
Tal: 82 31 330 6353
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hre. CDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:39947"
/clone="146alt--06-C16"
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/lab.host="Salt treated rice leaf lambda phage cDNA
library (145alt)
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/tissue type="leaf"
/dev stage="14 days after gernimation"
/lab host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
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/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                             /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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    Location/Qualifiers
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CV728196/c
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Oryza sativa (japonica cultivar-group)

ISM Oryza sativa (japonica cultivar-group)

ENkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryzea; Oryzea; Oryzea; Oryzea; Stim,J.S., Jun,K.M., Z., Geong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.F.K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact. Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db xref="taxon:39947"
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/tlabue_rype="leaf"
/dev stage="14 days after gernimation"
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Xhof; Laf was incubated at 4 C(360uM/m-zsec-1) for 2hrs.
CDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
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CV728197.1 GI:55430493
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library (14Salt)"

//note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
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/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                            Length 37;
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.8e+02;
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                                                   Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Evkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza,
(bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim, Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                           Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggblo.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol type="mkNa"
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/db xeef="teaxon: 3947"
/clone="FLO-03-F09"
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/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with XhoI site."
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/organism="Oryza sativa (japonica cultivar-group)"
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    Location/Qualifiers
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                     CV730003.1 GI:55433779
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/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

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/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with Xhol site."
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaae; Oryza.

1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Rim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                            y (FLO)"
Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongln, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                            /tissue_type="flower"
/lab_host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at end with EcoRI and 3' end with XhoI site."
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FLO--05-110.b1 Rice flower lambda phage cDNA library (FLO) Oryza
Bativa (japonica cultivar-group) cDNA clone FLO--05-110, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                                                   100.0%; Prec. ...
                                                                                                                                                                                                                         Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="flower"
/lab_host="E.coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--05-110"
                    /db_xref="taxon:39947"
/clone="FLO--03-J09"
cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:55436672
                                                                                                                                                                                                                         1.3%;
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Matches 35; Conservative
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                                                                                                                                                                                                                         Query Match
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AZ321759
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CV731472/c
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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hattp://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp. (gil-4732114 [gb]-RA129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (Bases 1 to 37)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Miederhausern, A. and Wright, D., Weiss, R., Disamid inserts

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculs C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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Pred. No. 1.8e+02;
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1.3%; Score 35; DB
Best Local Similarity 100.0%; Pred. No. 1.8
Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 1272 row: E column: 23
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC1M0272E23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 37.
Location/Qualifiers
                                                                                         Mus musculus (house mouse)
                                 AZ463801.1 GI:10621926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: plasmid ends
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Fax: 801 585 7177
                                                                                                                           Mus musculus
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                                                                                                                                                                      /Glone="UUGCIMO042P22"
/Glone="UUGCIMO042P22"
/Glone="UUGCIMO042P22"
/Glone 11b="Mouse 10kb plasmid UUGCIM library"
/Clone 11b="Mouse 10kb plasmid UUGCIM library"
/Clone 12b="Mouse 10kb plasmid UUGCIM library"
/Clone="Vector: PWD47nv; Purified genomic DNA from M:
musculus G75BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|q132114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
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                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0042 row: P column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: 0042 row: P column: 22
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C578L/6J"
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Location/Qualifiers
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                                                                                            Mus musculus (house mouse)
AZ321759
AZ321759.1 GI:10374820
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Best Local Similarity 100.
Matches 35; Conservative
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Fax: 801 585 7177
Email: ddunn@genet
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AZ463801/c LOCUS DEFINITION

RESULT 150

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Length 37; 0; Indels 67

Page

ORGANISM

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ACCESSION VERSION KEYWORDS REFERENCE AUTHORS

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/ Collivar="mixed background W23/A188/B73/K55" |
/ (Collivar="mixed background W23/A188/B73/K55" |
/ (Collivar="mixed background W23/A188/B73/K55" |
/ (Lissue type="laaf" |
/ (Lisue t
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KBrB081A15F KBrB, Brassica rapa BamHI BAC library Brassica rapa seubsp. pekinensis genomic clone KBrB081A15, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                              Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
Contact: Walbot V
Contact: Walbot V
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 2227
Fax: 650 728 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013006 row: H column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Busaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases I to 37)
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Chol, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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100.0%; Pred. No. 1.8e+02;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Zea mays"
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                                    GI:71931035
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DX071328.1 GI:84765624
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Best Local Similarity 100.(
Matches 35; Conservative
                                                                                                                                                                                                                                                                                   (bases 1 to 37)
CZ914427
CZ914427.1
                                                                                                                                                                                                                                                                                                          Walbot, V.
                                                                                                          Zea mays
                                                                                                                                           Zea mays
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DX071328/c
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4013006H08.2EL_y1 4013 - RescueMu Grid O Zea mays genomic, genomic
survey sequence.
                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/clome_lib="Mouse 10kb plasmid UUGClM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                 1 (bases I to 37)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)
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121: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
.....h. 10000 Std Birg: 0.00
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Bate: 0.110 row: P column: 16
Seq primer: CACACAGAAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0110P16"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
                                                                                           Mus musculus (house mouse)
                             AZ831214.1 GI:13001122
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Best Local Similarity 100.0
Matches 35; Conservative
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RESULT 152 CZ914427/c LOCUS

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/db_xref="taxon:51351"
/clone="KBrB081A15"
/lab_host="E.coli DH108"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCuGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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KBrB082M17F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB082M17, genomic survey
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
I Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosida II; Brassicaeles; Brassicaceae; Brassica.
I (bases I to 37)
Yang T.J. Kwon, S.J. Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Hang T.J. Kwon, S.J. Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
End sequence of Brassica rapa Bamil (KBrB) BAC clone Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Bamil BAC clone
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Brassica Genomics Team
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Tel: +82-31-299-1670
Fax: +82-31-299-1672
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1. 37
/organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/culTivar="Chiffu"
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/organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/culcivar="Chiifu"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Danio.

1 (bases I to 37)

Humphray, S. J., Huckle, E. and Hunt, S. E. Direct Submission
Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
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Gypriniformes; Cyprinidae; Danio.

I (bases 1 to 37)

Humphray, S. J., Huckle, E. and Hunt, S.E.

Direct Submission

Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: hunguery@sanger.ac. uk Unpublished

This sequence was generated from the T7 end of BAC 102P24. 102P24

is part of the Daniokey BAC Library created by R. Plasterk and N.V.
             /lab host="E.coli DH10B"
/clome_lib="KBrB, Brassica rapa BamHI BAC library"
/clome_lib="KBrB, Brassica rapa BamHI; Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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Danio rerio genomic clone DKEY-102P24, genomic survey sequence.
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Danio rerio genomic clone DKEY-102P2, genomic survey sequence.
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Location/Qualifiers
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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1.3%; Score 35; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.8e+0
Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="DKBY-102P24"
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/db_xref="taxon:7955"
.one="KBrB082M17"
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Danio rerio
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Conservative
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nes 35; Conserv
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CF301164/c
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/mol type="mRNA"
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Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: 
Inqueryeasanger. ac.uk Unpublished 
This sequence was generated from the T7 end of BAC 102P2. 102P2 is 
part of the Daniokey BAC Library created by R. Plasterk and N.V.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

(bases 1 to 38)
(km,J.S., Oheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
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Location/Qualifiers
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nes 0;
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                                                                                                                                                                 /mol_type="genomic DNA"
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/clone="DKB+102P2"
/tissue type="Testis"
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                                                                                                                                                                                                                                                                                 DB 1;
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/organism="Danio rerio"
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Best Local Similarity
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les 35; Conserv
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CF291176/c
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryotta; (idiglalnate; Streptophyta; Embryophyta; Tracheophyta; Eukaryotta; Magnoliophyta; Liliopsida; Embryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza; Oryza; (brand, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-Grale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yonglin, Kyeonggi, Korea
Tel: 82 31 320 6193

Fax: 82 31 321 6195

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Cr301164 38 bp mRNA linear EST 15-AUG-2003 7LEAF--05-013.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-013, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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with oligoribonucleotides and then used as templates for
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/mol_type="mRNA"
/cultivar="Nackdong"
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FEATURES

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CF328351 18-AUG-2003 NACL--03-D10.gl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--03-D10, mRNA
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Clade; Ehrhartoidee; Oryzeae; Oryza.

I (bases 1 to 38)
Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
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cultivar="Nackdong"

/cultivar="Nackdong"

/db xref="taxon 39947"

/clone="NACL-03-D10"

/tissue_trype="callus"

/dev stagge="proliferated callus on 2N6 media for 30 days"

/lab_nost="E.coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 3330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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//note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for RT-PCR."
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   Pred. No. 1.9e+02;
Mismatches 0;
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Pred. No. 1.9e+02;
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100.0%; Pred. No. ...
0; Mismatches
Best Local Similarity 100.0%; Pred. No. 1.5
Matches 35; Conservative 0; Mismatches
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CF328351.1 GI:33804947
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//wolltype="mrnA"
//wolltype="mrnA"
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/dab host="E.Coll DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
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Oryza sativa (japonica cultivar-group)
Dryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 38)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HD--12-H08.bl OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--12-H08, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongli, KyeongJi, Korea
13130 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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1.9e+02;
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0; Mismatches
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/cultivar="Nackdong"
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cDNA_library (HD)"
          Korea
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      Yongin, Kyeonggi, Ko
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 35; Conservative
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LOCUS DEFINITION RESULT 160 CF321261/c

ò 셤 ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

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FEATURES

AUTHORS REFERENCE

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EST 18-AUG-2003

Query Match

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Homo sapiens (human)
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

El (base 1 to 38)
Sim, J.S., Jun, K.M., Cheong, P.J., Kim, J.V., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Lupublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 21 221 6355
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/db xref="taxon:39947"
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/tissue type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yeongji, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Rice callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."
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                                                                                                                                                                                                                         Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
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Location/Qualifiers
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with oligoribonucleotides and then used as templates for \mathtt{RT-PCR}."
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DB 1; Le
ch 1.3%; Score 35; DB 1 Similarity 100.0%; Pred. No. 1.9 35; Conservative 0; Mismatches
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2709 ААВАВАВАВАВАВАВАВАВАВАВАВАВАВАВАВ 2743

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EST 18-AUG-2003
(CL) Oryza
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                           NACL--05-C15.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-C15, mRNA
linear
mRNA
                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group)
38 bp
                                                                                                                                                               GI:33807676
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioliformatics, MyongJi University
Yorgin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gDjoio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nackdong"

db_xref="taxon:39947"

/clone="NACL--05-C15"

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/dav_bost="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOP0; Site_1: BCORI; mRNA was capped
with_oligoribonucleotides and then used as templates for

Gaps .. 0 Query Match 1.3%; Score 35; DB 1; Length 38; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 35; Conservative 0; Mismatches 0; Indels

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2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

38 bp mRNA linear EST 11-DEC-2000 60200592F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4212527 BF525501 Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, BF525501.1 GI:11612862

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Best Local Similarity
Matches 35; Conserv
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CV725198/c
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                                                                                                                                                                                                                                                                                                                                                                                                        /organisme"Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
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/clone="IMAGE:421252"
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Site_2: Sall; Cloned unidirectionally. Primer:—Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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BF526154 GI:11613430
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I (bases 1 to 38)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9733 row: g column: 24
High quality sequence stop: 38.
Location/Qualifiers
                    Hominidae; Homo.

1 (bases 1 to 38)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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100.0%; Pred. No. 1.9e+02;
:ive 0; Mismatches 0;
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les 35; Conservative
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CV/24657
14Salt--01-F18.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--01-F18, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 38)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm, B.H.
Iarge-scale Sequencing Analysis of Rice ESTs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 33 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
/tissue_type="glioblastoma with EGFR amplification"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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/mol type="mRNA"
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hes 0; Indels
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100.0%; Pred. No. 1.9e+02;
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EST 04-NOV-2004
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Cryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

(bases 1 to 38)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
14Salt--02-C15.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--02-C15, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 38)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K., and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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                                                                                                                                                                                                                                                                                                                                                                                            Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bioinformatics, MyongJi University
Yougin, KyeongJi, Korea
Tel: 82 31 330 6193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
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/lab_nost="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
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1.9e+02;
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14Salt--03-M16.bl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--03-M16, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridolplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                              /noterry virtual, /noterry SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360m/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
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//note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-2AP KR vector at 5' end with EcoRI and 3' end with XhoI site."
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                         db_xref="taxon:39947"
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/tissue_type="leaf"
/dev_stage="14 days after gernimation"
/lab_host="R_coli SOLR"
/clone_lib==Salt treated rice leaf lambda phage cDNA
library (14Salt)
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/cultivar="Nackdong"
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/tissue_type="leaf"
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/db host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
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                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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1.9e+02;
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100.0%; Pred. No. 1.9
live 0; Mismatches
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade, Ehrhartoideae; Oryzeae; Oryza,
I (basea: I to 38)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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YongJi, KyeongJi, Korea
YongJi, KyeongJi, Korea
Fax: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahn@ggbio.com, bhnahn@bio.myongji.ac.kr.
  Gaps
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/clone_lib="Salt treated rice leaf lambda phage cDNA
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/cultivar="Nackdong"
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Best Local Similarity 100.0
Warrhes 35; Conservative
  35, Conservative
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CV726534/c
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Oryza sativa (japonica cultivar-group)

(SM Oryza, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

(Sativar, Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

(Sativar, Sativar, Shan, 
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/lab_host="E.coli SOLR"
/lab_host="E.coli SOLR"
/lab_host="E.coli SOLR"
/lab_host="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(350hM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
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/cultivar="Nackdong"
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Location/Qualifiers
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(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Strepcphyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clada; Ehrhatcoideae; Oryzae; Oryza.

1 (bases 1 to 38)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.L., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xho1: Leaf was incubated at 4 C(360W/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
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/dev_stage=14 days after gernimation"
/lab_host="B.coli Solk"
/lab_host="B.coli Solk"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (145alt)
/note="Wector: pBluescript SK(+); Site 1: EcoRI, Site 2:
Xhol; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with Xhol site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongln, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                   2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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                                                                                                                                                                      Score 35; DB 1; Le
Pred. No. 1.9e+02;
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/cultivar="Nackdong"
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                                                                                                                                                                  Query Match
Best Local Similarity
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CV727096/c
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CV727478/c
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzea.

El (bases 1 to 38)
SKim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
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/mol_type="mRNA"
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/culTivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="1.coli SOLR"
/clone="11bi="Salt treated rice leaf lambda phage cDNA
/clone="libi="Salt treated rice leaf lambda phage rice"
/clone="libi="Salt treated rice" lambda phage 
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza,
1 (bases 1 to 38)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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CV727478
                                                                                                                              CV727478.1 GI:55415102
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SM Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Enthartoideae; Oryza.

El (bases 1 to 38)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Lupublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 bp mRNA linear EST 04-NOV-2004 (14Salt--06-F06.bl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--06-F06, mRNA sequence. CV727921 GI:55415545
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                                                                                                                                                                                                                                                               /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhOI; Leaf was incubated at 4 C(360uM/m-28ec-1) for Zhrs. CDNA was inserted into landa Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhOI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /molutype="mRNA"
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                                                                                                                /db_xrefe"taxon:39947"
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/lab.host="8.51"
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library (148alt)"
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                                                                                                                                                                                                                                                                                                                                                                   Length 38;
                                                                                                                                                                                                                                                                                                                                                                 1.3%; Score 35; DB 1; Length 38;
Larity 100.0%; Pred. No. 1.9e+02;
Conservative 0; Mismatches 0; Indels
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
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                                                                            /mol_type="mRNA"
/cultivar="Nackdong"
                   Location/Qualifiers
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les 35; Conserv
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Oryza sativa (japonica cultivar-group)

ENKaryca, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Enkarycata; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

EX Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTB

Unpublished (2003)

Contact: Nahm B.H.

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Tel: 82 31 330 6193

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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                            CV/ZB176
14Salt--06-L22.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--06-L22, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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/lab_host="E.coli SOLR"
/lab_nost="E.coli Kolk"
/tibre lib="Salt treated rice leaf lambda phage CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nackdong"
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2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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1.3%; Score 35; DB 1; L4
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0;
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/clone="14Salt--06-L22"
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CV728835/c
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CV729857/c
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Oryza sativa (japonica cultivar-group)

Bukaryota, viridiplantae; Strepophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae; Strepophyta; Embryophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

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I (bases 1 to 38)

Song, S. I., Kim, Y. K. and Nahm, B. H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B. H.

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@ggblo.com, bhnahm@bio.myongji.ac.kr.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H. Genemics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea and Bioinformatics, MyongJi University Fax: 82 31 320 6193
Fax: 82 31 321 6535
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
                                                                                                                                                                                                                                                                      1.38
// Organism="Oryza sativa (japonica cultivar-group)"
// organism="Oryza sativa (japonica cultivar-group)"
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// cultivar="mackdong"
// db xref="taxon:39947"
// clone="145alt--06-N02"
// tissue type="laf"
// dev stage="14 days after gernimation"
// lab_host="E.coli SOLR"
// clone=lib="Salt treated rice leaf lambda phage cDNA
library (145alt)"
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FLO--01-F07.g1 Rice flower lambda phage cDNA library (FLO) Oryza
Bativa (japonica cultivar-group) cDNA clone FLO--01-F07, mRNA
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/db_xref="taxon:39947"
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CV728835 38 bp mRNA linear EST 05-NOV-2004 FLO--01-F21.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-F21, mRNA
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
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/lab_host="E.coli SOLR"
/lab_host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xhoi; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yorgin, Kyeongqi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="mRAdong"
/db xref="taxon:39947"
/clone="FLO--01-F21"
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1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels
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Location/Qualifiers
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Oryza sativa (japonica cultivar-group)
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CV728835.1 GI:55431639
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Matches 35; Conserv
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DW337683/c
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BSP clade; Enhantoideae; Oryza.

E 1 (basea 1 to 38)
S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Oryza sativa (japonica cultívar-group)
Oryza sativa (japonica cultívar-group)
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

YongIn, KyeongJi, Korea
Pers: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongJi.ac.kr.
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/db_xref="reaxon:39947"
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/lab host="8.col; SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
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XhoI; cDNA was inserted into lamda ubi_ZAP XR vector at 5 end with EcoRI and 3' end with XhoI site."
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/mol_type="mRNA"
/cultivar="Nackdong"
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0; Indels
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/cultivar="Nackdong"
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CV731476.1 GI:55436680
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Best Local Similarity 100.8
Matches 35, Conservative
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Lorm Guingo Diloga

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgophyta; Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, W., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.

Espressed tag sequences from Ginkgo megasporophyll (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Fazen Genome Sequencing Center
Cold Spring Harbor Laboratory, VP DO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M31Univeev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Ginkgo megasporophyll (NYBG)"
hote="Organ: megasporophyll; Vector: pBK-CMV; Site_l:
Xhol; Site_2: Eco RI; Stratagene ZAP Express CDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DW337683 38 bp mRNA linear EST 06-JAN-2006 EST-AR18G8 Sus scrofa mixed tissue cDNA library Sus scrofa cDNA
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Sus acrofa
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DR064343
ip76h05.g1 Ginkgo megasporophyll (NYBG) Ginkgo biloba cDNA 3', mRNA
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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                                                                                                                                     1.3%; Score 35; DB 1; Length 38; 100.0%; Pred. No. 1.9e+02; ative 0; Mismatches 0; Indels
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Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                   1.3%; Scc. No. 1.00.0%; Pred. No. 1.00.0%; Pred. No. 1.00.0%; Mismatches
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/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ginkgo biloba (maidenhair tree)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DR064343.1 GI:66987911
                                                                                                                                                              Watches 35; Conservative
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Fmail: wrink@govmail.state.nv.us

Tissues and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of Staphylococcus
implant-associated infection using 1000 cfu of Staphylococcus
aureus in a tibial transection, reduced and internally fixed with a
dynamic compression plate. NOTE: The sequences contain a 'CDNA
adapter' between the EcoRI site and the start of the EST. The
adapter' between the EcoRI site and the start of the EST. The
Location/Qualifiers
1. 38
/organism="Sus scrofa"
/mol_type="mmNA"
/mol_type="mmNA"
/gtrain="crossbreed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /close_15b="Sus scrofa mixed tissue cDNA library"
/note="Vector: pBSK; Site_1: Eco RI; Site_2: XhoI; Tissues
and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of
Staphylococcus aureus in a tibial transection, reduced and
internally fixed with a dynamic compression plate. NOTE:
The sequences contain a 'CDNA adapter' between the EcoRI
site and the start of the EST. The adapter sequence is
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2M002B106R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0028106 R, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
(bases 1 to 38)
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Rink, A., Santschi, E.M. and Beattie, C.W.
Normalized cDNA libraries from a porcine model of orthopedic implant-associated infection
Mamm. Genome 13 (4), 198-205 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:9823"
/clone="AR18G8"
/tissue_type="mixed"
/cell_type="mixed"
/dev stage="control, 5 month old castrated male"
/lab_host="SOLR"
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                                                                                                                                                                      Contact: Rink, A
Animal Disease and Food Safety Laboratory
Nevada Department of Agriculture
350 Capitol Hill Avenue, Reno, NV 89502, USA
TTE: 775-688-1180 Ext. 232
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live 0; Mismatches
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Best Local Similarity
Matches 35; Conserv
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LOCUS
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PUBMED
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                                         AUTHORS
TITLE
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="WetCor: PWD42ruy; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|APL29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
putified. The sheared, adaptored mouse DNA was annealed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 39)

Nath-MOC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                        Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Parrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC2M0028106"
                                                                                                                                                                                                                                                            High quality sequence stop: 38.
                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
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University of Utah
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        308, L.
USA
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DEFINITION
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BG287495
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KEYWORDS
SOURCE
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CF302356.1 GI:33674117
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              Query Match
Best Local Similarity 100.
Matches 35; Conservative
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Best Local Similarity
Matches 35; Conserv
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ORGANISM
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CF302356/c
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                                                                                                                                                                                                                                                                                                                                 RESULT 189
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AUTHORS
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603342221F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5369956 5',
BI694035
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/clone="IMAGE:5369956"
/clone="type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="PH108"
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/clone_lib="NCI_CGAP_Mam2"
/clone_lib="NCI_CGAP_Mam2"
/cloned_unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mamalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Hitp://image.llnl.gov
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM10400 row: i column: 02 High quality sequence stop: 36.
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NIH-MC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/organism="Homo sapiens"
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/strain="FVB/N-3"
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/organism="Oryza sativa (japonica cultivar-group)"

mol type="mRNA"

(ultivar=wackdong"

/ultivar=wackn:3947"

/ulsue_type="leaf"

/dev stage="7 days after germination"

/lab_host="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoR1; mRNA was capped

with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                     CF298508 19-by mRNA linear EST 15-AUG-2003 7LEAF--01-019.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-019, mRNA
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TLEAF--07-M16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-M16, mRNA
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                  Gaps
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             Length 39;
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    Location/Qualifiers
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100.0%; Pred. No. 1.9e+02;
                                         1.9e+02
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CF321323

HD--12-117.bl OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone PD--12-117, mRNA sequence.

CF321323
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza

1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Xim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Nahm B.H.
Contact: Nahm B.H.
Genomics and Generics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Yengin, Kyeonggi, Korea
Fax: 82 31 32 16355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                            /note="Vector: pCR4-TOPO, Site_1: EcoRI, Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
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    .39
    Organism="Oryza sativa (japonica cultivar-group)" /mol type="mRNA" /cultivar="Nackdong" /cultivar="Nackdong"

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iive 0; Mismatches 0;
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/clone="HD--12-I17"
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          CDNA library (HD) "
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CF330732/c
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/mol type="mRNA"
/cultivar="NacKong"
/db xref="taxon:39947"
/clone="HD-04-M06"
/clone="HD-04-M06"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_nost="E.coli DH108"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryzae; Dun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                      /db.xref="t_axon:39947"

/clone="TLEAF--07-M16"

/tissue_type="lags after germination"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lb="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonuclectides and Then used as templates for
                                                                                                                 Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeongqi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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19 bp mRNA linear EST 15-AUG-200
HD--04-M06,bl OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--04-M06, mRNA sequence.
CF315736

CF315736.1 GI:33687497
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division Genomics and Genetics Institute, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongJi.ac.kr.
Location/Qualifiers
1 (bases 1 to 39)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/mol_type="mRNA"
/cultivar="Nackdong"
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100.0%; Pred. No. 1.9e+02;
iive 0; Mismatches 0;
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High quality sequence stop: 39.
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Best Local Similarity
Matches 35; Conserv
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BE891613
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                                                                                                   Oryza sativa (japonica cultivar-group)

SM Oryza sativa (japonica cultivar-group)

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryzae; Oryza.

E 1 (bases 1 to 39)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTS

Lonpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6355
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/db xref="taxon:33947"
/clone="NACL--06-J06"
/tissue trype="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_nost="R.coli DH10B"
/clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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1 (bases 1 to 39)

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurent: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF032623 39 bp mRNA linear EST 20-OCT-20
601453114F1 NIH_MGC_66 Homo sapiens CDNA clone IMAGE:3857019 5',
    sativa (japonica cultivar-group) cDNA clone NACL--06-J06, mRNA
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100.0%; Pred. No. 1.9e+02;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/cultivar="Nackdong"
                                                                  CF330732.1 GI:33809685
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Homo sapiens
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Best Local Similarity 100.
Matches 35; Conservative
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39 bp mRNA linear EST 20-OCT-2000 601434505F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919584 5', BEE91613
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                                                              /clone="IMAGE:3857019"
/tissue_type="adenocarcinoma"
/tish host="DH10B (phage-resistant)"
/clone_lib="NHH_MGC_66"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 72"
/note="Corgan: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Ollgo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC/DCTD/DTP
Tissue Procurement: ATC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9749 row: j column: 01
High quality sequence stop: 39.
High quality sequence stop: 39.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 39)

NIH-MG http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 1.9e+02;
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Best Local Similarity 100.0%; Pred. No. 1.>
Matches 35; Conservative 0; Mismatches
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/clone="IMAGE:3919584"
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Homo sapiens
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.
El (bases 1 to 39)
S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
L Dhpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                 CV724457

14Salt--01-A17.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--01-A17, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Wettor: pBluescript SK(+); Site 1: EcoR1; Site 2: XhoI; Leaf was incubated at 4 C(360uM/\overline{m}-2sec-1) for 2\overline{h}re, cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoR1 and 3' end with XhoI site."
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/organism="Oryza sativa (japonica cultivar-group)"
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Hel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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hes 0; Indels
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CV724457.1 GI:55412081
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CV724623.1 GI:55412247
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Best Local Similarity 100.
Matches 35; Conservative
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CV724623/c
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39 bp mRNA linear EST 04-NOV-2004
14Salt--02-C12.gl Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-C12, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2frs. CDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
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sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division Genomics and Genetics Institute, GreenGene Biotech Inc.; Division Yongin, Kleenece and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Exar: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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library (148alt)"
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/lab_host="E-Coli SOLR"
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                                                                                                                                                                                                                            /organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
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Pred. No. 1.9e+02;
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100.0%; Pred. No. ...
0; Mismatches
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Location/Qualifiers
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84

Query Match

Matches

ò g ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION CV725228/c

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Oryza sativa (japonica cultivar-group)

Eukaryota, diaponica cultivar-group)

Eukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatcphyta; Magnoliophyta; Embryophyta; Engertophyta; Engles, Embryophyta; Magnoliophyta; Liliopsida; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Cadeo; Sin, K.M., J.K., Kim, Y.-K. and Nahm, B.H.

Large-Gracia Saquencing Analysis of Rice ESTS

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

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Fax: 82 31 321 6355

Location/Qualifiers
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Contact: Nahm B.H.

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Fax: 82 31 3121 6355
Exax: 82 31 321 6355
Email: bhnahm@gdpio.com, bhnahm@bjo.myongji.ac.kr.
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/lab_host="s.coli SOLR"
/clone_libe="Salt_treated rice leaf lambda phage cDNA
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CV725570.1 GI:55413194
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhatcoideae; Oryzeae; Oryza.

(bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yonglin, Wasonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/lab.host="E.coli SOLR"
/lab.host="E.days after gernimation"
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/mol_type="mRNA"
/cultivar="Nackdong"
        cDNA was inserted into lamda Uni-ZAP XR vector with EcoRI and 3' end with XhoI site."
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                                                                                       y Match 1.3%; Score 35; DB 1; Length 39; Local Similarity 100.0%; Pred. No. 1.9e+02; nes 35; Conservative 0; Mismatches 0; Indels
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Location/Qualifiers
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AUTHORS

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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhatcoideae; Oryzea; Oryza.

(bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Boinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:39947"
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/dev stage="leaf"
/dev stage="leaf"
/dev stage="leaf"
/lab_host="E.coli SOLR"
/clone lib="Salt treated rice leaf lambda phage cDNA
library (148alt)"
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0;
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Oryza sativa (japonica cultivar-group)

Cryza sativa (japonica cultivar-group)

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatcphyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryzeae; Oryzea

l (bases 1 to 39)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-escale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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EST 04-NOV-2004
            14Salt--03-H22.bl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--03-H22, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantaa, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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/clone="14Salt--03-H22"
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/dev_stage="14 days after gernimation"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
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/mol_type="mRNA"
/cultivar="Nackdong"
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100.0%; Pred. No. 1.9e+02;
vative 0; Mismatches 0;
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                                                                                           Conservative
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SM Oryza sativa (japonica cultivar-group)

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

E 1 (bases 1 to 39)

SKim,J.S., Jun,K.M., Cheong, J.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

L. Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/clone lib="Salt treated rice leaf lambda phage cDNA
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/lab_bost="8.coli SOLR"
/clone_lib==Salt treated rice leaf lambda phage cDNA
library (14Salt)
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/mol_type="mRNA"
/cultivar="Nackdong"
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Location/Qualifiers
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/clone="14Salt--03-011"
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CV726361.1 GI:55413985
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14Salt--04-L17.bl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--04-L17, mRNA sequence.
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14Salt--04-I09.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--04-I09, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Enrhartoideae; Oryzeae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice BSTs
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Yongin, Kyeonggi, Korea
Yel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/lab_host="E.coli SOLR"
/clone lib="Salt treated rice leaf lambda phage cDNA
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/mol type="mRNA"
/cultivar="Nackdong"
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0;
  1.3%; Score 35; DB 1; Le
100.0%; Pred. No. 1.9e+02;
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantaa, Streptophyta, Embryophyta, Tracheophyta,
Spermarophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza
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Oryza sativa (japonica cultivar-group)
bukaryota, Viridiplantea; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida, Poales; Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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/clone="14Salt--04-L17"
/tissue type="leaf"
/dev_stage="14 days after gernimation"
/lab host="E.coli SOLR"
/clone lib="Salt treated rice leaf lambda phage cDNA
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|mol_type="mRNA"
|cultivar="Nackdong"
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0; Indels
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CV726936.1 GI:55414560
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/tissue_type="leaf"
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library (14Salt)"
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/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
/note="Vector into lamda Uni-ZAP XR vector at 5: end
with EcoRI and 3' end with XhoI site."
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14Salt--04-O07.gl Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--04-O07, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                              /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhOI; Leaf was incubated at 4 C(360uM/m-2sec-1) for Zhrs. CDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhOI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee, T.H., Shin, Y.C.,
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                                                                                                            /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
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Location/Qualifiers
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/clone="14Salt--04-N10"
/tissuc_type="lasf"
/dev stage="14 days after gernimation"
/lab_host="E.coli SOLR"
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Erge-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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100.0%; Pred. No. 1.9e+02;
ive 0; Mismatches 0;
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Pred. No. 1.9e+02;
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.

E 1 (bases 1 to 39)

S Kim,J.S., Jun,K.M., K.M., Y.-K. and Nahm, B.H.

Lupublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
                         39 bp mRNA linear EST 04-NOV-2004 (14Salt--04-P01.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--04-P01, mRNA sequence.
CV727002
CV727002.1 GI:55414626
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyte; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 39)
1 (klamed 1 to 39)
2 (Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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/clone="145alt--04-Pol"
/tissue_type="leaf"
/dev_stage="14 days after gernimation"
/lab_host="E.coli SOLR"
/clone_lib="salt treated rice leaf lambda phage cDNA
library [145alt)
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Location/Qualifiers
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/cultivar="Nackdong"
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Oryza sativa (japonica cultivar-group)

ISM Oryza sativa (japonica cultivar-group)

Eukaryota, (infdiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatcphyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryzea

clade; Ehrhartoideae; Oryzeae; Oryzea

clade; Ehrhartoideae; Oryzeae; Sang, S.I., Kim,J.K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Large-scale Sequencing Analysis of Rice ESTs

Contact: Nahm B.H.

Goncact: Nahm B.H.

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Location/Qualifiers

Location/Qualifiers
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                                                                                                                                                                                                              /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/mol_tyne="Nackdong"
/db_xref="taxon:3994"
/clone="14Salt--04-P09"
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Bioscience and Bioinformatics, MyongJi University
                                                                                                                         bhnahm@bio.myongji.ac.kr
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100.0%; Pred. No. 1.9e+02;
ative 0; Mismatches 0;
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                                                                                                                         Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
                             Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Best Local Similarity 100.0
Matches 35; Conservative
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CV727680/c
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39 bp mRNA linear EST 04-NOV-2004
14Salt--05-H08.gl Salt treated rice leaf lambda phage cDNA library
(14Salt-) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-H08, mRNA sequence.
                                                                                                                                                                                                        linear EST 04-NOV-2004
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

(kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-Gcale Sequencing Analysis of Rice ESTE
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[Ince="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: Xho!; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.cDNA was inserted into lamba Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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100.0%; Pred. No. 1.9e+02;
ive 0; Mismatches 0; Indels
     Length 39;
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Location/Qualifiers
                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol type="mRNA"
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/clone="148alt--65-E03"
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/dev stage="14 days after gernimation"
/lab_host="E.coli SOLR"
                                                                          2709 АААААААААААААААААААААААААААААА
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     Score 35; DB 1; Le
Pred. No. 1.9e+02;
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Oryza sativa (japonica cultivar-group)
1.3%; Score 35; DB
ilarity 100.0%; Pred. No. 1.9
Conservative 0; Mismatches
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CV727351.1 GI:55414975
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Best Local Similarity 100.0
Matches 35; Conservative
                      Similarity
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Best Local ?
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SOURCE
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CV727215/c
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CV727351/c
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                                      Matches
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CV727680 39 bp mRNA linear EST 04-NOV-2004 145alt-05-P01.gl Salt treated rice leaf lambda phage cDNA library (145alt) Oryza sativa (japonica cultivar-group) cDNA clone 145alt--05-P01, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryzeae; Oryzeae; Oryzeae; Oryzeae; Oryzeae; Ciade; Ehrhartoideae; Chan, Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Kim, J.S., Jun, K.M., J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                       Contact: Nature B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Eax: bhahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                          Tobases I to 39)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, Z.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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/dev_stage="14 days after gernimation"
/lab/bost="8.coli SOLR"
/clone_lib==23lt treated rice leaf lambda phage cDNA
library_(145alt)"
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    .39
        Coganism="Oryza sativa (japonica cultivar-group)" /mol type="mRNA" /cultivar="Nackdong" /cultivar="Nackdong"

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100.0%; Pred. No. 1.9e+02;
cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mkNA"
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Matches 35; Conservative
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library (14Salt)"
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CV728278.1 GI:55430594
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Best Local Similarity
Matches 35; Conserv
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CV729217
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Kim,J.S., Jun,K.M., Cheong P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6155
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                          1953LT-06-N13.91 Salt treated rice leaf lambda phage cDNA library (145alt) Oryza sativa (japonica cultivar-group) cDNA clone 145alt-06-N13, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantas, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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//note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: Xhoi; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
                                                                                                                /note="Vector: pBluescript SK(+); Site_1: EcoR1; Site_2: Xho1; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoR1 and 3' end with Xho1 site."
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/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:39947"
/clone="14Salt--06-N13"
/tissue type="leaf"
/dev stage="leaf"
/lab host="fs.coli SOLR"
/lab host="fs.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
               Gaps
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                                                                                                                                                                                                                Length 39;
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1.3%; Score 35; DB 1; Le
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Matches 35; Conservative 0; Mismatches 0;
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   'clone="14Salt--05-P01"
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RESULT 217

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E 1 (bases 1 to 39)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
L Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Exa: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
14Salt--06-012.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt-06-012, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyra; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:39947"
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/dev_stage="14 days after gernimation"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
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/mol_type="mRNA"
/cultivar="Nackdong"
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100.0%; Pred. No. 1.9e+02;
ative 0; Mismatches 0;
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CV732729 39 bp mRNA linear EST 05-NOV-2004 FLO--07-F09.gl Rice flower lambda phage cDNA library (FLO) Oryza Bativa (japonica cultivar-group) cDNA clone FLO--07-F09, mRNA
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/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5, end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
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    Location/Qualifiers
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100.0%; Pred. No. 1.9e+0
tive 0; Mismatches
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flower lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-F09"
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CV733026/c
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                                                                                                                                                                                                      /mol type="markedong"
/cultivar="Nackdong"
/cultivar="Nackdong"
/db xxef="texon:39947"
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/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: BcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at S'end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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FLO--03-H21.gl Rice flower lambda phage cDNA library (FLO) Oryza
Bativa (japonica cultivar-group) cDNA clone FLO--03-H21, mRNA
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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/organism="Oryza sativa (japonica cultivar-group)"

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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.96
.ive 0; Mismatches
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                                                                                RESULT 223
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spernatcophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza,
I (basea) I to 30
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Unpublished (2003)
Contact: Nahm B.H.
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/lab_hogt="E.coli SOLR"
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/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at send with EcoRI and 3' end with XhoI site."
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Yongin, KyeongJi, Korea
1. 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                        /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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of Bioscience and Bioinformatics, MyongJi University YongJi, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Pred. No. 1.9e+02;
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clone="FLO--07-P05"
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clone="FLO--07-M05"
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/cultivar="Nackdong"
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CV733431
FLO--08-F12.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--08-F12, mRNA
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryza.

1 (bases 1 to 39)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Yongin, Kyeongqi, Korea
Yel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with XhoI site."
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100.0%; Pred. No. 1.9e+02;
ative 0; Mismatches 0;
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CV733935.1 GI:55441239
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/tissue_type="flower"
/lab host="E.coli SOLR"
/lab host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uhi-ZAP XR vector at 5, end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Vizidjantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
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5 (khangari to 30)
6 (khangari to 30)
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yorgin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Yongin, KyeongJi, Korea
Yongin, KyeongJi, Korea
Fax: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/cultivar="Nackdong"
/cultivar="Nackdong"
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/clone="FLO--09-C05"
/tissue type="flower"
/lab_host="E.coli Solk"
/clone=lib="Rice flower"
/note="Vector: pBluescript SK(+); Site_l: EcoRI; Site_2: Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at Eed with EcoRI and 3' end with Xhol site."
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/organism="Oryza sativa (japonica cultivar-group)"

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ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0;
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/db_xref="taxon:39947"
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Matches 35; Conserv
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Gaps

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Conservative

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/dex="Male" Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4772114|gp|AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xii0-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                          AZ639088 14-DEC-2000 1M0499A20F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0499A20 F, genomic survey sequence.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 18
4112, USA
Tel: 801 858 5606
Fax: 801 858 7177
Email: 604un@enetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0499 row: A column: 20
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus; Lo 39)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
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2709 ААААААААААААААААААААААААААААААААА
                                  Seq primer: CGTTGTAAAACGACGCCAGT

    .39
    /organism≃"Mus musculus"

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/strain="C57BL/6J"
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/clone="UUGC1M0499A20"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordai
Mammalia; Eutheria; Euarch
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AZ639088/c
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2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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1.3%; Score 35; DB 1; I
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.9e+0
tive 0; Mismatches
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                                                                                                                              technique"
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CF311814/c
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                                                                                                                                                                                   DKF2554E1872 rl 564 (synonym: hfbr2) Homo sapiens cDNA clone DKF2p564E1872, mRNA sequence.
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Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Blum, et al.)
Unpublished (1999)
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/lab_host="X1-2blue"
/clone_lib="564 (synonym: hfbr2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: Sal1"
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Location/Qualifiers
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0; Indels
2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="DKFZp564E1872"
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Location/Qualifiers
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Homo sapiens
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Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae; Homo.
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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/docurref="Laxon:9606"
/clone="INAGE:4447702"
/tissue_type="hypernephroma, cell line"
/tish host="BH10B (phage-resistant)"
/clone lib="NIH (phage-resistant)"
/clone lib="NIH MGC 89"
/note="Organ: kIdney; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
/site_2: Sall; cloned unidirectionally; oligo-dT primed.
/Average insert size 1.3 kb. Library enriched for
/full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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ABF--07-D23.bl ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--07-D23, mRNA sequence.
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602339795F1 NIH_MGC_89 Homo sapiens CDNA clone IMAGE:4447702 5',
mRNA sequence.
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1. (Dasse 1 to 40)

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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
/tissue type="Testis"
/clone lib="Homo sapiens Testis (Stavrides GS)"
/note="CDNA fragment isolated using a cDNA end rescue
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                                                    Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplancae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzae, Oryza.

1 (bases 1 to 40)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Buyza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP

Glade; Ehrhatoidaes; Oryzae; Oryza.

(Dases 1 to 40)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yorgin, KyeongJi, Korea Tel: 82 31 330 6193 Fax: 82 31 31 21 6355 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /notes "Vector: pCR4-TOPO, Site 1: EcoRI, Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcribtion factor 3 overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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NACL--01-F11.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-F11, mRNA
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0; Indels
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CF327027.1 GI:33802307
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Best Local Similarity 100.'
Matches 35, Conservative
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CF328199 40 bp mRNA linear EST 18-AUG-2003 NACL--02-P21.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-P21, mRNA
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                           /dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, KyeongQi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonuclectides and then used as templates for
RT-PCR."
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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'organism="Oryza sativa (japonica cultivar-group)"
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Location/Qualifiers
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100.0%; Pred. No. 1.9e+02;
iive 0; Mismatches 0;
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                              /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--01-F11"
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35, Conservative
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                                            CF328306 A0 bp mRNA linear EST 18-AUG-2003 NACL--03-C09.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--03-C09, mRNA
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/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza,
1 (bases 1 to 40)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Uridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 40)
1 (bases 1 to 40)
1 (kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Nahm B.H.

Contact: Nahm B.H.

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Tel: 82 31 330 6193
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Email: bhnahm@plio.myongji.ac.kr.

Location/Qualifiers
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
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mol_type="mRNA"
/cultivar="Nackdong"
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels
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/clone="NACL--03-C09"
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RESULT 233
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Oryza sativa (japonica cultivar-group)

Gryza sativa (japonica cultivar-group)

Eukaryota, Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota, Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryzea;

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

NL Unpublished (2003)

Contact: Nahm B.H.

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Fax: 82 31 321 6355
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/dev_stage="14 days after gernimation"
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0;
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/cultivar="Nackdong"
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Location/Qualifiers
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com,
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Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

El (bases lto 40)

Ekim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Gong, S. J., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Gontact: Nahm B.H.

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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Oryza sativa (japonica cultivar-group)
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
I (basea: 1 to 40)
Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Unpublished (2003)
Contact: Nahm B.H.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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YongJin, KyeongJi, Korea
13 1330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade, Brhartoideae, Oryzae, Oryza.

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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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/clone_lib="Salt treated rice leaf lambda phage cDNA
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                                                                                                              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0;
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/clone="14Salt--02-001"
/tissue_type="leaf"
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/clone="14Salt--04-K06"
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Query Match

Matches

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RESULT 239

SOURCE ORGANISM

TITLE JOURNAL COMMENT

AUTHORS REFERENCE

ACCESSION VERSION KEYWORDS

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CV727587.1 GI:55415211
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza,

1 (bases 1 to 40)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
/tissue_type="leaf"
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/dev_stage="14 days after gernimation"
/lab_nost="S.coli SOLR"
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library (14Salt)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for Zhrs.
CDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6155
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers
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/dev_stage="15.0dl SOLR"
/clone_lib="Salt_treated rice leaf_lambda_phage_CDNA_library_(14Salt)"
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/mol_type="mRNA"
/cultivar="Nackdong"
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0; Indels
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1es 35; Conservative
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RESULT 240 CV727587/c

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14Salt.-05-M20.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt.-05-M20, mRNA sequence. 40 bp mRNA linear EST 04-NOV-2004 [14Salt--06-C07.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone CV727805 ö Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaa.

1 (bases 1 to 40)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-Grale Sequencing Analysis of Rice ESTs Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhatroideae; Oryzeae; Oryza.

1 (bases 1 to 40)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.J., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs /tissue_type="leaf"
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library (14Salt)"
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Xho!; Leaf was incubated at 4 C(360um/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site." Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Vongin, Kyeonggi, Korea
Tel: 82 31 330 6133
Fax: 82 31 321 6555
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Gaps /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="wackdong"
/db xrt="taxon:39947"
/cione="148alt_-05_M20" 0 1.3%; Score 35; DB 1; Length 40; 100.0%; Pred. No. 1.9e+02; /ative 0; Mismatches 0; Indels 2709 ААААААААААААААААААААААААААААААААА

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Pred. No. 1.9e+02;
100.0%; Preα. ....
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                        35; Conservative
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       Best Local Similarity
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CV727858/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Nahm B.H.
Generics and Genetics Institute, GreenGene Biotech Inc.; Division Genomics and Genetics Institute, GreenGene Biotech Inc.; Division Objain, Expendent Boinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@pio.myongji.ac.kr.
Location/Qualifiers
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/dev_stage="14 days after gernimation"
/lab_host="Rc.oli SOLR"
/lone_lib="Salt treated rice leaf lambda phage cDNA
library (145alt)
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 Tel: 82 31 330 6193
Fax: 82 31 321 6335
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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1.3%; Score 35; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0;
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DB 1; Length 40;

1.3%; Score 35;

Query Match

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Dryza sativa (japonica cultivar-group)

Eukaryorota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryorota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; O
                                                                                                                                                                                                                                                                                                                                                                                         v///8b8 14Salt--06-D16.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt-06-D16, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
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/clone="14Salt--06-D16"
/tissue_type="leaf"
/dev.stage="14 days after gernimation"
/lab_host="E-coli SOLR"
/clone_lble=Salt treated rice leaf lambda phage cDNA_lbbrary (14Salt)"
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/cultivar="Nackdong"
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1.3%; Score 35; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0;
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CV730371.1 GI:55434492
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Best Local Similarity 100.0
Matches 35; Conservative
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Local 35; Conserva
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CV731031/c
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clade; Ehrhartoideae; Oryzeae; Oryza.

E. (Dasses I to 40)
S. Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahn, B.H.
Large-scale Sequencing Analysis of Rice ESTs
L. Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeonggJi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhaahm@ggDio.com, bhnahm@bio.myongji.ac.kr.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Tongln, Kyeonggi, Korea
Tel: 82 31 330 6193
Pax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hra. CDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa (japonica cultivar-group)"
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/clone=lib="S.coli SOLR"
/clone=lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/cultivar="Nackdong"
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Best Local Similarity
Matches 35; Conserv
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CV731031 40 bp mRNA linear EST 05-NOV-2004 FLO-04-N24.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO-04-N24, mRNA
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/lab host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pRluescript SK(+); Site_1: EcoRI; Site_2:
Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with Xhol site."
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/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with Xhol site."
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Clade; Ehrhartoidaea; Oryzeae; Oryza.

1 (bases 1 to 40)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Kim,J.S., Zun,K.M., Zie, and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Yel: 82 31 33.0 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/mol type="mRNA"
/culTivar="Nackdong"
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100.0%; Pred. No. 1.9e+02;
ative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.9e+02;
ative 0; Mismatches 0;
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/clone="FLO--03-005"
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/tissue_type="flower"
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CV732353.1 GI:55438119
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CV732353/c
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="wackdong"
/db xref="taxon:19947"
/clone="FLO--04-N24"
/tissue_type="flower"
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/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="wector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

El (Dasses I to 40)

Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzeae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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FLO--05-E21.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--05-E21, mRNA
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/mol type="mRNA"
/cultivar="wackdong"
/db x="taxon:39947"
/clone="FLO--05-E21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                            Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.3%; Score 35; DB 1; Length 40; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 35; Conservative 0; Mismatches 0; Indels
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Location/Qualifiers
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CV731319.1 GI:55436371
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CV731319/c
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhatroideae; Oryzeae; Oryza.

(bases 1 to 40)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/lab_host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
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Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5:
end with EcoRI and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Nahm B.H.
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yorgin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5
end with EcoRI and 3' end with XhoI site."
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100.0%; Pred. No. 1.9e+02;
ive 0; Mismatches 0; Indels
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CV732676.1 GI:55438756
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CV732676/c
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.

E 1 (bases 1 to 40)
S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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FLO--07-D02.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-D02, mRNA
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             Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
                                                                                                             (bases 1 to 40)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Blotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Torgin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="FLO--06-M17"
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Xho1; cDNA was inserted into lamda ubi-ZAP XR vector at 5 end with EcoRI and 3' end with Xho1 site."
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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1.9e+02;
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KEYWORDS
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| Organism="Oryza sativa (japonica cultivar-group)"
| organism="Oryza sativa (japonica cultivar-group)"
| wol transm="Nackdong" |
| cultivar="Nackdong" |
| clone="PLO-07-E04" |
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/tissue_type="flower"
/lab_host="E.coli SOLR"
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
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Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Enrhartoideae; Oryzeae; Oryza.

(bases 1 to 40)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bloinformatics, MyongJi University
Yongin, KyeongGi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gpio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Pred. No. 1.9e+02;
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100.0%; Pred. No. ...
0; Mismatches
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/db xref="taxon:39947"
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CV733422/c
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AUTHORS
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Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhattoideae; Oryzae; Oryza.

El (bases 1 to 40)

SKim,J.S., Jun,K.M., Cheong, V.-K. and Nahm, B.-H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.-H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongjin, Kyeonaggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
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                                           Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Spermatophyta; Viridiplantae; Streptcophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

1 (bases 1 to 40)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="flower"
/lab_host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_l: EcoRI; Site_2:
Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with Xhol site."
                                                                                                                                                                                                                                                                                                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6555
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nackdong"
/db xraf=xnon:39947"
/clone="FLO--07-L19"
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0; Indels
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Location/Qualifiers
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/cultivar="Nackdong"
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Matches 35; Conserv
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CV733017/c
                                                                     ORGANISM
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryzae.
El (bases 1 to 40)
SKim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice EST8
LD Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Biocience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CV733422 40 bp mRNA linear EST 05-NOV-2004 FLO--08-F08.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-F08, mRNA
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/lab_host="E.coli SOLR"
/lab_host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with Xhol site."
/clone="FLO--07-M01"
/tissue_type="flower"
/lab_host="E.col: SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with XhoI site."
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Location/Qualifiers
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1.3%; Score 35; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0;
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1.3%; Score 35; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0;
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/cultivar="Nackdong"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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DEFINITION
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Seg primer: T7
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murcidea; Muridae; Murinae; Mus.

1 (bases 1 to 40)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Menen,B., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

University of Utah Genome Center
University of Utah Genome Center
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/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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                                                             Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplancae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza,
1 (bases 1 to 40)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Seepnecing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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2M0112K02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0112K02 F, genomic survey sequence.
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/mol type="mRNA"
/cultivar="Nackdong"
/db_xrefertxoon:39947"
/clone="FPLO-08-K08"
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100.0%; Pred. No. 1.9e+02;
trive 0; Mismatches 0; Indels
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Location/Qualifiers
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Insert Length: 10000 Std Error: 0.00
                         GI:55440654
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Fax: 801 585 7177
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Matches 35; Conserva
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CV733638.1
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84112, USA
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(http://www.house_DNA.Resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gilfa732114 [gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 sequence of Brassica rapa ssp. pekinensis SauJAI BAC clone
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Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                     /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse lokb plasmid UGGCIM library"
/note="Wector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JUN35034 SECTOR TINEAR GSS 22-DEC-2(
KBrS015N17F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS015N17, genomic survey
sequence.
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Contact: Beom-Seok Park
Brassica Genomics Team
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.3%; Score 35; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0;
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 40.
Location/Qualifiers
                                                                                                                                                                                                         organism="Mus musculus"
                                                                                                                                                                                                                                      /mol_type="genomic DNA"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                         /clone="UUGC2M0112K02"
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CF291539
CF291539.1 GI:33660572
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Best Local Similarity 100.
Matches 35; Conservative
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                   ACCESSION
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(14ROOT) Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Lamiales; Plantaginaceae; Antirrhineae;
                                                                                                                                                                /clome_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bey, M., Stueber, K., Fellenberg, K., Schwarz-Sommer, Z., Sommer, H., Saedler, H. and Zachgo, S.
Saedler, H. and Zachgo, S.
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
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14-AUG-20 MRNA linear EST 14-AUG-20 14ROOT--02-A03.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-A03, mRNA
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                                             /organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:4151"
/clone="0.12 12 h22"
/tissue type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
                                                                                                                                                                                                                                                    Length 40;
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Pred. No. 2e+02;
Pred. no. 7e+nes 0; Indels
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Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                        Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
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/organism="Antirrhinum majus"
                                                                                                                                                                                                                                                             100.0%; Pred. No.
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                                                                                          /sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS015N17"
/lab_host="E. coli_DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3%; Score 35;
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Antirrhinum majus
               location/Qualifiers
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Class: BAC ends
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Best Local Similarity
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Oryza sativa (japonica cultivar-group)

Eukaryotea, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryotea, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryotea, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryzea;

Clade; Ehrhartoideae; Oryzeae; Oryzea;

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 320 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                     CF310464 1inear EST 18-AUG-2003 NACL--06-D01.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--06-D01, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="callus" /dev_stage="proliferated callus on 2N6 media for 30 days" /dev_stage="proliferated callus on 2N6 media for 30 days" /lab host="E.coli DH10B" /clone_lib="Rice callus plasmid cDNA library (NACL)" /note="Vector: pCR4-TOP0; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JMT--04-A03.g1 AtJMT-overexpressing transgenic rice plasmid CDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
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Kim, U.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophy
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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100.0%; Pred. No. 2e+02;
vative 0; Mismatches 0; Indels
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/cultivar="Nackdong"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab host="E.coli DH10B"
/clone lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was reversed with ABA(20um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
                                                                                                  db_xref="taxon:39947"
| Clone="HD--08-009" |
| /tissue | Lype="callus" |
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| /dev_stage="proliferated callus on 2N6 media for 2 weeks" |
| /dev_stage="proliferated callus on 2N6 media for 2 weeks" |
| /dev_stage="proliferated callus on 2N6 media for 2 weeks" |
| /dev_stage="proliferated callus" 
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhatroideae; Oryzeae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-Gcale Sequencing Analysis of Rice ESTE
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR: mRNA was derived from rice Histone Deacetylase overexpression line."
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/mol_type="mRNA"
/cultivar="Nackdong"
       'organism="Oryza sativa (japonica cultivar-group)"
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
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Location/Qualifiers
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                                   /mol_type="mRNA"
/cultivar="Nackdong"
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CF320203.1 GI:33691964
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CV725993/c
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sulvaryca, Viridiplantes, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade, Ehrhartoideae, Oryzaee, Oryza.

1 (bases 1 to 41)
Kim,J.S., Uun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                /db_xref="taxon:39947"
/clone="UMT--04-A03"
/tissue_type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division Genomics and Genetics Institute, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@pio.myongJi.ac.kr.
Location/Qualifiers
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                                                                                                                                                                                                                        /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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thes 0; Indels
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/clone="14Salt--03-D07"
/tissue_type="leaf"
/dev stage="14 days after gernimation"
/lab_host="E.coli SOLR"
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100.0%; Pred. No. 2e+(
tive 0; Mismatches
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cDNA_library_(JMT)"
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Matches 35; Conservative
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41 bp mRNA linear EST 04-NOV-2004 (14Salt--03-M18.gl Salt treated rice leaf lambda phage cDNA library 14Salt-07yza sativa (japonica cultivar-group) cDNA clone 14Salt--03-M18, mRNA sequence.
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41 bp mRNA linear EST 04-NOV-2004
145alt--03-G10.bl Salt treated rice leaf lambda phage cDNA library
(145alt) Oryza sativa (japonica cultivar-group) cDNA clone
145alt--03-G10, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yogin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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100.0%; Pred. No. 2e+02;
cive 0; Mismatches 0; Indels
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CV725993.1 GI:55413617
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.
E (bases 1 to 41)
S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
L Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza,
I (basea I to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTB
Unpublished (2003)
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//note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
Xhoi; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
CDNA was inserted into lamda Uni-2AP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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| Alab_host="E.coli SOLR"
| /done_lib="8salt treated rice leaf lambda phage cDNA
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100.0%; Pred. No. 2e+02;
iive 0; Mismatches 0; Indels
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Location/Qualifiers
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CV726393.1 GI:55414017
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Best Local Similarity 100.0°
Matches 35, Conservative
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CV726393/c
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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/lab_host="E.coli SOLR"
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library (145alt)"
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Xhoi, Leaf was incubated at 4 C(350uM/m-2aec-1) for Zhre.
CDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with BcoRI and 3' end with XhoI site."
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Contact: Nahm B.H.

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Genomics and Bioinformatics, MyongJi University
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Tel: 82 31 330 6193
Fax: 82 31 321 635
Eax: 82 31 321 635
Email: bhnahm@gGpio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers
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/mol_type="mRNA"
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/dev stage="14 days after gernimation"
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/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (145alt)"
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Pred. No. 2e+02;
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v 100.0%; Pred. No. ...
0; Mismatches
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SOURCE

TITLE JOURNAL COMMENT

FEATURES

AUTHORS

REFERENCE

ACCESSION VERSION KEYWORDS

RESULT 270 CV727015/c DEFINITION

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XhoI; Leaf was incubated at 4 C(560wM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
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14Salt--05-118.bl Salt treated rice leaf lambda phage CDNA library (14Salt) Oryza sativa (japonica cultivar-group) CDNA clone 14Salt--05-118, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yeongji, Kveongji, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongGi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/organism="Oryza sativa (japonica cultivar-group)"
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
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Location/Qualifiers
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| Organism="Coryza sativa (japonica cultivar-group)"
| Mol type="mRNA"
| Mol type="mRNA"
| Cultivar="NacKdong"
| Cultivar="NacKdong"
| Cultivar="Yasalt--04-P08"
| Cidome="14pe="leaf"
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14Salt.--04-P08.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--04-P08, mRNA sequence.
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14Salt--05-D24.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--05-D24, mRNA sequence.
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Oryza sativa (japonica cultivar.group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of the contact of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 41)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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hes 0; Indels
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100.0%; Pred. No.
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DEFINITION RESULT 271 CV727210/c

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RESULT 273 CV727841/c DEFINITION

ઠે 셤 ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

FEATURES

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148alt-06-NO5.gl Salt treated rice leaf lambda phage cDNA library (148alt) Oryza Bativa (japonica cultivar-group) cDNA clone L148alt--06-NO5, mRNA Bequence.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Enrhatcoideae; Oryzeae; Oryza
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Yongin, KyeongGi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/dev_stage="14 days after gernimation"
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/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa (japonica cultivar-group)"
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100.0%; Pred. No. 2e+02;
ative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 35; Conservative
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Organ sativa (japonica cultivar-group)

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Espermatophyta; Maglantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Maglantae; Streptophyta; Embryophyta; Tracheophyta; Clade; Ehrhartoideae; Oryzeae; Oryza.

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El (Masses It of 41)

Contact: Nam, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/lab_host="E.coli 501R"
/clone_lib="Salt_treated rice leaf lambda phage cDNA
library (145alt)"
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                   cDNA was inserted into lamda Uni-ZAP XR vector with EcoRI and 3' end with XhoI site."
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                                                                                                                             1.3%; Score 35; DB 1; Length 41;
100.0%; Pred. No. 2e+02;
cive 0; Mismatches 0; Indels
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Matches 35; Conservative
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LOCUS CV728055/c

ACCESSION VERSION KEYWORDS

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Page 111

EST 05-NOV-2004

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae.
El (Bases I to 41)
SKim,J.S., Jun,K.M., Cheong, D.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
U Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bloinformatics, MyongJi University
YongIn, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 11 321 6355
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/clone="FLO--01-J08"
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/lab host="E.coli Solk"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
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Xho1; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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                     CV728978

FLO--01-J08.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-J08, mRNA
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FLO--01-K21.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-K21, mRNA
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/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
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100.0%; Pred. No. ...
'... 0; Mismatches
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CV729041/c
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/tissue_type="14 days after gernimation"
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/clone_lib="salt treated rice leaf lambda phage cDNA
library (14Salt) "treated rice leaf lambda phage cDNA
library (14Salt) "treated at 4 C(360uM/m-2sec-1) for 2rx Xhol; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hxs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with Xhol site."
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41 bp mRNA linear EST 05-NOV-2004 FLO--01-D04.bl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-D04, mRNA
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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KhOI; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with XhOI site."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bloscience and Bioinformatics, MyongJi University
Yongin, Kyeongji, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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|mol_type="mRNA"
|cultivar="Nackdong"
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100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 2e+(
cive 0; Mismatches
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Matches 35; Conserv
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SOURCE ORGANISM

TITLE JOURNAL COMMENT

AUTHORS REFERENCE

ACCESSION VERSION KEYWORDS

LOCUS DEFINITION CV728716/c

RESULT 276

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Gaps

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EST 05-NOV-2004

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

41

RESULT 277 CV728978/c

Query Match

Matches

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source

FEATURES

EST 05-NOV-2004

FEATURES

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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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41 bp mRNA linear EST 05-NOV-2004 FLO--06-G04.bl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--06-G04, mRNA
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm BH.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bloinformatics, MyongJi University
                                 CV731668 1inear EST 05-NOV-20 FLO-05-M20.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--05-M20, mRNA
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ilarity 100.0%; Pred. No. 2e+02;
Conservative 0; Mismatches 0; Indels
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/cultivar="Nackdong"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Local 35; Conserve
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Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.

E 1 (bases 1 to 41)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

L Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
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FLO--05-H10.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--05-H10, mRNA
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                                                                                                                                                                                                                                                                                                           /tissue_type="flower"
/lab_host="E.coli SOLR"
/lab_host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5, end with EcoRI and 3' end with XhoI site."
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XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoR1 and 3' end with XhoI site."
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| Organism="Oryza sativa (japonica cultivar-group)"
| Amol type="mRNA"
| Mol type="mRNA"
| Cultivar="Maxokdong"
| Ab xref="taxon:39947"
| Clone="FLO--05-H10"
| Cistone="FLO--05-H10"
| Cistone="FLO--05-H10"
| Cistone="Type="flower"
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organism="Oryza sativa (japonica cultivar-group)"
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100.0%; Pred. No. 2e+02;
cive 0; Mismatches 0; Indels
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hes 0; Indels
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1.3%; Score 35; DB
Best Local Similarity 100.0%; Pred. No. 2e+
Matches 35; Conservative 0; Mismatches
                                                                                                                                     /mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="FLO--01-K21"
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CV731427.1 GI:55436582
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CV731427/c
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DEFINITION

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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS RESULT 280

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Length 41;

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CV734304 linear EST 05-NOV-2004 FLO-09-J18.bl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO-09-J18, mRNA
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/clone="FLO--09-J18"
/tlab.host="E.Glower lambda phage cDNA library (FLO)"
/hote="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/hots="vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/hoty: cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A2775066 10kb plasmid UUGCIM library Mus musculus genomic UUGCZM0007101F, genomic survey sequence.
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/mol type="mRNA"
/cultivar="Nackdong"
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5. 2e+02;
0; Indels
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Mus musculus
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                        CV734304.1 GI:55441966
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AZ775066.1 GI:12901172
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Best Local Similarity 100.
Matches 35; Conservative
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-Gcale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                 /clome_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Wector: planescript SK(+); Site_l: EcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with XhoI site."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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// Organism="Oryza sativa (japonica cultivar-group)"
// Organism="Nackdong"
// Cultivar="Nackdong"
// Chone="FLO--06-GQ4"
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    bhnahm@bio.myongji.ac.kr.
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Location/Qualifiers
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2e+02;
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/cultivar="Nackdong"
/db xref="taxon 39947"
/clore="FLO--08-022"
/tissue type="flower"
/lab host="E.coli SOLR"
/clone_lib="Rice flower 1
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Pred. No.
Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
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Matches 35; Conserv
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Matches 35
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GSS 16-FEB-2001

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DU834001/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /Bab. maie...
/ Jab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/ clone_lib="Mouse 10kb plasmid UUGCIM library"
/ clone_lib="Wouse 10kb plasmid UUGCIM library"
/ note="Vector: PWD421v; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was blut cand-repaired by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated from a frep
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gil | 4732114 | gb| AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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2M0103107F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0103107 F, genomic survey sequence.
AZ827008
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rislam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, K., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Walss, R.
       E., SLC,
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       S. 2030
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
308, Biomedical Polymers Research Bldg., 20
12, USA
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0007 row: I column: 01
                                                                                                                                                                             Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plaamid ends
High quality sequence stop: 41.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C578L/6J"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:10090"
clone="UUGC2M0007101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     'sex="Male'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.3
Best Local Similarity 100.
Matches 35; Conservative
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AZ827008
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwnot (gilly 4732114|gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (stratagene) cells and selected for ampicillin resistance."
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Fukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

I (bases 1 to 41)
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus G57BL/60 (male) was obtained from the Jackson
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 41;
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
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Fax: 801 585 7177
Email: ddunmgenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: I column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
                                                                                                                                                                                              plate: 0103 row: I column: 07
Seg primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0103107"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
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GI:84743707
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Class: BAC ends
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DX049410.1
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DX049410/c
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KBrS014M09F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS014M09, genomic survey sequence.
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             Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Wagnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
I (bases I to 41)
Yang T.J. Kwon,S.J. Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Institute of Agricultural Biotechnology 225 Seodun-Dong, Suwon, 441-707, Korea 151: 482-31-299-1670 Fax: +82-31-299-1670 Email: pbeom@rda.go.kr
                                                                                                                                                                                                                                                  /clone="KBrS013D19"
/lab_host="E. coli DH10B"
/clone lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
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/db_xref="taxon:51351"
/db_ne="KBrS014M09"
/lab_hot=="coli DH10B"
/clone lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBACI; Site_1: Sau3AI; Brassica rapa spekinensis var. Chiifu BAC library (KBrS BAC) is
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/mol type="genomic DNA"
/cultivar="Chiifu"

    1. .41
    /organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
    /cultivar="Chiifu"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sub_species="pekinensis"
/db_xref="taxon:51351"
                                                                                                                        Location/Qualifiers
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Brassica Genomics Team
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Tel: +82-31-299-1670
Fax: +82-31-299-1672
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                                                                                      Seq primer: T7
Class: BAC ends.
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available at NIAB."
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Albp DNA linear GSS 10-JAN-2006 KBrB052A12F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB052A12, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantae Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
                                                                                                                                                                                                                                                                                                                              DU835000 41 bp DNA linear GSS 22-DEC-20
KBrS015L21F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS015L21, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBACI; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Hahn, J. H. Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., End sequence of Brassica rapa Sau3AI (KBrS) BAC clone Unpublished (2005)
Contact: Boom-Seok Park Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Park: +82-31-299-1672
                                                             Gaps
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/mol type="genomic DNA"
/cultivar="Chiifu"
   Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.3%; Score 35; DB 1; Length 41; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels
                                                                                                                     2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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|db_xref="taxon:51351"
|clone="KBrS015L21"
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mRNA sequence.
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Matches 35; Conserv
EH25 9PS,
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KEYWORDS
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                 FEATURES
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Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Sitel: EcoRI
R. Site2: Smal 5' Seq Primer T3 Normalised library constructed from
Dovine ovary. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovinae; Bos.

1. (bases 1 to 42)
Anderson, S. I., Finlayson, H. A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="KBrB052A12"
/lab host="E.coli DH10B"
/lab host="E.coli DH10B"
/lone lib="WarB, Brassica rapa BamHI BAC library"
/note="Vector: pcUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AJ691919 KN261 Bos taurus CDNA clone KN261-025_M11, mRNA sequence.
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  Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases I to 41)
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Hahn, J.H., and Park, B.S.
                                                                                                                                                                                                                                                                   Brassica Genomics Team
Mational Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Exar: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                  End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.3%; Score 35; DB 1; Length 41; 00.0%; Pred. No. 2e+02;
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/db_xref="taxon:51351"
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Bos taurus
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Matches 35; Conservative
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Class: BAC ends
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JOURNAL
COMMENT
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AJ691919
                                       ORGANISM
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ઠે 셤

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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="kaxon:9606"
/dlone="InvAGE:451403"
/tissue_type="transitional cell papilloma, cell line"
/lab host="Blios (phage-resistant)"
/clone lib="NIH MGC 93"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 Ab. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                      /mol_type="mRNA"
/db xref="taxon:9913"
/clone="KNS0="0.05_M11"
/tissue_type="0.04zy"
/clone_lib="KNS61"
/note="vector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2:
/note="vector: pBlueScriptII(SK+); Normalised library
constructed from bovine ovary."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 21-FEB-2001
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S I (bases I to 42).

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC

CDNA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

Cloe distribution: MGC clone distribution information can be found through the I.M. AG.E. Consortium/Link at:

http://image.llnl.gov

Plate: LiAMI0405 row: c column: 20

High quality sequence stop: 42.

Location/Qualifiers
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG292448 11-FEB-20
602386574F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4515403 5',
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5. 2e+02;
6; Indels
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100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 2e+0z
---ive 0; Mismatches

    .42
    /organism="Bos taurus"

www.arkgenomics.org.
Location/Qualifiers
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100.0%; Pre-
0; N
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 35; Conservative
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RESULT 292 CF318540/c DEFINITION

ORGANISM

ACCESSION VERSION KEYWORDS TITLE JOURNAL COMMENT

AUTHORS REFERENCE

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/dev_stage="pointerated callus on 2N6 media for 2 weeks" /lab_host="E.coli DH10B" /clone lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEGATED (115.91 OSHDAC1-overexpressing transgenic rice plasmid CDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--10-115, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Yel: 82 31 33 30 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University Yongin, KyeongJi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR: mRNA was derived from rice Histone Deacetylase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                                                                                                                                                                                                                         /organism="Oryza sativa (japonica cultivar-group)"
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/mol type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.3%; Score 35; DB 1; Length 42;
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1.3%; Score 35; DB
Best Local Similarity 100.0%; Pred. No. 2e+
Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                           /mol_type="mRNA"
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/clone="HD--09-E19"
/tissue_type="callus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:39947"
/clone="HD--10-115"
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                                                                                                                                                                        Location/Qualifiers
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CF319867.1 GI:33691628
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CF319867/c
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JOURNAL
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                                                             42 bp mRNA linear EST 15-AUG-2003
11brary (HD) Oryza sativa (japonica cultivar-group) cDNA clone
CF318540.
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cDNA library (HD)"
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Spermatophyta; Viidiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 42)
Xim,J.S., Jun,K.M., Cheong,P.J., Xim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Xim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeongqi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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2e+02;
hes 0; Indels
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100.0%; Pred. No. 2e+
ive 0; Mismatches
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Best Local Similarity 100.
Matches 35, Conservative
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FEATURES

RESULT 293 CF318962/c LOCUS

ò d ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL

AUTHORS REFERENCE

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Gaps

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602015993F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4151542
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B. I (bases 1 to 42)

S. NIH-MGC Netp://mgc.nci.nih.gov/.

Intional Institutes of Health, Mammalian Gene Collection (MGC)

Intoublished (1999)

Contact: Robert Strausberg, Ph.D.

Charl: cgapbs-remant: David N. Louis, M.D.

Collo Library Preparation: Life Technologies, Inc.

Collo Library Preparation: Life Technologies, Inc.

Colno Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Cloe distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov.

Plate: LLAM9416 row: j column: 23

High quality sequence stop: 39.

Location/Qualifiers
                                                                                                    Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Nahm B.H. Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
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   CF332408.1 GI:33813036
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhattoideae; Oryzaa.

E (hases 1 to 42)

I (bases 1 to 42)

Is Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

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Tel: 82 31 330 6193

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treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
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                                                                                                                                                                                      Length 42;
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Location/Qualifiers
                                                                                                                                                                                                                                                         0; Indels
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CF320056.1 GI:33691817
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Best Local Similarity 100.
Matches 35; Conservative
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FEATURES

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

DEFINITION

RESULT 295

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 296 CF332408/c LOCUS DEFINITION

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Page 119

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(davg bost anthesis)"
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/lab host="DHOB (life Technology)"
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/clone_lib="Barley EST endosperm lissues of the Barley cultivar
/note="Vector: _zipLox; Site_l: Sal 1; Site_2: Not I; mRNA
was prepared from endosperm tissues of the Barley cultivar
Himalaya. CDNA was synthesised from pooled 10, 12, and 15
dpa endosperm using Not I-oligo(dT)18 primer/adapter
(Pharmacia Biotech), and then ligated to the Sal I-Not I
site of _zipLox vector (Life Technology) after adding a
Sal I-Xho I adapter (Stratagene). Constructed by Shahjahan
Ali and Bill Taylor."
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S Ali, S, Holloway, B. and Taylor, W.C.

Normalisation of cereal endosperm EST libraries for structural and functional genomic analysis

L Plant Mol. Biol. Rep. 18, 123-132 (2000)

Contact: Bill Taylor

Commonwealth Scientific and Industrial Research Organisation

Division of Plant Industry.

CSTRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia

Tel: 61 2 6246 5000

Email: Bill Taylor@csiro.au

Seq primer: M13 reverse primer

High quality sequence stop:

Location/Qualifiers
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145alt--02-I06.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-I06, mRNA sequence.
                                                                                                                                                                                 Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Pooideae, Triticeae, Hordeum.
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Oryza sativa (japonica cultivar-group)
Cura sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
     vulgare cDNA clone BNEL75e2 5' similar to Unknown Function, mRNA
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    .42
/organism="Hordeum vulgare subsp. vulgare"
/mol type="mRNA"
/cultivar="Himalaya"

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live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sub_species="vulgare"
/db_xref="taxon:112509"
/clone="BNEL75e2"
                                                                                                                                Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
                                                                               GI:51525163
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CV725428.1 GI:55413052
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Best Local Similarity 100.0
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CV062024.1
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/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
P. carinii organisms (3x109) from a single rat (59-1-6, sacrificed on 3/17/9) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard conditions described by vendor, Stratagene. Further details see www.uky.edu/Project/Pneumocystis/"
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                                                                                                                        /tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally, Primer: Oligo dr.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW334133 42-1 Pneumocystis carinii cDNA 3', mRNA sequence.
AW34133
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1 (bases 1 to 42)

Smllan,A.G., Arnold,J., Weise,M., Wunderlich,J., Sledman,J.C., Kovacs,J. and Cushion,M.

Expressed sequence tags from Pneumocystis carinii
                                                                                                                                                                                                                                                                                                                                    1.3%; Score 35; DB 1; Length 42; 100.0%; Pred. No. 2e+02; ative 0; Mismatches 0; Indels
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100.0%; Pred. No. 2e+02;
cive 0; Mismatches 0; Indels
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1. .42
forganism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4151542"
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/db_xref="taxon:4754"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: staben@pop.uky.edu.
Location/Qualifiers
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Pneumocystis carinii
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Best Local Similarity 100.0
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Tel: 606 257 2161
Fax: 606 257 1717
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S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 bp mRNA linear EST 04-NOV-2004 (14Salt--03-P05.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--03-P05, mRNA sequence. CV726363 CV726363.1 GI:55413987
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridollantaa, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Yel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhOI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hre. CDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhOI site."
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="145alt--03-P05"
/tissue_type="leaf"
/dev_stage="14 days after gernimation"
/lab_host="S.coli SOLR"
/clone lib="S.coli SOLR"
/clone lib="Salt treated rice leaf lambda phage cDNA
library (145alt)"
                                                                                                                                                                                                                                  /mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="145alt--02-106"
/tissue_type="leaf"
/dev_stage="14 days after gernimation"
/lab_host="E.coli SOLR"
/clone_libe="Salt treated rice leaf lambda phage CDNA
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14Salt--03-P10.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone L4Salt--03-P10, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bloinformatics, MyongJi University
YongJi, KyeongGi, Korea
Tel: 82 31 330 6193
Fax: 82 31 31 22 655
Email: bhnahm@pio.myongji.ac.kr.

Location/Qualifiers
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/clone="148alt--03-P10"
/tissue_type="leaf"
/dev_stage="14 days after gernimation"
/lab_host="E.coli SOLR"
/clone=lib="Soli treated rice leaf lambda phage cDNA
library (148alt)"
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/mol_type="mRNA"
/cultivar="Nackdong"
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Pred. No. 2e+02;
Orinnarian 0; Indels
                                                                                                     Score 35; DB 1; Length 42;
Pred. No. 2e+02;
...matches 0; Indels
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1.3%; Score 35; DB 3Best Local Similarity 100.0%; Pred. No. 2e+
Matches 35; Conservative 0; Mismatches
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CV728634.1 GI:55431251
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35; Conservative
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                               Coryaa sativa (japonica cultivar-group)

Coryaa sativa (japonica cultivar-group)

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

El (bases 1 to 42)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

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y (FLO) Oryza
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantas (Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
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| Mol Lypg="mRNA"
|cultivar="Nackdong"
| db_xref="taxon:39947"
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iive 0; Mismatches
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.

El (Dasse) 1 to 42)
SKim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Lu Dupublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                       /tissue_type="flower"
//lab_host="E.coli SOLR"
//lab_host="E.coli SOLR"
//clone lib="Rice flower lambda phage cDNA library (FLO)"
//note="Vector: pBluescript SK(+); Site_l: EcoRI; Site_2:
Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with Xhol site."
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42 bp mRNA linear EST 05-NOV-2004
FLO--02-A05.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--02-A05, mRNA
CV729267
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/lab_host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_l: EcoRI; Site_2:
Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at 5, end with EcoRI and 3' end with Xhol site."
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FLO--01-P01.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-P01, mRNA
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/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Wackdong"

/db_xref="taxon:39947"

/clone="FLO--01-P01"
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Location/Qualifiers
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0;
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100.0%; Pred. No. 20.
... 0; Mismatches
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/clone="FLO--01-F05"
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/db_xref="taxon:39947"
/clone="FLO--06-A23"
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/cultivar="Nackdong"
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Best Local Similar
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Matches 35
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CV732835/c
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DEFINITION
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CV731845/c
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JOURNAL
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                                   Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Enrhartoideae; Oryzeae; Oryza.

El (Bases I to 42)

El (Bases I to 42)

El (Ram,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)

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Tel: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xxef="taxon:19947"
/clone="FLO--02-A05"
/tissue_type="FLO-02-A05"
/lab_host="R.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site=1: EcoRI; Site=2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
of Bioscience and Bioinformatics, MyongJi University
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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2e+02;
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tive 0; Mismatches
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Pred. No.
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/cultivar="Nackdong"
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/cultivar="Nackdong"
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    GI:55432491
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Best Local Similarity 100.
Matches 35; Conservative
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    CV729267.1
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JOURNAL
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VERSION
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SOURCE
                                                                                                                                                               AUTHORS
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CV732835 FLO-07-H20.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-H20, mRNA
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FLO-06-A23.bl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO-06-A23, mRNA
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaee; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTB
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 655
Exar: 82 31 31 22 655
Email: bhahm@pio.myongji.ac.kr.
Location/Qualifiers
/clone="FLO--05-121"
/tissue type="flower"
/lab host="E.coli Soln"
/lab host="E.coli Soln"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Weetor: pBluescript SK1+); Site_1: EcoRI; Site_2:
Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at send with EcoRI and 3' end with XhoI site."
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/lab host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at end with EcoRI and 3' end with XhoI site."
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100.0%; Pred. No. 2e+02;
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches
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cultivar="Nackdong"
                                                                                                                                                                                                                                                  Best Local Similarity
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CV733323/c
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CV733275/c
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AUTHORS
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Bukaryota; diagonica cultivar-group)

Bukaryota; diagonica cultivar-group)

Bukaryota; didiglalnate; Streptophyta; Embryophyta; Tracheophyta; Spermatcphyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 42)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-escale Sequencing Analysis of Rice ESTs
Unpublished (2003)

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Fax: 82 31 321 6195

Email: bhnahm@ggblo.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
/mol type="manA"
/cultivar="Nackdong"
/cultivar="13947"
/cultivar="13947"
/clone="FLO--07-H20"
/tissue_type="flower"
/lab host="E.col; SOLR"
/lab host="E.col; SOLR"
/lab host="Rice flower lambda phage cDNA library (FLO)"
/note="vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/note="vector: pBluescript SK(+); Site_1: XNoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
                                                           Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzeae; Oryza.
I (bases 1 to 42)
Song, S. I., Kim, J. K., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B. H.
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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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FLO--07-110.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-110, mRNA
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/mol_type="mRNA"
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                      CV732835.1 GI:55439068
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Best Local Similarity
Matches 35; Conserv
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/db_xref="txxon:33947"
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/lab host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="vector: pBluescript SK(+); Site. 1: EcoRI; Site. 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at Send with EcoRI and 3' end with XhoI site."
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzae, Oryza.

1 (bases 1 to 42)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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| db_xref="taxon:39947"
| fclone="FLO--08-B2"
| fissue_type="flower"
| lab_host="E.oli SOLR"
| clone lib="Rice flower lambda phage cDNA library (FLO)"
| note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with XhoI site."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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FLO--08-B22.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-B22, mRNA
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hea 0; Indels
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Location/Qualifiers
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0; Mismatches
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/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                      Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Bhrhartoideae; Oryzeae; Oryza.
1 (bases I to 42)
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Larges-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm_B.H.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza,
1 (bases 1 to 42)
1 (kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
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/tissue_type="tlower"
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/mol_type="mRNA"
/cultivar="Nackdong"
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2e+02;
hes 0; Indels
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CV733544.1 GI:55440468
                       CV733323.1 GI:55440025
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Best Local Similarity 100.0'
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CV733544/c
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Tel: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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LOCUS CV733690 42 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--08-L13.b1 Rice flower lambda phage cDNA library (FLO) Oryza
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/lab host="E.coli Solk"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/clone="lowertor" lambda phage cDNA librar
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Xhoi; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyra; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
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/mol type="mRNA"
/cultivar="Nackdong"
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1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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CV734112 42 bp mRNA linear EST 05-NOV-2004 FLO--09-F07.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--09-F07, mRNA
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/lab_host="E.coli SOLR"
/lab_host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplancae, Streptophyta; Embryophyta; Foaceae, BEP
clade, Ehrhartoideae, Oryzae, Oryza,
1 (bases 1 to 42)
1 (bases 1 to 42)
1 (kim,J.K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., X., and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                     /mol type="mrNA"
/culTivar="Nackdong"
/db xref="teaxon:39947"
/clone="FLO-09-B08"
/tissue type="flower"
/lab_host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
                                                                                                                                                                                                 /notes="Vector: pBluescript SK(+); Site 1: EcoRI, Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with XhoI site."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongjin, Kyeongji, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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     organism="Oryza sativa (japonica cultivar-group)"
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100.0%; Pred. No. 2e+02;
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100.0%; Pred. No. 2.
... 0; Mismatches
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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-F07"
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Matches 35; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae;

Li (bases 1 to 42)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/db_xxef=taxon:39947"
/db_xxef=taxon:39947"
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/tissuc_type="flower"
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/clone lib="Rice flower lambda phage cDNA library (FLO)"
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Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5, end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzeae; Oryza.

(bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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FLO--09-B08.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--09-B08, mRNA
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sativa (japonica cultivar-group) cDNA clone FLO--08-L13, mRNA
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Location/Qualifiers
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Oryza sativa (japonica cultivar-group)
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Matches 35; Conserv
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

CV733938/c LOCUS RESULT 316

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FEATURES

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TITLE JOURNAL COMMENT

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ACCESSION VERSION KEYWORDS

GSS 22-DEC-2005

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/mol_type="genomic_DNA"
/cultivar="Chiifu"
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Class: BAC ends.
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Chuang, C.K., Chen, M.Y., Liu, M.L., Hsu, M.C., Yang, K.T., Fan, Y.H.,

Lin, J.H., Liu, C.C., Huang, C.H., Chen, Y.C. and Lin, D.T.

Porcine testis EST project

Unpublished (2005)

Contact: Mu-Chiou Huang

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Department of Animal Science, National Chung-Hsing University

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Fax: 886 4 22870613 (ext.) 239

Email: mchang@mail.nchu.edu.tw

The EST project for testis from Duroc was granted by Council of

Agriculture, Taiwan, Material with normal function was tested and
heat stress experiments of animals were conducted by Divisions of
Biotechnology and Animal Resources, Animal Technology Institute

Taiwan (ATIT). Library was constructed and EST clones were

sequenced by Graduate Institutes of Veterinary Microbiology and
Department of Animal Science, National Chung-Hsing University.

Bioinformatic work was conducted by a network from ATIT, National
Cheng-Kung University, and Chung-Hua University. The sequences

scolled and alt_trimmed with phred v0.020425.c. Vector identified
and masked by Gross_match. Sequences were cleaned of vector,
adaptors and repetitions.

Plate: 28 row: Any and chung-Hua Diversity.

Plate: 28 row: Any and chung-Hua Diversity.

Plate: 28 row: Any and chung-Hua Diversity.
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/lab_host="DH10B (Life Technologies)"
/clone_lbb="porcine testis cDNA library II"
/note="Organ: testis cDNA library II"
/note="Organ: testis, Vector: pSPORT1; Site_1: NotI;
Site_2: Sall; Material with normal function was tested and heat stress experiments of animals were conducted by Divisions of Biotechnology and Animal Resources, Animal Technology Institute Taiwan (ATIT): First strand cDNA was synthesized by using nick translational replacement of the mRNA. Double-strand cDNA was added with Sall adapter, then digested with NotI and cloned into the NotI and Sall sites of pSPORTI vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi;
Laurasiatheria; Cetartiodactyla; Suina; Suidae;
PDUts2028G11 Porcine testis cDNA library II Sus scrofa cDNA clone PDUts2028G11 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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100.0%; Pred. No. 2e+02;
iive 0; Mismatches 0; Indels
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/mol_type="mRNA"
/strain="Duroc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9823"
/clone="PDUts2028G11"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seg primer: T7 promoter primer
High quality sequence stop: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                        CX058845
CX058845.1 GI:84134987
EST.
                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                      Sus scrofa (pig)
Sus scrofa
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Best Local Similarity
Matches 35; Conserv
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Bource

FEATURES

RESULT 319 DU835485/c

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Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Supernyota; Viridiplantae; Streptophyta; Euchicotyledons;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaces; Brassica.

El (bases 1 to 42)

Yang, T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,

Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,

Hahn,J. H. and Park,B.S.

End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team 43 bp mRNA linear EST 10-JUN-2005 TAC21610_plka, mRNA sequence. ö Email: pbeom@rda.go.kr BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone Ludels, Renauld, H., Berriman, M., Murphy, L., Yeats, C.A., Weir, W., Rerhornou, A., Aslett, M., Bishop, R., Bouchier, C., Cochet, M., Coulson, R., M. R., Erser, A., Cronin, A., de Villiers, E., Fraser, A., Fosker, N., Gardner, M., Goble, A., Griffiths-Jones, S., Harris, D.E., Karzer, R., Larke, N., Lord, A., Maser, P., McKellar, S., Mooney, P., Morton, F., Meney, V., Oveil, S., Price, C., Quaill, M.A., Rabbinowitsch, E., Rawlings, N. D., Rutter, S., Saunders, D., Seeger, K., Shah, T., Squares, R., Squares, R., Walker, A.R., Woodward, J., DUB35485 42 bp DNA linear GSS 22-DEC-2(KBrS016M05R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS016M05, genomic survey sequence. /sub_species="p&kinensis"
/db_xref="taxon:51351"
/clone="KBrS016M05"
/lab_host="E. coli DH10B"
/clone_lib="KBrS. Brassica rapa Sau3AI BAC library"
/note="vector: pCUGIBACI; Site_1: Sau3AI, Brassica rapa spekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB." Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae; Gapa ö organism="Brassica rapa subsp. pekinensis" 1.3%; Score 35; DB 1; Length 42; 100.0%; Pred. No. 2e+02; ative 0; Mismatches 0; Indels National Institute of Agricultural Biotechnology 225 Seodun-Dong, Suwon, 441-707, Korea Tel: +82-31-299-1670 2709 АВАВАВАВАВАВАВАВАВАВАВАВАВАВАВАВА 2743

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Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                          mRNA sequence.
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BG028362
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ORGANISM
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ALSB7884 BP Chicken Brain Library Gallus gallus cDNA clone
ROSO64G06, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                              ö
Dobbelaere, D.A.E., Langsley, G., Rajandream, M.-A., McKeever, D., Shiels, B., Tait, A., Barrell, B. and Hall, N.
The genome of the host-cell transforming parasite Theileria annulata and a comparison with T. parva
Unpublished (2005)
Contact: Pain A
The Pathogen Sequencing Unit
The Wellcome Trust Sanger Institute
Genome Campus, Call 18A, UNITED KINGDOM
Piroplasm cDNA library: Frank Katzer and Brian Shiels, Division of
Veterinary Infection and Immunity, ICM, University of Glasgow, UK.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Email: frazer.murray@bbsrc.ac.uk
GCGGCCGCTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                     /db_xref="taxon:5874"
/clone="TAC21c10_plka"
/dev_stage="picoplasm"
/lab_host="Bos taurus (cow)"
/clone lib="Theileria annulata piroplasm"
/note="country: Turkey:Ankara"
                                                                                                                                                                                                                                                                                                                                                                                         1.3%; Score 35; DB 1; Length 43; 100.0%; Pred. No. 2e+02; Ve 0; Mismatches 0; Indels
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1.3%; ccc. -., 2e+
Best Local Similarity 100.0%; Pred. No. 2e+
Matches 35; Conservative 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS064G06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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BP Chicken Brain Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL587884.1 GI:13192918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (chicken)
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AL587884/c
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TITLE
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                                    TITLE
                                                                                     COMMENT
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Clonetech (*6854-1)"
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/ organism="Homo sapiens"

mol_type="mRNA"

/db_xref="taxon:9606"

/db_xref="taxon:9606"

/clone="TMAGE:4389940"

/tissue_type="osteosarcoma, cell line"

/tab.host="bH108 (phage-resistant)"

/clone_lib="NHH MGC 96"

/note="organ: bone; Vector: pCMV-SPORT6; Site_l: NotI;

Site_2: Sall; Cloned unidirectionally; oligo-dT primed.

Average insert size 1.533 kb. Library enriched for full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG028362 43 24-JAN-2001
602295420F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4389940 5',
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I (bases 1 to 43)

S NIH-MGC http://mgc.nci.nih.gov/.

INIH-MGC http
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                            Gaps
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Query Match 1.3%; Score 35; DB 1; Length 43; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 35; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /uzer="IMAGE:521376"
/tissue_type="leukocyte"
/lab_host="NH108"
/lab_host="NH108"
/clone lib="NH108"
/clone lib="NH MCC:118"
/note="Vector: pcNv-SpORT6; Site_1: Not1; Site_2: EcoRV
/clone lib="NH MCC:118"
/note="Vector: pcNv-SpORT6; Site_1: Not1; Pite_2: EcoRV
/clone lib="NH Rource leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
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7LEAF--08-123.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--08-123, mRNA
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 43)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIISI row: a column: 09
High quality sequence stop: 43.
Location/Qualifiers
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongln, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                           Hominidae; Homo.

1 (bases 1 to 43)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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Location/Qualifiers
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Best Local Similarity 100.
Matches 35; Conservative
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CF302744/c
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/.vs.ur.au. - vs.u. mann.
/mol type="mRNA"
/cultivar="Nackdong"
/db.xref="Laxon:3994"
/clone="JEAF--09-123"
/tissue_type="leaf"
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/clone="lib="Rice leaf plasmid cDNA library II (7LEAF)"
/none="Vector: pCR4-TOPO; Site 1: ECORI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Nahm B.H.
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Boinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@pio.myongji.ac.kr.
Location/Qualifiers
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/dev stage="14 days after germination"
/lab_hosts=E.coli DH10B"
/clone lib="#clMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 bp mRNA linear EST 18-AUG-20
JMT-03-J17.gl AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT-03-J17, mRNA sequence.
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'organism="Oryza sativa (japonica cultivar-group)"
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Pred. No. 2e+02;
--rohem 0; Indels
                                                                                                                                                                                                                                                                                                                                            Length 43;
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Le Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
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100.0%; Pred. No. 2.
10.0%; Mismatches
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/clone="JMT--03-J17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/cultivar="Nackdong"
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Matches 35; Conservative
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35; Conservative
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/dev_stage="developing endosperm tissue 10, 12, 15 dpa

/dev_stage="developing endosperm tissue 10, 12, 15 dpa

/days_post_anthesis"

/lab_host="DH108 (Life Technology)"

/clone_lib="Barley EST endosperm library"

/note="Vector: ZipLox; Site_1: Sal I; Site_2: Not I; mRNA

was prepared from endosperm tissues of the barley cultivar

Himalaya. CDNA was synthesised from pooled 10, 12, and 15

dpa endosperm using Not I-oligo(dT)18 primer/adapter

(Pharmacia Blotech), and then ligated to the Sal I-Not I

site of ZipLox vector (Life Technology) after adding a

Sal I-XhO I adapter (Stratagene). Constructed by Shahjahan

Ali and Bill Taylor."
                                                EST 24-AUG-2004
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                                                                                                                                                                                  Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bokaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Pooideae; Triticeae; Hordeum.
1 (bases I to 43)
Ali, S. Holloway, B. and Taylor, W.C.
Normalisation of cereal endosperm EST libraries for structural and functional genomic analysis
Flant Mol. Biol. Rep. 18, 123-132 (2000)
Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                            CV062138

SNEL76g12 Barley EST endosperm library Hordeum vulgare subsp.
vulgare cDNA clone BNEL76g12 5' similar to Unknown Function, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Division of Plant Industry.
CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
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/cultivar="Himalaya"
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 61 2 6246 5223/
Fax: 61 2 6246 5000
Email: Bill.Taylor@csiro.au
Seg primer: M13 reverse primer
High quality sequence stop: 43.
Location/Qualifiers
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/db_xref="taxon:112509"
/clone="BNEL76g12"
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Best Local Similarity 100.0
Matches 35, Conservative
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CV724539/c
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RESULT 326
CV062138
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

El (Dases I to 43)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs

U Unpublished (2003)

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:39947"
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/clone="148alt--01-021"
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/clone_lib="S.coli treated rice leaf lambda phage cDNA
library (148alt)"
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/mol_type="mRNA"
/cultivar="Nackdong"
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Location/Qualifiers
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/clone="14Salt--01-M23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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LOCUS
DEFINITION
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

El (Bases I to 43)
El (Asses I to 43)
El (Man,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongdi University
Vongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                   43 bp mRNA linear EST 04-NOV-2004 [145alt-01-N04.gl Salt treated rice leaf lambda phage cDNA library [145alt) Oryza sativa (japonica cultivar-group) cDNA clone CV724969 CV724969.1 GI:55412593
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                /dev stage="Left" days after gernimation"
/lab_host="E.coli SOLR"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14salt)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xhoi, Leaf was inneubated at 4 (360uW/m-2sec-1) for 2hrs.
CDNA was inserted into lamba Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
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/tissue_type="loaf"
/dev stage="14 days after gernimation"
/lab_host="E.coli SOLR"
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                                                                                                                                                                                                                                               0; Indels
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1.3%; Score 35; DB
Best Local Similarity 100.0%; Pred. No. 2e+
Matches 35; Conservative 0; Mismatches
    tissue_type="leaf"
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Best Local Similarity
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RESULT 330 CV725127/c

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Oryza sativa (japonica cultivar-group)

ISM Oryza sativa (japonica cultivar-group)

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryzea

I (bases to 43)

RS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Clade; Ehrhartoideae; Oryzeae; Oryza.

Stim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S. I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, MyongJi University
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43 bp mRNA linear EST 04-NOV-2004
14Salt--02-K02.bl Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-K02, mRNA sequence.
145alt--02-A20.bl Salt treated rice leaf lambda phage cDNA library (145alt) Oryza sativa (japonica cultivar-group) cDNA clone CY725127
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/dev_stage="14 days after gernimation"
/lab_host="E.coli SOLR"
/clone_lib="Salt_treated rice leaf lambda phage cDNA
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/mol_type="mRNA"
/cultivar="Nackdong"
/db xackdong.
/db xacm:39947"
/clone="14Salt--02-A20"
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CV725506.1 GI:55413130
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Best Local Similarity 100.0
Matches 35, Conservative
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Best Local Similarity 100.
Matches 35; Conservative
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CV725720/c
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AUTHORS
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzeae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                           /note="Vector: pBluescript SK(+), Site 1: EcoR1, Site 2: XhoI; Leaf was incubated at 4 C(360uM/\overline{m}-2sec-1) for 2\overline{h}rs, CDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoR1 and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Yongin, KyeongJi, Korea
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/ Organism="Oryza sativa (japonica cultivar-group)"
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// lab_host="E.coli SOLR"
// lab_host="E.coli SOLR"
// clone=_lib="Salt treated rice leaf lambda phage cDNA
library (145alt)"
                                                                                                               Gaps
                                                                                                        'organism="Oryza sativa (japonica cultivar-group)"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
_Location/Qualifiers
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Best Local Similarity 100.
Matches 35; Conservative
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DB 1; Length 43;

1.3%; Score 35;

Query Match

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Oryza sativa (japonica cultivar-group)

Ewlaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatcphyta; Magnollophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 43)

Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. - K. and Nahm, B. H.

Large-excale Sequencing Analysis of Rice ESTs
Unpublished (2003)

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Email: bhnahm@ggblo.com, bhnahm@bio.myongji.ac.kr.
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/culone="145alt--02-P03"
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XhOI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni_ZAP KR vector at 5' end
with EcoRI and 3' end with XhOI site."
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43 bp mRNA linear EST 04-NOV-2004
145alt--02-P03.gl Salt treated rice leaf lambda phage cDNA library
(145alt) Oryza sativa (japonica cultivar-group) cDNA clone
145alt--02-P03, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
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                               Indels
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0;
                                                                                     2709 ААААААААААААААААААААААААААААААА
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CV725720.1 GI:55413344
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CV726694.1 GI:55414318
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CV726751/c
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clade; Ehrhartoideae; Oryzeae; Oryzaa.

E. (bases 1 to 43)

S. Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs

L. Unpublished (2.03)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Tel: 82 31 321 6355
Email: bhaahm@aggbio.com, bhnahm@bio.myongji.ac.kr.
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Oryza sativa (japonica cultivar-group)
Coryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Gentaci: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Tyongli, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; Leaf was incubated at 4 C(360 \mu/\machine{m}-2 \text{sec}-1) for 2 \text{firs}. CDNA was inserted into landa Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa (japonica cultivar-group)"
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    Location/Qualifiers
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CV726349.1 GI:55413973
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14Salt--04-H13.bl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--04-H13, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

1 (bases 1 to 43)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song S. I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Contact: Nahm B.H.

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Location/Qualifiers
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                                                                                                                    /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; Leaf was incubated at 4 C(360uW/m-2sec-1) for 2hre.cDNA was inserted into lamda Uni-2AP XR vector at 5' end with EcoRI and 3' end with XhoI site."
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/mol type="mRNA"
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100.0%; Pred. No. 2e+02;
ative 0; Mismatches 0; Indels
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Page 133

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/lone_lib="salt treated rice leaf lambda phage cDNA

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Xhoi; Leaf was incubated at 4 (360uM/m-2sec-1) for 2hrs.

CDNA was inserted into lamda Uni-ZAP XR vector at 5' end

with EcoRI and 3' end with XhoI site."
                                                                                                                           Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermarcophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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  14Salt--04-I22.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--04-I22, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                          Genomics and Genetics Institute, GreenGene Blotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yorgin, Kyeongqi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
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/mol_type="mRNA"
/cultivar="Nackdong"
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhOI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hre. CDNA was inserted into lamda Uni-Zh RR vector at 5' end with EcoRI and 3' end with XhoI site."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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//note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xhoi; Leaf was incubated at 4 C(360uM/m-28ec-1) for 2hrs.
CDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with Xhoi site."
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, Y.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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/mol_type="mRNA"
/cultivar="Nackdong"

    .43
/organism="Oryza sativa (japonica cultivar-group)"

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0
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2e+02;
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FLO--01-C09.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-C09, mRNA
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/db xrefa="tackcoing"
/clone="FLO--01.-C09"
/labuost="E.coli Solx"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Wocror: pBluescript SK(+); Site_l: EcoRI; Site_2:
XhoI; cDNA an inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spernatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Xim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Pax: 82 31 321 6355
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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100.0%; Pred. No. 2e+
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   Matches 35; Conservative
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CV728737 1inear EST 05-NOV-2004 FLO--01-D16.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-D16, mRNA
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/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
xhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, KyeongJi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/lab_hogt="E.coli SOLR"
/lab_hogt="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xhoi; cDNA was inserted into lamda Uni-ZAP XR vector at send with EcoRI and 3' end with XhoI site."
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Kim, J. S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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/mol_type="mRNA"
/cultivar="Nackdong"
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/mol type="mRNA"
/culTivar="Nackdong"
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Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches (
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/clone="FLO--01-C11"
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Xho1; CDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with Xho1 site."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 43)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantaa, Streptophyta, Embryophyta, Tracheophyta,
Spermarophyta, Magnollophyta, Liliopaida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
11. 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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FLO--01-J22.b1 Rice flower lambda phage cDNA library (FLO) Oryza
Sativa (japonica cultivar-group) cDNA clone FLO--01-J22, mRNA
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Kim, M.J., Lee, T.H., Shin, Y.C.,
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
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/organism="Oryza sativa (japonica cultivar-group)"
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                             Indels
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            Pred. No.
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/cultivar="Nackdong"
           ilarity 100.0%; P. Conservative 0;
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CV729000.1 GI:55431960
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Matches 35; Conserv
         Best Local Similarity
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CV728887/c
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CV729000/c
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Estativa (japonica cultivar-group)

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryzae;

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,Y.-K., and Nahm B.H.

Large-scale Sequencing Analysis of Rice ESTs

Lupublished (2003)

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Fax: 82 31 321 6355
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/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with Xhol site."
Song, S. I., Kim, J. K., Kim, Y. - K. and Nahm, B. H.
Large-scale Sequencing Analysis of Rice ESTB
Unpublished (2003)
Contact: Nahm B. H.
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Yorgin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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FLO--01-N17.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-N17, mRNA
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/mol_type="mRNA"
/cultivar="Nackdong"
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Location/Qualifiers
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100.0%; Pred. No. ...
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="flower"
/lab_host="E.coli SOLR"
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/cultivar="Nackdong"
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RESULT 346 CV729970/c

ò g LOCUS DEFINITION

ORGANISM

KEYWORDS SOURCE

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

ACCESSION VERSION

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/db xxef="caxon:39947"
/clone="FLO--04-121"
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
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Xhol; DNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with Xhol site."
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/clone lib="rece flower lambda phage cDNA library (FLO)"
/clone lib="recer pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; CDNA was inserted into lamda Uni-ZAP XR vector at 5:
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice EST8
Large-scale Sequencing Analysis of Rice EST8
Uppublished (2003)
Contact: Nahm B.H.
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Tel: 82 31 330 6355
Fax: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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/cultivar="Nackdong"
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/cultivar="Nackdong"
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Location/Qualifiers
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Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 43)
Kim,J.S., Vun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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/lab ho
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                1.3%; Score 35; DB 1; Length 43;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
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    Location/Qualifiers
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                    Query Match
Best Local Similarity 100.(
Matches 35; Conservative
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RESULT 347 CV730586/c

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CV732091 43 bp mRNA linear EST 05-NOV-2004 FLO--06-G15.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--06-G15, mRNA
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/note="Vector: pBluescript SK(+); Site 1: BcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
                       Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Far: 82 31 330 6355
Bmail: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/organism="Oryza sativa (japonica cultivar-group)"

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100.0%; Pred. No. 2e+
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryzea; Oryzea
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Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with Xhol site."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantas Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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FLO--05-111.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--05-111, mRNA
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FLO--04-016.bl Rice flower lambda phage cDNA library (FLO) Cry
8ativa (japonica cultivar-group) cDNA clone FLO--04-016, mRNA
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0, 2e+02;
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Score 35; DB 1; Lengtn wo. Pred. No. 2e+02;
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Location/Qualifiers
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      1.3%; Scor.
100.0%; Pred. No. 20.
... 0; Mismatches
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Pred. No.
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CV731060.1 GI:55435848
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                   Query Match
Best Local Similarity 100.0
Matches 35, Conservative
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Best Local Similarity 100.
Matches 35; Conservative
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VERSION KEYWORDS SOURCE ORGANISM

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clade; Ehrhartoideae; Oryzeae; Oryza.
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/mol type="mRNA"
/mol type="mRNA"
/cultivar="Nackdong"
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/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/hol; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 43)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantea: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Nahm B.H.
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 635
Exax: 82 31 321 635
Email: bhnahm@gpio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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end with EcoRI and 3' end with XhoI site."
                                              1.3%; Score 35; DB 1; Length 43; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
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CV732533/c
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/mol type="mmx" or to the color of the color
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Jun, K.M., Cheong, P.J., Kim, N.J., Lee, T.H., Shin, Y.C., Song, S.I., Jun, K.M., Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Contact: Nahm B.H.
Contact: Nahm B.H.
Contact: Nahm B.H.
Yonghin, Kyeonggi, Korea
Pal 31 310 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bloinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="PLO--07-D21"
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/organism="Oryza sativa (japonica cultivar-group)"

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100.0%; Pred. No. 2e+02;
trive 0; Mismatches 0; Indels
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Oryza sativa (japonica cultivar-group)

Cryza sativa (japonica cultivar-group)

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatcphyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

El (basea 1 to 43)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Unpublished (2003)

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Email: bhnahm@ggblo.com, bhnahm@bio.myongji.ac.kr.
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryzae.

E. (Loases 1 to 43)

S. Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
L Unpublished (2003)
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with XhoI site."
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"

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/organism="Oryza sativa (japonica cultivar-group)"

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Location/Qualifiers
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100.0%; Pred. No. 2e+02;
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/cultivar="Nackdong"
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyra; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

E I (bases 1 to 43)
S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
L Onpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                      EST 05-NOV-2004
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/lab host="B.coli SOLR"
/lab host="B.coli SOLR"
/lone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: BcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at end with EcoRI and 3' end with XhoI site."
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FLO--07-021.bl Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-021, mRNA
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/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                       1.3%; Score 35; DB 1; Length 43;
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
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Matches 35; Conservative 0; Mismatches
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/clone="FLO--07-N05"
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                                                                  Query Match
Best Local Similarity 100.0
Matches 35; Conservative
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CV733143/c
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AUTHORS
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/mol type="mRNA"
/mol type="mRNA"
/cultivar="Nackong"
/db xref="type="flower"
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/fissue [rype="flower"
/lab host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: Ahol; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with Xhol site."
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Yun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Tyonglu, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at end with EcoRI and 3' end with XhoI site."
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                                                                                     Length 43;
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Location/Qualifiers
                                                                                                                              0; Indels
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                                                                                   Query Match 1.3%; Score 35; DB 1; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 35; Conservative 0; Mismatches 0
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Oryza sativa (japonica cultivar-group)
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CV734334.1 GI:55442029
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CV733316/c
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 43)

1 (bases 1 to 43)

2 Kim,JS., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.
Genenics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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CX002408 CX002408.1 GI:56273824
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Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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/dev stage="3 month old normal canine"
/lab_host="XL10 gold"
/clone lib="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site_1:
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/organism="Oryza sativa (japonica cultivar-group)"
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Balija,V.S., Nascimento,L.U. and McCombie,W.R.
Balija,V.S., Nascimento,L.U. and McCombie,W.R.
Bryte from Canis familiaris left cardiac ventricle (dog)
Unpublished familiaris left cardiac ventricle (dog)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
Po Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8884
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/organism="Canis familiaris"
/mol_type="mRNA"
/db xref="taxon:9615"
/sex="Unknown"
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Location/Qualifiers
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Canis familiaris
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EcoRI; Site_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel
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1M0095D02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0095D02 R, genomic survey sequence.
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/note="Vector: PUMP4Znv; Purified genomic DNA from M. musculus C57BL/64 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sciurognathi; Murcidea; Murinae; Mus.

1 (bases 1 to 43)

1 Ubases 1 to 43)

1 Ubun, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

1 Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)
                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                Length 43;
                                                                                                                                                                                                         1.3%; Score 35; DB 1; Length 43;
100.0%; Pred. No. 2e+02;
ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: 0095 row: D column: 02
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0095D02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 43.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ355703.1 GI:10468288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert Length: 10000
Plate: 0095 row: D c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: plasmid ends
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 35; Conserv
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84112, USA
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AZ355703/c
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ORGANISM
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AUTHORS
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TITLE

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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-GOld (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CR762707

40 bp mRNA linear EST 23-SEP-2004
DKFZp469F0617_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
DKFZp469F0617_5', mRNA sequence.
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Nolecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact
RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469F0617
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pongo pygmaeus mRNA (Ansorge, W., Krieger, S., Regiert, T., et al.)
Unpublished (2004)
Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Pongo.
1 (bases 1 to 40)
Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,F
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                            Score 35; DB 1; Length 43; Pred. No. 2e+02; 0; Mismatches 0; Indels
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                                                                                                                                                                               Query Match 1.3%; Score 35; DB Best Local Similarity 100.0%; Pred. No. 2e+Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pongo pygmaeus"
/mol type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp469F0617"
/tissue_type="kidney"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pongo pygmaeus (orangutan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CR762707.1 GI:52600068
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CV066153.1 GI:51529330
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KEYWORDS
SOURCE
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Bombyx mori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue types"endosperm"
/dev_stage="endosperm"
/dev_stage="endosperm"
/dev_stage="endosperm"
/dev_stage="endosperm"
/lab_host=="bH10B (Life Technology)"
/lab_host=="bH10B (Life Technology)"
/clone_lib="Wheat EST endosperm library"
/clone_lib="Wheat EST endosperm lissues of the "heat cultivar was prepared from endosperm tissues of the "heat cultivar Hartog. cDNA was synthesised from pooled 6, 8, and 10 dpa endosperm using Not I-oligo(dT)18 primer/adapter
(Pharmacia Biotech), and then ligated to the Sal I-Not I site of _zipLox vector (Life Technology) after adding a Sal I-Xho I adapter (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group)

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 36)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                              1 (bases 1 to 43)
All, 5, Holloway, B. and Taylor, W.C.
Normalisation of cereal endosperm EST libraries for structural and functional genomic analysis
Plant Mol. Biol. Rep. 18, 123-132 (2000)
Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Pooideae, Triticeae, Triticum.
                                                                                                                                                                                                                                                                                                                   Division of Plant Industry.

SIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia Tels: 61 2 6246 5223

Fax: 61 2 6246 5000

Email: Bill.Taylor@csiro.au
Seq primer: Mil reverse primer
High quality sequence stop: 43.

Location/Qualifiers
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongGi, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Hartog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group)
                      Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:4565"
/clone="WNEL30e11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CV725617.1 GI:55413241
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CV725617/c
                                                  ORGANISM
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AUTHORS
TITLE
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycoidea; Bombycoidea; Bombycoidea; Bombyx.

I (bases I to 41)
Zhang, Y. Z., Xu, J., Chen, J., Wang, D., Nie, Z.M., Lv, Z.B., Jiang, C.Y., Liu, L., Song, L., He, P.A., Chen, F. and Wu, X. F.

The full-length cDNA library construction of silkworm pupae (Bombyx mori) and large-scale sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DY231388 41 bp mRNA linear EST 03-FEB-2006 EST02142 BmP Bombyx mori cDNA clone BmpK_K44_2005-10-30_WD-051030 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; Leaf was incubated at 4 C(360wM/m-2sec-1) for Zhrs. cDNA was inserted into lamda uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="whole pupae body but for the skin"
/dev_stage="metaphase"
/clone_lib="Bmp"
/note="vector: pHelix; Site_I: Hind II; The synthesis of
double-stranded cDNA from mRNA was based on the method
described by Gubler and Hoffman. The obtained cDNA were
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                                                                                                                                                                                                                                                                                /tissue_type="leaf"
/dev btage="14 days after gernimation"
/lab host="E.coll SOLK"
/clone_lib="Salt treated rice leaf lambda phage cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                      /organism="Oryza sativa (japonica cultivar-group)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 36;
                                                       bhnahm@bio.myongji.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="0ingsong-Haoyue"
/db_xref="taxon:709!"
/clone="BmpK K44 2005-10-30_WD-051030"
/sex="male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 TCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%; Score 34.4; DB 1
97.2%; Pred. No. 2e+02;
ative 0; Mismatches
                                                                                                                                                                 /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-M17"
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Fax: 86 571 86841198
Email: yaozhou@chinagene.com
Seq primer: M13 Forward
High quality sequence stop: 41
POLYA=Yes.
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/organism="Bombyx mori"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: brahm@ggbio.com, bhne
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                               library (14Salt)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DY231388.1 GI:86465516
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Best Local Similarity 97.2
Matches 35; Conservative
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EST
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Taukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .34

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/mol_type="mRNA"
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                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                     CJ038300 tull-length enriched swine cDNA linear EST 22-OCT-2004 CJ038300 full-length enriched swine cDNA library, adult uterus Sus scrofa cDNA clone UTR01C110090 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uenishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., Okumura, N., Hamasima, N. and Awata, T.
PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319 Low quality bases were trimmed based on the quality values.

Location/Qualifiers
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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ligated into the plasmid vector pHelix and subsequently the ligation product was tranformed into B.coli competent cells TG1. At last, the recombinant clones were screened by blue-white plaques."
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                                                                                                      1.3%; Score 34.4; DB 1; Length 41;
97.2%; Pred. No. 2.1e+02;
tive 0; Mismatches 1; Indels
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                                                                                                                                                 Conservative
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                                                                                                                         Best_Local Similarity
Matches 35; Conserv
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LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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COMMENT
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Xhoi; Leaf was incubated at 4 c(36OuM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
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14Salt.-03-M05.bl Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt.-03-M05, mRNA sequence.
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                                                                                                                                                                Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
of Styceongji, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 34)
Kim,J.S., Uun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 34)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-Scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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    .34
/organism="Oryza sativa (japonica cultivar-group)"

(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--01-A16, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2709 ААААААААААААААААААААААААААААААА
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CV726231.1 GI:55413855
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                                                                                                                            RESULT 370
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JOURNAL
COMMENT
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SM Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.

E 1 (bases 1 to 34)

S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Lunpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 11 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14Salt--04-J17.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--04-J17, mRNA sequence.
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                                                                                                                                                                                                                                                                            /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: ShoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. CDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
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                                                                                                                         /db_xref="taxon:39947"
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/clone_11b=E.coli SOLR"
/lab_ray (14Salt treated rice leaf lambda phage cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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/mol type="mRNA"
/culcivar="Nackdong"
/db xref="taxon:39947"
/clone="14Salt--04-J17"
/tissue_type="leaf"
/dev_stage="leaf"
/lab host="E.coli SOLR"
/lab host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
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                                                              'organism="Oryza sativa (japonica cultivar-group)"
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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Location/Qualifiers
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                                                                                  /mol_type="mRNA"
/cultivar="Nackdong"
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Device sativa (japonica cultivar-group)

Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryz
                                                                                                                                                                                                                                                                                                                        34 bp mRNA linear EST 04-NOV-2004 (14Salt--05-G14.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--05-G14, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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/tissue_type="leaf"
/dev_stage="14 days after gernimation"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)
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/cultivar="Nackdong"
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Query Match 1.2
Best Local Similarity 100.
Matches 34; Conservative
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XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhatroideae; Oryzeae; Oryza.

1 (bases 1 to 34)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Tyongli, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
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|mol_type="mRNA"
|cultivar="Nackdong"
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0. 2e+02;
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Location/Qualifiers
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100.0%; Pred. No. 2e+C
:ive 0; Mismatches
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Best Local Similarity 100.0
Matches 34; Conservative
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CV730644 34 bp mRNA linear EST 05-NOV-2004 FLO--04-E17.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--04-E17, mRNA
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/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_l: EcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5, end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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/organism="Oryza Bativa (japonica cultivar-group)"

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DB 1; Lenc.
3. 2e+02;
0; Indels
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    Location/Qualifiers
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                           ch 1.2%; Score 34; DB 1 Similarity 100.0%; Pred. No. 2e+34; Conservative 0; Mismatches
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Tel: 801 585 5606
Fax: 801 585 7177
                                                                    Similarity
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84112, US
                                           Query Match
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AZ465350/c
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Minoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae.

El (Bases I to 34)
El (Bases I to 34)
El (Man, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H.

Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B. H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 312 6155
Email: bhanhm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxxxx:39947"
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/clone lib="Rice flower service SK(+); Site 1: BcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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/lab host="E.coli SOLR"
/lab host="E.coli SOLR"
/loof="lab"erice flower lambda phage cDNA library (FLO)"
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XhoI; cDNA was inserted into lamda Uni=ZAP XR vector at 5'
            Kim, J.S., Jun, K.M., Cheong, P.J., Kim, W.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
YongIn, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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FLO--09-K11.g1 Rice flower lambda phage cDNA library (FLO) Oryza
Bativa (japonica cultivar-group) cDNA clone FLO--09-K11, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 34;
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Location/Qualifiers
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2e+02;
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100.0%; Pred. No. 2e+
tive 0; Mismatches
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/db_xref="taxon:39947"
/clone="FLO--09-K11"
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/cultivar="Nackdong"
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Best Local Similarity 100.
Matches 34; Conservative
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Imboratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114 |gb|A123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
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1M0275012F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0275012 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (Bases 1 to 34).

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Bondaern, B., Dedersen, T., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
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end with EcoRI and 3' end with XhoI site.
                                                                  Length 34;
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                                                           1.2%; Score 34; DB 1;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches
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Insert Length: 10000 Std Error: 0.00
Plate: 0275 row: 0 column: 12
Seg primer: GGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 34.
Location/Qualifiers
                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
Mus musculus
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RESULT 378
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34 bp DNA linear GSS 05-OCT-200
1M0339P09R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 34)
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                          Gaps
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                                                     Length 34;
                                                                                                          Indels
and selected for ampicillin resistance."
                                               1.2%; Score 34; DB 1; Le
100.0%; Pred. No. 2e+02;
ative 0; Mismatches 0;
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Fax: 801 585 7177

Email: ddunm@genetics.utah.edu

Inmert Length: 10000 Std Error: 0.00

Plate: 0339 row: P column: 09

Seq primer: CACACAGGAAAACAGCTAATGACC
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C578L/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0339P09"
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Location/Qualifiers
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                                          Query Match
Best Local Similarity 100.0
Matches 34; Conservative
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TITLE

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciuropanthi; Muroidae; Murinae; Mus.
E (Dases 1 to 34)
Sunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ809643 34 bp DNA linear GSS 20-FEB-2001 2M0073C14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic close UUGC2M0073C14 R, genomic survey sequence.
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/clone lib="Mouse 10kb plasmid UGGCIM library"
/note="Vector: PWD42ry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                   Gaps
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                                                            Query Match 1.2%; Score 34; DB 1; Length 34; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 34; Conservative 0; Mismatches 0; Indels
and selected for ampicillin resistance."
                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: C column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 34.
Location/Qualifiers
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/clone="UUGC2M0073C14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ809643.1 GI:12976135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnalolophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

El (bases i Lo 35)
El (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /aub species="rekinensis"
/db xref="taxon:5131"
/clone="KBrB036016"
/lab host="E.coli DH10B"
/clone lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pcUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CV730365 15-NOV-2004 ELO-03-001.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO-03-001, mRNA
                Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons;
rosids; eurosids II, Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                                                                                                                                                                              Yang T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/culTivar="Chiffu"
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                                                                                                                                                                                                                                                                                                                                                                                                                  National Institute of Agricultural Biotechnology 225 Secdun-Dong, Suwon, 441-707, Korea 11 + 82-31-299-1670 Fax: +82-31-299-1672 Email: pbeom@rda.qo.kr
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100.0%; Pred. No. 2e+02;
ative 0; Mismatches 0;
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Class: BAC ends.
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KBEB036016R KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB036016, genomic survey
sequence.
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Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: pbecom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                      DUB15285
KBrS016F23F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS016F23, genomic survey
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Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.Y.
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J. H. and Park, B.S.
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/clone="KBrS016F23"
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/clone="E. coli DH10B"
/clone=lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBACI; Site_1: Sau3AI; Brassica raj
spp_pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
                                                                                                                                Gaps
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Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organisme"Brassica rapa subsp. pekinensis"
|mol_type="genomic DNA"
|cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.2%; Score 34; DB 1; Length 34; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 34; Conservative 0; Mismatches 0; Indels
                                                         1.2%; Score 34; DB 1; Length 34; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Pax: +82-31-299-1672
                                                                                                                                                                                                2709 ААААААААААААААААААААААААААААААА
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Class: BAC ends.
Loaction/Qualifiers
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DX037933.1 GI:84732230
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RESULT 380

ò a DX037933

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FEATURES

REFERENCE AUTHORS

DEFINITION

RESULT 379

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Matches

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Oryca sativa (japonica cultivar-group)
Oryca sativa (japonica cultivar-group)

Oryca sativa (japonica cultivar-group)

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Orycae; Orycae;
Clade; Ehrhartoideae; Orycae; Orycae;
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim, Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJn, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@glbio.com, bhnahm@bio.myongji.ac.kr.
                           CF330901 42 bp mRNA linear EST 18-AUG-2003 NACL--06-N01.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--06-N01, mRNA
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42 bp mRNA linear EST 04-NOV-2004
14Salt--03-K15.gl Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-K15, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa (japonica cultivar-group)"
/mol type="makNA"
/cultivar="NackOng"
/b xref="texon:39947"
/clone="NACL--06-N01"
/cissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptrophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Rice callus plasmid cDNA library (NACL)" /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K. Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Matches 34; Conservative
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/ Mol type="mRNA"
/ Cultivar="Nackdong"
/ db xref="texon:3994"
/ clone="14ROOT--02-G07"
/ tissue type="root"
/ dev stage="14 days after germination"
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/ clone lib="Rice root plasmid cDNA library (14ROOT)"
/ clone lib="Rice root plasmid cDNA library (14ROOT)"
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                                        /mol type="mmx"
/mol type="mx"
/mol type="mx"
/mol type="mx"
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/cultivar="wackdong"
/cultivar="wackdong"
/cultivar="wacknon:3947"
/cultivar="wacknon:3947"
/cultivar="wacknon:3947"
/cultivar="wacknon:30x"
/cone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="vector: pBluescript SK(+); Site 1: Ecohi; Site 2:
Xhoi; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 bp mRNA linear EST 14-AUG-2003 14ROOT--02-G07.gl Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-G07, mRNA
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-Gcale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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    .35
/organism="Oryza sativa (japonica cultivar-group)"

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. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                   1.2%; Score 34; DB
100.0%; Pred. No. 2.1
ive 0; Mismatches
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CF291807.1 GI:33660840
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Best Local Similarity
Matches 34; Conserv
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Matches 34; Conserv
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LOCUS DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Query Match

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Bource

FEATURES

TITLE JOURNAL COMMENT

AUTHORS REFERENCE

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CF331029.1 GI:33810274
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  1.2%;
                   94.68;
  Query Match
Best Local Similarity 94.6
Matches 35; Conservative
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Best Local Similarity
Matches 35; Conserv
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/db_xref="teaxon:51351"
/clone="KBE0407815"
/lab_host="E.0401 DH10B"
/clone lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCu(GBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DX045841 1inear GSS 10-JAN-2006 KBrB047E15F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB047E15, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                     /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Exx: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
                                                                                                                                           /db_xref="taxon:39947"
/clone="lasalt--03-K15"
/tissue_type="leaf"
/dev_stage="14 days after gernimation"
/lab.host="R-coli SOLR"
/clone_lib=="Salt treated rice leaf lambda phage cDNA
library (14Salt)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                Organism="Oryza sativa (japonica cultivar-group)"
mol type="mRNA"
'cultivar="Nackdong"
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0
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/organism="Brassica_rapa subsp. pekinensis"
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 42;
2.3e+02;
hes 0; Indels
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/cultivar="Chiifu"
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Class: BAC end
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Best Local Similarity
Matches 34; Conserva
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DX045841/c
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E 1 (bases 1 to 42)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bloinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Eax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                  42 bp mRNA linear EST 05-NOV-2004 (14Salt--06-K03.bl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone L14Salt--06-K03, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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                                                                Gaps
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/clone="14Salt--06-K03"
/tissue type="leaf"
/dev stage="14 days after gernimation"
/ab host="E.coli SOLR"
/clone lib="Salt treated rice leaf lambda phage cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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/mol type="mRNA"
/cultivar="Nackdong"
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Score 33.8; DB 1; Length 41;
Pred. No. 2.3e+02;
0; Mismatches 2; Indels
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Pred. No. 2.3e+02;
0; Mismatches 2;
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Homo sapiens
   36; Conservative
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                                                                                                                                                                                                             mRNA sequence.
BE894837
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     Matches
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                             E 1 (bases 1 to 40)

S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, Kyeonggi, Korea
Tel: 82 31 321 6555
Fax: 82 31 321 6555
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKFZDS6CC0246_r1 S66 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp56GC0246, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:39947"
/clone="NACL--06-P22"
/tissue_type="callus"
/dev stage="rooliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Rice callus plasmid cDNA library (NACL)" /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 42)
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                   organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="DKRZp566C0246"
/tissue_type="kidney"
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/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: Sall"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.2%; Score 33.6; DB 1; Length 40; Best Local Similarity 90.0%; Pred. No. 2.4e+02; Matches 36; Conservative 0; Mismatches 4; Indels
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST (Ottenwaelder, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
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Homo sapiens
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Best Local Similarity
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AL038483
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BE894837 35 bp mRNA linear EST 20-OCT-2000 001434018F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919061 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 72"
/note="Yorgan: Skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 35)

NIH-MGC http://mgc.nci.nih.gov/.

NiH-mdC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Ambystoma mexicanum
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bmail: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9748 row: d column: 06
High quality sequence start: 4
High quality sequence stop: 35.
Location/Qualifiers
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0; Mismatches
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3919061"
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Homo sapiens
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CV724804/c
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TITLE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetophyta; Gnetopsida; Gnetales; Gnetaceae; Gnetum.
E 1 (bases 1 to 35)
S Brenner, B.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
L Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mana"
/db_xref="taxon:g826"
/db_xref="taxon:g826"
/tisue_type="rail Blastema"
/cell type="rail Blastema"
/coll type="rail Blastema"
/colne_lib="6-Day Axolot! Tail Blastema" (6DAxBL)"
/clone_lib="6-Day Axolot! Tail Blastema" (6DAxBL)"
/note="Vector: pCWNSport6; Site_l: Not1; Site_2: Sall;
/noremalized cDNA plasmid library prepared by_Invitrogen.
Size fractionated mRNA was polydT primed and cloned into
Not1-Sall site of pCMVSport6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.67 kB.
TAG_LIB=6DAxBL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DN955388 135 bp mRNA linear EST 04-MAY-2005 it87b05.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
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Habermann, B., Bebin, A.G., Herklotz,S., Volkmer,M., Eckelt,K., Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M. An Ambystoma mexicanum EST sequencing project: Analysis of 17,352 expressed sequence tags from embryonic and regenerating blastema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                        Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
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1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                    Pfotenhauerstrasse 108,01307 Dresden, Germany Tel: 0049 351 210 2620 Eax: 0049 351 210 1489 Email: tanakami-domi-coloum: Helate: BL284A row: 08 column: Helate: BL284A row: 08 column: Location/Qualifiers
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/organism="Ambystoma mexicanum"
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/db_xref="taxon:3382"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 516 367 8874
Email: mccombie@cshl.org
Seg primer: -21M13UnivRev.
Location/Qualifiers
                                                                                                         Genome Biol. (2004) In press
Contact: Elly M. Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DN955388.1 GI:63027526
                                                                                             cDNA libraries
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CV724804 145alt treated rice leaf lambda phage CDNA library (145alt) Oryza sativa (japonica cultivar-group) CDNA clone 145alt--01-J08, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE894682 36 bp mRNA linear EST 20-OCT-2000 c01435925F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920911 5',
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/note="Organ: mature, unfertilized reproductive strobili; Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date: Completed 02/11/02, submitted for sequencing 02/12/02. Library: Stratagene ZAP Express CDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts. Sample: NYBG accession number #436/84"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 36
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Clone="IndAGE:3920911"
// Clone="IndAGE:3920911"
// Clone="IndAGE:3920911"
// Clone="Inb="NIH MGC 72"
// Orde="Organ: skin; Vector: pcMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9753 row: a column: 08
High quality sequence stop: 30.
Location/Qualifiers
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1 (bases 1 to 36)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-AdC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                            Score 33.4; DB 1; Length 35;
Pred. No. 2.2e+02;
0; Mismatches 1; Indels
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97.1%;
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Best Local Similarity 97.1
Matches 34; Conservative
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                                                                                     Oryza sativa (japonica cultivar-group)

Sukaryota, (japonica cultivar-group)

Eukaryota, (japonica cultivar-group)

Eukaryota, (japonica cultivar-group)

Eukaryota, (japonica cultivar-group)

Spermatophyta; Magnoliophyta; Enliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryzea.

(jade; Ehrhartoideae; Oryzeae; 
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Contact: Walbot V
Contact: Walbot V
Spacement of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 2227
Fax: 650 728 8221
Email: Walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4012010 row: G column: 11
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/dev_stage="14 days after gernimation"
/lab_host="scoli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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/clone="14Salt--01-J08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/cultivar="Nackdong"
CV724804.1 GI:55412428
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CZ912531/c
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/Local lib="4012 - RescueMu Grid BB"
/Clone lib="4012 - RescueMu Grid BB"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BanHI; Site2: BglII; RescueMu is a 4-9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transposon units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/. BB was grown at UC Berkeley in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII; and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grid
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
EMAG end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS007101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica rapa subsp. pekinensis
Bruszyota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (Bases I to 36)
Yang T.J. Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DU830895 S. D. DNA linear GSS 22-DEC-20
KBrS007101F KBrS, Brassica rapa Sau3A1 BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS007101, genomic survey
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0
                                                                                                                         /mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissuc_type="leaf"
/dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rapa subsp. pekinensis"
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/db_xref="taxon:51351"
/clone="KBrS007101"
/lab_host="E. coli DH108"
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/cultivar="Chiifu"
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                                                                                              organism="Zea mays"
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/organism="Brassica
                                    location/Qualifiers
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transposon-tagged
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Class: BAC ends.
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/sex="Male"
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Best Local Similarity
Matches 34; Conserv
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AZ824309/c
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37 bp mRNA linear EST 04-SEP-2003
DKFZD566M083 r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 37)
Kim,J.S., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Rim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site_l: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae, Homo.

1 (bases 1 to 37)

Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/dob_xref="taxon:9606"
/clone="DKPEp566M083"
/tissue_type="kidney"
/dob stage="fetal"
/dob stage="fetal"
/lab_host="X1-2blue"
/clone=lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
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                                                                                               Score 33.4; DB 1; Length 36;
Pred. No. 2.3e+02;
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                                                                                                   1.2%; Score 33.4; D. Best Local Similarity 97.1%; Pred. No. 2.3e Matches 34; Conservative 0; Mismatches
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Homo sapiens
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/mol type="makAom"
/mol type="makAom"
/mol type="makAom"
/dolon="Ref="taxon:3994"
/clone="FLO-06-M19"
/lab host="E.Coli SOLR"
/hote="Yector: pBluescript SK(+); Site_1: ECORI; Site_2: Ahol; CDNA was inserted into lamda Uni-ZAP KR vector at 5, end with ECORI and 3' end with XhoI site."
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Contact: Nahm B.H.
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
of Kyeongji, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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Dunn, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0098 row: O column: 17
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 37.
Location/Qualifiers
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    37
    organism="Mus musculus"

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University of Utah Genome Center
University of Utah
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/strain="C578L/6J"
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/clone="UUGC2M0098017"
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Mus musculus
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Query Match
Best Local Similarity
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plssmid UUGCIM library"
/note="Vector: PWD42nr; Purified genomic DNA from M.
musculus C57BL/G/ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dhares/). The DNA
was bylordynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by loopymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gql |4732114|gpl |AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli Xillo-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_l: BamHI; Brassica rapa spp
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Brassica rapa subsp. pekinensis
Brassica, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae; Brassica.
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BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J7 bp DNA linear GSS 10-JAN-2 KBrB068M24F KBrB, Brassica rapa subsp. pekinensis genomic clone KBrB068M24, genomic survey
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Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33.4; DB 1; Length 37; Pred. No. 2.3e+02;
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/mol_type="genomic DNA"
/cultivar="Chiifu"
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225 Seodun Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
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/db_xref="taxon:51351"
/clone="KBrB068M24"
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Class: BAC end
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Best Local Similarity
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AUTHORS
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CF302184 15-AUG-2003 7LEAF--07-H22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-H22, mRNA
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Bhrhartoideae; Oryzeae; Oryzeae; Oryzea.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioschence and Bioinformatics, MyongJi University

Yongli, KyeongJi, Korea

Tel: 82 31 330 6193

Fax: 82 31 3121 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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/mol type="mRNA"
/cultivar="Nackdong"
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                                                                                            Length 37;
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                                                                                            ch 1.2%; Score 33.4; DB 1; Length 3 1 Similarity 97.1%; Pred. No. 2.3e+02; 34; Conservative 0; Mismatches 1; Indels
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Oryza sativa (japonica cultivar-group)
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/clone="7LEAF--07-H22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF302184
CF302184.1 GI:33673945
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CF316791.1 GI:33688552
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Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         sequence
                                                                                                                                            Query Match
Best Local Simil
Matches 34; C
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AZ589726/c
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VERSION
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AUTHORS
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JOURNAL
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SOURCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Enhantoideae; Oryza.

E 1 (bases 1 to 38)
S Kim.J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab_nost="E.coli DH10B"
/clone lib="collADH21-overexpressing transgenic rice plasmid
cDNA library (HD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 31-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCR4-TOPO, Site_1: EcoRI; Callus was treated with ABA(20um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR: mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pneumocystis carinii
Pneumocystis carinii
Bukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
1 (baess 1 to 38)
Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,
Edman, J.C., Kovacs, J. and Cushion, M.
Expressed sequence tags from Pneumocystis carinii
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
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AWJJJ9BS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pneumocystis carinii"
/mol_type="mRNA"
/mol_type="nRNA"
/lab_ref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33.4; DB 1;
Pred. No. 2.4e+02;
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/clone="HD--06-D18"
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Fax: 606 257 1717
Email: staben@pop.uky.edu.
Location/Qualifiers
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1.2%;
Best Local Similarity 97.1%;
Matches 34; Conservative (
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AW333985/c
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AZ589726 13-DEC-2000 1M0398124R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0398124 R, genomic survey sequence.
/note="vector: Lambda ZAP II, Site_1: EcoRI; Site_2: XhoI; P. carinii organisms (3x10e9) from a single rat (99-1-6, sacrificed on 3/17/9) at Cincinnati VA facilities. Trizol extracted RNA. Oligo dT priming, standard conditions described by vendor, Stratagene. Further details see www.uky.edu/Project/Pneumocystis/"
                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                   DR074451 38 bp mRNA linear EST 08-JUN-2005
ik94004.gl Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Ginkgo male leaf (NYBG)"
/note="Organ: leaf, Vector: pBK-CWY; Site_1: XhoI; Site_2:
Eco RI; Stratagene ZAB Express CDNA Synthesis Kit. The
library was size-fractionated to enrich for large
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Pred. No. 2.4e+02;
0; Mismatches 1; Indels
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    .38
    /organism="Ginkgo biloba"

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Ginkgo biloba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:3311"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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DR074451.1 GI:67052436
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GSS.
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Best Local Similarity 97.1
Matches 34; Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil47321141gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
121: 801 S85 5606
Fax: 801 S85 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UANOUD: 14 SERIB 18 bp DNA linear GSS 10-JAN-2006 KBrB066N13F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB066N13, genomic survey sequence.
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                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sclurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                               1 (bases 1 to 38)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von. Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0398 row: I column: 24
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol type="genomic DNA"
/strain="CS7BL/6J"
/db xref="taxon:10090"
/clone="UUGCIM0398124"
   Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DX060574
DX060574.1 GI:84754870
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                               ORGANISM
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VERSION
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SOURCE
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Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicotyledons; cosids; eurosids II; Brassicales; Brassicaces; Brassica.

El (bases 1 to 38)

Syang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.

End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)

Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Aggicultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab.host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
bekinensis var. Chilfu BAC library (KBrB BAC) is provided
hy yong-bon Lim (CMI)!
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                          Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB066N13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HD--10-A16.bl OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--10-A16, mRNA sequence.
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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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1.2%; Score 33.4; DB 1; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | sub_species="pekinensis"
| db_xref="taxon:51351"
| clone="KBrB066N13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/cultivar="Chiifu"
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by Yong-Pyo Lim (CNU)
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Class: BAC ends.
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CF319510
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Ultract Submission

LE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr - The Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on by 8p, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genome survey sequence TET3 end of BAC # BACSIODI2 of RPCI-98 library from Drosophila melanogaster (fruit concent concent concent concentration)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila,
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Indels
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR10D12"
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   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     fly), genomic survey sequence.
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   34; Conservative
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                                                                                                                                           db_xref="taxon:39947"
|Colone="MbD-10-A16"
|/tissue_type="callus"
|/dev_stage="proliferated callus on 2N6 media for 2 weeks"
|/dev_stage="proliferated callus"
|/dev_stage="prolif
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Habbermann, B., Bebin, A.G., Herklotz, S., Volkmer, M., Eckelt, K.,
Habbermann, B., Bebin, A.G., Herklotz, S., Volkmer, M., Eckelt, K.,
Andystcoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
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/db_xref="taxon:8056"
/tifsue_type="Tail Blastema"
/cell_type="regenerating tail blastema"
/colne_lib="6-Day Axolot! Tail Blastema (6DAxBL)"
/note="Wector: pCWYSport6; Site_1: Not!; Site_2: Sall;
/note="Wector: pCWYSport6; Site_1: Not!; Site_2: Sall;
/note-"Went blasmid library prepared by Invitrogen.
Size fractionated mRNA was polydT primed and cloned into
Not!-Sall site of pCMVSport6. Bacterial host is
EMDH108-TONA. Average insert size is 1.67 kB.
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Amphibia, Batrachia, Caudata, Salamandroidea, Ambystomatidae,
                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(10um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
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    ^Arganism="Orryza sativa (japonica cultivar-group)" /mol type="mRNA" /mol type="mRNA" /cultivar="Nackdong"

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Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: BL285D row: 07 column: F
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Ambystoma mexicanum"
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Contact: Elly M. Tanaka
Tanaka Lab
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CDNA library (JMT)"
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

El (Basse I to 40)
El (Basse I to 40)
El (Man,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, KyeongGJ, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gGplo.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                        Hinkton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Kenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: LIESg04.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Asron M. Zorn.
Location/Qualifiers
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 1 (bases 1 to 40)
Workle.E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
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/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.2%; Score 33.4; DB 1; Length 40;
77.1%; Pred. No. 2.4e+02;
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/clone="JWT--06-H01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
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/organism="Xenopus tropicalis"
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                                                                        Contact: Huckle E
Sanger Institute
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Best Local Similarity
Matches 34; Conserv
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/note="Vector: pCR4-TOPO, Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBluescript II SK(+); Site_1: NotI; Site_2: EcoRI; Normalized oligo dT primed cDNA library using poly A+ RNA from mixed embryonic stages of Nematostella vectensis. Cloned directionally into pBluescript II SK(+). Ligated in NotI, EcoRI"
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Technau, U., Rudd, S., Maxwell, P., Gordon, P.M.K., Saina, M.,
Technau, U., Rudd, S., Maxwell, P., Gordon, P.M.K., Holstein, T.W.,
Ball, B. E. and Miller, D. J.
Maintenance of ancestral complexity and non-metazoan genes in two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nematostella vectensis
Nematostella vectensis
Eukaryota; Metazoa; Cnidaria; Anthozoa; Hexacorallia; Actiniaria;
Edwardsiidae; Nematostella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      327-384-37_010 KS Nematostella vectensis normalized cDNA library 327 Nematostella vectensis cDNA clone 327-384-37_010_KS, mRNA
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KBrB087J22F KBrB, Brassica rapa BamHI BAC library Brassica rapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trends Genet. (2005) In press
Contact: Ulrich Technau
Sars Centre for Marine Molecular Biology
High Technology Building, Thormohlensgt. 5 5008 Bergen, Norway
Tel: +47-55584340
Email: ulrich.technau@sars.uib.no
Plate: 37 row: 10 column: 0
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                                                                                                                                  Length 40;
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4; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                    1; Indels
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DV082973.1 GI:82864366
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2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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Best Local Simi
Matches 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab host="E.coli DH10B"
/clone lib="KBrB, Brassica rapa BamHI BAC library"
/clone lib="KBrB, Brassica rapa BamHI; Brassica rapa spp
/clone evertor: pCUGIBACI; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiftu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhatroideae; Oryzeae; Oryza.
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                          Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                   National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
121: 482-31.299-1670
Fax: +82-31-299-1670
Email: pbeom@rda.go.kr
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                                                                                                                                                                                                                                       Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
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subsp. pekinensis genomic clone KBrB087J22, genomic survey
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1.2%; Score 33.4; DB 1; Length 40;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels
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/organism="Brassica rapa subsp. pekinensis"
/organism="Genomic DNA"
/culTivar="Chilfu"
/sub speciaes="pokinensis"
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Brassica Genomics Team
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                                                               DX076358.1 GI:84770654
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CF300448/c
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δ g

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1. .41

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="12EF--04-NI5"
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/tissue_type="leaf"
/dev stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
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7LEAF--07-C22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-C22, mRNA
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
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/clone="7LEAF--07-C22"
/clsue type="leaf"
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/lab_host="Coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 41)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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/mol type="mRNA"
/cultivar="Nackdong"
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94; Conservative 0; Mismatches 1; Indels
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Tel: 82 31 330 6193
Fax: 82 31 321 6358
Email: bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Location/Qualifiers
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Conservative
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Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6135
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                   CF305364 the mRNA linear EST 15-AUG-2003 CLD1--01-105.bl Rice cold treated leaf plasmid cDNA library (CLD1) Oryza sativa (japonica cultivar-group) cDNA clone CLD1--01-105,
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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I (bases 1 to 41)

I (bases 1 to 41)

Chen, S., Mao, M. Wu, X., Gu, J., Huang, Q., Zhou, J., Shen, Y., Han, Z.,

Chen, S., Mao, M. and Chen, Z.

Homo sapiens CB library cDNA clones

Unpublished (2000)

Contact: Zhu Chen
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/tiSoue_type="leaf"
/dev_stage="leaf"
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(CD1)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV742106 AV Homo sapiens cDNA clone CBCAAC09 5', mRNA sequence. AV742106
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/ roganism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/culTivar="Nackdong"
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                    CF305364.1 GI:33677125
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Homo sapiens
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Matches 34; Conservative
                                                                                                                                                                            mRNA sequence.
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                                                                              RESULT 415
CF305364/c
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryzea; 
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end with EcoRI and 3' end with XhoI site."
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/clone="CBCAACO:9666"
/cione="CBCACO9"
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/lab_hogt="BAS.8"
/clone_lib="CB"
/note="Vector: pBluescript; Site_1: EcoRI; The insert is cloned randomly with the EcoRI digestion"
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Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
197 Rui-Jin II Road, Shanghai 200025, P. R. China
198 86-21-64743206
Eax: 86-21-64743206
Email: mbshi@ms.stn.sh.cn
Email: mbshi@ms.stn.sh.cn
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
Location/Qualifiers
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Location/Qualifiers
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Hominidae; Homo
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/clone lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKF2p56611946 r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKF2p56611946, mRNA sequence.
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Bukaryota, Virighlantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons, core eudicotyledons,
rosida, eurosida II, Brassicales, Brassicaceae, Brassica.
1 (bases 1 to 41)
1 (bases 1 to 41)
1 (bases 1 to 41)
1 (bases 2 to 41)
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1 (bases 3 to 41)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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National Institute of Agricultural Biotechnology
225 Seodum-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Exa: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
  Gaps
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Contact: Beom-Seok Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Brassica rapa subsp. pekinensis"
|mol_type="genomic DNA"
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                                      2709 ААААААААААААААААААААААААААААААА
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  34; Conservative
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Class: BAC ends.
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KEYWORDS
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CF128529

NACL--03-H18.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--03-H18, mRNA
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/clone="NACL--03-H18"
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Torgin, Kyeongqi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
1 (bases 1 to 38)
Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stagé="fetal""
/lab_host="X1-2blue"
/otone_lib="566 (gynonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: Sall"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                        D-85764 Neuherberg, Germany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33.2; DB 1; Length 38;
Pred. No. 2.4e+02;
0; Mismatches 3; Indels
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/clone="DKFZp56611946"
                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="kidney"
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/cultivar="Nackdong"
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Location/Qualifiers
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Location/Qualifiers
                                                      Wiemann, S.
EST (Ottenwaelder, et al.)
Unpublished (1999)
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92.1%;
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Best Local Similarity 92.1
Matches 35; Conservative
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33; Conservative
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CF326967.1
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Matches 33;
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/mol type="mRNA"
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/cultivar="NacKdong"
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/note="Vector: pCR4-TOPO; Site_1: BcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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                                                                                                                                                            CF291613 33 bp mRNA linear EST 14-AUG-2003 14ROOT--02-B21.bl Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-B21, mRNA
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Enrhartoideae; Oryzeae; Oryza.

(bases 1 to 33)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Cyza sativa (japonica cultivar-group)

Eukaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

Clade; Ehrhartoideae; Oryzeae; Oryza.

( (Dases 1 to 33)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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 Indels
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Conservative
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CF311229/c
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DEFINITION
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CF326967 33 bp mRNA linear EST 18-AUG-2003 NACL--01-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-E04, mRNA
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                            /dev stage="14 days after germination"
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cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2nrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
                                                                       Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Exar: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/mol type="mRNA"
/cultivar="Nackdong"
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Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
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100.0%; Pred. No. 2.3e+02;
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ive 0; Mismatches
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/clone="ABF--06-F23"
                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="leaf"
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Tue Nov

DEFINITION

RESULT 424

ઠે 유 CF328313

ORGANISM

ACCESSION VERSION KEYWORDS SOURCE

TITLE JOURNAL COMMENT

FEATURES

AUTHORS REFERENCE

RESULT 425 CF336752/c DEFINITION

ઠે 셤 ACCESSION VERSION KEYWORDS

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Oryza sativa (japonica cultivar-group)

Elwaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoidee; Oryzea; Oryza.

El (baees 1 to 33)

Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db xref="taxon.39947"
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/tissue_type="ladf"
/dev_stage="lad days after germination"
/lab_host="B.coli DH10B"
/lab_host="B.coli DH10B"
/clone_lib="AtJWT-overexpressing transgenic rice plasmid cDNA library (JWT)"
/note="Wetor: pCR4-TOPO; Site_l: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTB
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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33 bp mRNA linear EST 18-AUG-20
MTM--07-G18.bl AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--07-G18, mRNA sequence.
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/mol_type="mRNA"
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100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0;
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/cultivar="Nackdong"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhna
Location/Qualifiers
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Location/Qualifiers
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Best Local Similarity 100.(
Matches 33; Conservative
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CF337105/c
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/organism="NENA"
/organism="NENA"
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/db xref="taxon:19947"
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/clone="NACL--03-C14"
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/lab host="E.coli DH108"
/lone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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JMT-06-019.gl AtJMT-overexpressing transgenic rice plasmid cDNA
JMT-06-019, mRNA sequence.
CF336752
CF336752.1 GI:33821884
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NACL--03-C14.gl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--03-C14, mRNA
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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/note="Vector: pCR4-TOPO; Site_l: EcoRI; mRNA was capped
with oligoribonuclectides and then used as templates for
RT-PCR."
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                               1.2%; Score 33; DB 1; Length 33;
100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0; Indels
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    Location/Qualifiers
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Matches 33; Conservative
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Best Local Similarity 100.0
Matches 33; Conservative
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

El (Bases I to 33)
El (Bases I to 33)
El (Masses I to 33)
Contact: Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, Kyeonggi, Korea
Tel: 82 31 321 6153
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                       33 bp mRNA linear EST 04-NOV-2004 (14Salt--03-C19.bl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone CV725846
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CV725871.1 GI:55413495
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Oryza sativa (japonica cultivar_group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida; Poales, Poaceae; BEP
clade, Ehrhartoideae; Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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/lab_host="s.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
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/mol_type="mRNA"
/cultivar="Nackdong"
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1.2%; Score 33; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0;
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                            CV725846/c
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/clone="145alt--02-C18"
/clone="145alt--02-C18"
/tab_host="14 days after gernimation"
/lab_host="E.coli SOLR"
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/clone_lib="5alt treated rice leaf lambda phage cDNA
/lore="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xho1; Laf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
CDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with Xho1 site."
                                                                                                                                                                          /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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CV725203. GI:55412827
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplanteae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 33)
1 (bases 1 to 33)
1 (kim,J.K., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/tissue_type="leaf"
/dev_stage="leaf"
/dev_stage="leaf"
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
of Bioscience and Bioinformatics, MyongJi University
of Bioscience and Bioinformatics, MyongJi University
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggblo.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/organism="Orryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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Pred. No. 2.3e+02;
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1.2%; Score 33; DB Best Local Similarity 100.0%; Pred. No. 2.3 Matches 33; Conservative 0; Mismatches
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VERSION
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Gaps

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with EcoRI and 3' end with XhoI site."
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Best Local Similarity 100.
Matches 33; Conservative
                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nahm B.H.
                                                                                                         Similarity
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                                                                             Query Match
                                                                                                                Best Local
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LOCUS
DEFINITION
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CV726801/c
LOCUS
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AUTHORS
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JOURNAL
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KEYWORDS
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KEYWORDS
SOURCE
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viitidiplantae; Streeptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

E i (bases 1 to 33)
S Kim,J.S., Jun,K.M., Cheong, D.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.F. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14Salt--03-F12.g1 Salt treated rice lesf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone L4Salt--03-F12, mRNA sequence.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yrongli, Kveongqi, Kveongqi, Kveongqi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBluescript SK(+); Site_1: EcoR1; Site_2: XhOI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hre. CDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoR1 and 3' end with XhOI site."
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                                                                                                                                                                                                                                       1. 33
Arganism="Oryza sativa (japonica cultivar-group)"
And Ltype="Nackdong"
And xref="taxon:39947"
Ab xref="taxon:39947"
Alb xref="taxon
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/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="tastcon:39947"
/clone="148alt--03-F12"
/tissue_type="lasf"
/dev_stage="14 days after gernimation"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (148alt)"
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100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0; Indels
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Location/Qualifiers
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JOURNAL
COMMENT
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AUTHORS
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CV726984

14Salt--04-O15.bl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--04-O15, mRNA sequence.
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Yongin, KyeongGi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 33)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/lab/host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/culTivar="Nackdong"
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Length 33;
  1.2%; Score 33; DB 1; Le
100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0;
                                                                                                                   2709 ААААААААААААААААААААААААААААААААА
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/db xref="taxon:39947"
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Best Local Similarity
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DEFINITION
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KEYWORDS
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae, BEP clade; Ehrhartoideae, Oryzae, Oryza.

(kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantaa, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
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                                                                                                                                                                                                                       Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, KyeongGi, Korea 1913 131 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:39947"
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/clone="146alt--04-015"
/tissue_type="ladys after gernimation"
/dev_stage="14 days after gernimation"
/lab.host="s.coli SOLR"
/clone_lib="Solt treated rice leaf lambda phage cDNA
library (45alt)"
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"___
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/mol_type="mRNA"
/cultivar="Nackdong"
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100.0%; Pred. No. 2.3e+02;
Live. 0; Mismatches 0; Indels
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CV732151.1 GI:55437726
                                                                                                                                                                                                         Contact: Nahm B.H.
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XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'end with EcoRI and 3'end with XhoI site."
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/clone lib="Rice flower lambda phage cDNA library (FLO)"
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Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at 5, end with EcoRI and 3' end with Xhol site."
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Nahm B.H. Genemics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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/mol_type="mRNA"
/cultivar="Nackdong"
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Tel: 82 31 330 6193
Fax: 82 31 321 6365
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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1.2%; Score 33; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0;
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Pred. No. 2.3e+02;
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O; Mismatches
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CV732198.1 GI:55437812
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyra; Embryophyta; Tracheophyta; Spermatophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.
E l (bases 1 to 33)
S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa (japonica cultivar-group)"
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/note="Yector: pBluescript KK(+); Site_1: EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza,

1 (bases 1 to 33)
Kim,J.S., Uun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yorgin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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FLO--07-M18.g1 Rice flower lambda phage cDNA library (FLO) Oryza
Bativa (japonica cultivar-group) cDNA clone FLO--07-M18, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                     Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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CV733051.1 GI:55439486
    CV732853.1 GI:55439103
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Best Local Similarity 100.0
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CV733051/c
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryzae; Oryzae;

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,N.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.F., and Nahm,B.H.

Large-scale Sequencing Analysis of Rice EST9

Unpublished (2003)

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Tel: 82 31 330 6193

Fax: 82 31 321 6355
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/clone lib="Rice flower lambda phage cDNA library (FLO)"
/clone libe-macript SK(+); Site_1: EcoRI; Site_2:
/hote="Yector: pBluescript SK(+); Site_1: ecoRI; Site_2:
/hol; cDNA was inserted into lamda Uni-ZAP XR vector at 5;
end with EcoRI and 3' end with XhoI site."
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Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with Xho1 site."
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Location/Qualifiers
                                                                                                                                                                                                                                                                       Score 33; DB 1; Le
Pred. No. 2.3e+02;
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Pred. No. 2.3e+02;
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DEFINITION
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Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                     source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev stage="3 month old normal canine"
/lab_host="XL10 Gold"
/lab_host="XL10 Gold"
/clone libb="Whole Heart Library (DOGSST5)"
/note="Organ: Heart; Vector: pBluescript II SK; Site_1:
ECORI; Site_2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, Phb, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ486/95 Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0315P22 F, genomic survey sequence.
                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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1 (bases 1 to 3)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ralam, D., Aoyagi, A., Eacorn, T., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Unpublished (2000)
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                                                                                                                                                         l (Bases 1 to 33)
Balija,V.S., Nascimento,L.U. and McCombie,W.R. ESTS from Canis familiaris whole heart (dog) Unpublished (2004)
Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory Po Box 100, Cold Spring Harbor Laboratory Po Box 187 8894
Fax: 516 367 8874
Email: mccombie@cshl.org.
Location/Qualifiers
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2.3e+02;
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    .33
    /organism="Canis familiaris"
/mol_type="mRNA"
    /db_xref="taxon:9615"

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100.0%; Pred. No. 2.3
ative 0; Mismatches
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
  CX013914
CX013914.1 GI:56396325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Unknown"
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                                                           Canis familiaris (dog)
Canis familiaris
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Best Local Similarity 100.0
Matches 33; Conservative
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Fax: 801 585 7177
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84112, USA
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AZ486795/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gil-f732114 [gb]-RR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0474B02F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0474B02 F, genomic survey sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah
Contact Contex
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 33)
Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Pred. No. 2.3e+02;
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: P column: 22
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0315P22"
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                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 33; Conservative
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FEATURES

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/dev stage="adult"
//dev stage="adult"
//dev stage="adult"
//deb_host="DH10B"
//clone_lib="H021 - RescueMu Grid V"
//clone_lib="H021 - RescueMu Grid V"
//note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamH1; Site 2: BgJII;
RescueMu is a 4.9 kb, modified maize Mu transposon
Gesigned to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units: For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/' Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 bp DNA linear GSS 22-DEC-2005 KBrS006K01R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS006K01, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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BAC end sequence of Brassica rapa ssp. pekinensis Sau3Al BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 33)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Yang, T.J., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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/db_xref="taxon:51351"

/db_aref="KBTS.006K01"

/lab_host="KBTS.001 DH10B"

/clone_lib="KBTS, Brassica rapa Sau3AI BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                               /mol type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Brassica rapa subsp. pekinensis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.2%; Score 33; DB 1; L6
100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica rapa subsp. pekinensis
   Location/Qualifiers
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Brassica Genomics Team
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: M13 Reverse
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ampicillin."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp [A732114]gb] AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C2917348 13 bp DNA linear GSS 08-AUG-2005 4021005C07.2EL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Unpublished (2001)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoldeae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021005 row: C column: 07
Class: transposon-tagged.
                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 2.3e+02;
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: B column: 02
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1.2%; Score 33; DB 1
Best Local Similarity 100.0%; Pred. No. 2.3¢
Matches 33; Conservative 0; Mismatches
                                                   Plate: 0474 row: B column: 02
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/64"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0474B02"
                                                                                                                                                  High quality sequence stop: 33.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                       sex="Male"
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Zea mays
                                 Insert
Plate:
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KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT AUTHORS REFERENCE

ACCESSION VERSION

DEFINITION

RESULT 441

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AL587876.1 GI:13192910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Brassica rapa subsp. pekinensis"
/organism="genomic DNA"
/oulTivar="Chift"
/sub_apecies="pekinensis"
/sub_apecies="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB031H14"
/lab_host="K.coli DH108"
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/clone lib="KBrB Brassica rapa BamHI BAC library"
/clone lib="KBrB Brassica rapa BamHI BAC library"
/clone lib="KBrB Brassica rapa spp
pekinensis var. Chiftu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantaa, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnollophyta, eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institute of Agricultural Biotechnology
225 Seedun-Dong, Suwon, 441-707, Korea
121: 482-31-299-1670
Fax: +82-31-299-1670
Email: pbeom@rda.go.kr
BAC.end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
/note="Vector: pCUGIBAC1; Site_1: Sau3A1; Brassica rapa
Bep pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
                                                                                                                                                                                                                                                                                                            DNA linear GSS 10-JAN-2 KBrB031H14F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB031H14, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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1.2%; Score 33; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.3a+02;
Matches 33; Conservative 0; Mismatches 0;
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Location/Qualifiers
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/dev_stage="Unknown"
/lab host="DH108"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: Not1; Site 2: Sal1; Cloned unidirectionally. Primer: Olfgo dT. 5' adaptor sequence: 5' TCGACTCGAG 3'; 3' adaptor sequence: 5' GCGGCGCTTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from clonetech (*6851)"
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                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (Sases 1 to 34)
Murray, F.
BP Chicken Brain Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Administry Bulling Bualtinoncoglines; Filmates; Catalling; Hominidae, Homo.

1 (bases 1 to 34)

S Nill-MGC http://Mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbe-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM570 row: e column: 18
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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1.2%; Score 33; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                     Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS064F10"
/tissue_type="Brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BU431799.1 GI:22770281
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BU431799
                               Gallus gallus
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FEATURES

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/lab host="DH108"
/clone_lib="NIH_MGC_l16"
/clone_lib="NIH_MGC_l16"
/clone_lib="Organ: pooled_colon, kidney, stomach; Vector:
pcMV-SPORT6; Site_l: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo female. Library is
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
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                                              BI761940 36 bp mRNA linear EST 25-SEP-2001 603048772F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189224 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC. clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1472 row: o column: 17
High quality sequence stop: 36.
High quality sequence stop: 36.
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                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 38)
Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
                                                                                                                                                                                                                                                                                                                           Hominidae, Homo.

1 (bases 1 to 36)

NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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100.0%; Pred. No. 2.4e+02;
ative 0; Mismatches 0;
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/db_xref="taxon:9606"
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Antirrhinum majus
                                                                                                                                                               BI761940.1 GI:15753518
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                                                                                                                                                                                                                      Homo sapiens (human)
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Best Local Similarity 100.0
Matches 33; Conservative
                                                                                                           mRNA sequence.
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Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

E 1 (bases 1 to 34)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Xim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Lupublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CV734277 34 bp mRNA linear EST 05-NOV-2004 PLO-09-J02.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--09-J02, mRNA
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/clone="FLO--09-J02"
/tissue_type="flower"
/lab host="E.coli Solk"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Yector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with Xhol site."
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                                                                                                     /mol_type="mRNA"
/db xref="taxon:9606"
/clone="lMAGE:385573"
/tissue_type="adenocarcinoma"
/tlab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_66"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Fechnologies.
Fechnologies.
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Location/Qualifiers
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1.2%; Score 33; DB 3
Best Local Similarity 100.0%; Pred. No. 2.3s
Matches 33; Conservative 0; Mismatches
                                                                                 organism="Homo sapiens"
High quality sequence stop: 31.
Location/Qualifiers
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/cultivar="Nackdong"
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CV734277.1 GI:55441908
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Email: Bill. Taylor@cceiro.au

Engaprimer: Mil reverse primer

High quality sequence stop: 38.

Location/Qualifiers

Location/Q
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Pooideae; Triticae; Triticum.

El (bases 1 to 38)
Ali,6, Holloway, B. and Taylor, W.C.
Normalisation of cereal endosperm EST libraries for structural and functional genomic analysis
AL Plant Mol. Biol. Rep. 18, 123-132 (2000)
Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry.

CSIRO Plant Industry.

CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
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Saedler, H. and Zachgo, S.
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
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/organism="Antirrhinum majus"
/mol type="mRNA"
/db_xref="taxon:4151"
/clone="0.18 __11.08"
/clone_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
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Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
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Plant Cell 16 (12), 3197-3215 (2004)
15539471
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Orygon Status (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryzea.

1 (bases 1 to 39)

SK Mim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

YongJin, Kyeonggl, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                             CF327755 39 bp mRNA linear EST 18-AUG-2003 NACL--02-F23.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-F23, mRNA
Sal I-Xho I adapter (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."
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/lab_host="E.coli DH10B"
/clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoR1; mRNA was capped
with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                               Gaps
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/mol type="mRNA"
/cultivar="Nackdong"
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Pred. No. 2.5e+02;
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100.0%; Pred. No. 2...
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/clone="NACL--02-F23"
/tissue_type="callus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                         33; Conservative
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Best Local Similarity
                                                                                                               Best Local Similarity
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CF315464.1 GI:33687225
                                                                                                                                              Query Match 1.2%;
Best Local Similarity 97.1%;
Matches 33; Conservative 0
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LOCUS
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/organismm="Oryza sativa (japonica cultivar-group)"
/ullivar="Mackdong"
/ullivar="Mackdong"
/ulsave="1940pe="1940"
/clone="14ROOT--02-L12"
/tisbue_rype="root"
/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/lab_host="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOOF); Site 1: ECORI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CF302250
7LEAF--07-J10.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-J10, mRNA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

(loases 1 to 37)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nahm B.H.

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Biosience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@pio.myongji.ac.kr.

Location/Qualifiers
                                                                                                                                                                                       Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yogin, KyeongJi, Korea Tel: 82 31 330 6193

Fax: 82 31 321 6355
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt sperarophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryzae; Oryzae; Ekin,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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/clone="7LEAF--07-J10"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/cultivar="Nackdong"
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14 bp. mRNA linear EST 15-AUG-2003 HD--04-G09.bl OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--04-G09, mRNA sequence.
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/dev_stage="proliferated"
/lab_nost="E.coli DH10B"
/clone lib="colabact-overexpressing transgenic rice plasmid cDNA library (HD)"
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LOCUS CZ906552 34 bp DNA linear GSS 08-AUG-2005
DEFINITION 4011001D06.1EL_y2 4011 - RescueMu Grid J Zea mays genomic, genomic
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                    2707 CTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
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/clone="HD--04-G09"
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/cultivar="Nackdong"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhrahm@ggbio.com, bhna
Location/Qualifiers
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Conteat: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 723 2227
Fax: 650 728 gaz1
Email: walboto@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4011001 row: D column: 06
Class: transposon-tagged.
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                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

    (Dases 1 to 34)

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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica, Viridiplancae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 34)
Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
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/organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
               CZ906552
CZ906552.1 GI:71917315
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Best Local Similarity 97.1'
Matches 33; Conservative
 sequence.
                                                                Zea mays
Zea mays
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/sub species="bekinensis"
/bub zref="taxon:51351"
/clone="KBrB058P12"
/clone="E.coli DH10B"
/clone lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pcUGIBAC1; Site 1: BamHI; Brassica rapa pp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."
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End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1670
Bmal: pbeom@rda.go.kr
BRAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrBOSSP12
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 34)
Yang, T.J. Kwon, S.J. Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
End sequence of Brassica rapa BamHI (KBrB) BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB063K14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA linear GSS 10-JAN-2 KBrB063K14F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB063K14, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                              rapa subsp. pekinensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 34;

    .34
/organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/cultivar="Chiifu"

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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.2%; Score 32.4; DB 1; 7.1%; Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                 1. .34
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/mol_type="genomic DNA"
/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Conservative
                                                                                                                                                                                                                                                                                         Seq primer: T7
Class: BAC ends.
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Class: BAC ends
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Contact: Ivens AC
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UMR 619 - Equipe
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Matches 33; Conserv
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CN545543/c
LOCUS
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ORGANISM
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AUTHORS
                     JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 34)

Humphray, S. J., Huckle, E. and Hunt, S. E.

Direct Submission

Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail contact: Humquery@sanger.ac.uk Unpublished

This sequence was generated from the T7 end of BAC 41A4. 41A4 is part of the Danlokey BAC Library created by R. Plasterk and N.V.
                /clone="KBrB063K14"
/lab_host="E.coli DH10B"
/lab_host="E.coli DH10B"
/clone lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                      ркатант 34 bp DNA linear GSS 22-NOV-2002
Danio rerio genomic clone DKEY-41A4, genomic survey sequence.
AL980969
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Schistosoma mansoni
Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigedida; Schistosomatoidea; Schistosoma.
1 (bases 1 to 36)
Billon, G.P., Fellwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaidou-Katsaridou,N., Quall,M.A., Wilson,R.A. and Ivens,A.C.
Microarray analysis identifies genes preferentially expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Further details: http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
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                                                                                                                                                              1.2%; Score 32.4; DB 1; 97.1%; Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
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                                                                                                                                                                                                    0; Mismatches
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xref="taxon:51351"
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Best Local Similarity
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AM047864/c
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DR41A4T
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CNS45543

EST 17487 Ripe Grape Skin Triplex2 Library Vitis vinifera CDNA clone B3CS00RL003C10 3', mRNA sequence.
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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/cone_lib="Ripe Grape Skin Triplex2 Library"

/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:

SfilR; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

1 (bases 1 to 38)
1 (bases 1 to 38)
2 (babal, P., Agases, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"
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Universite de Bordeaux I, Institut National de la Recherche
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the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
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36 AAAAAAAAAAAAAAAAYAAAAAAAAAAAAA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Vitis vinifera"
                                                                                         Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM
Location/Qualifiers
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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/note="Vector: pAMP1; Site_1: Not1; Site_2: Sall"
                      Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers
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Best Local S:
Matches 34,
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ORGANISM
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Matches
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AUTHORS
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/mol type="mRNA"
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/clone="B3CS00RL006F10"
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/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_l: SfilA; Site_1: SfilB; Oriented library"
                                                                        37 bp mRNA linear EST 30-APR-2004 EST 17891 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA Clone B3CS00RL006F10 3', mRNA sequence.
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
                                                                                                                                                                                                                                               Eukaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Viteceae; Vitis.

1 (bases 1 to 37)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo.
1 (bases 1 to 38)
Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2%; Score 32.2; DB 1; Length 37;
11.9%; Pred. No. 2.7e+02;
ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seg primer: T7.
Location/Qualifiers
                                                                                                                                                                       CN545945.1 GI:46910570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL037916
AL037916.1 GI:49682063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST (Bloecker, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 91.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                             Vitis vinifera
Vitis vinifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MIPS
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Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
ORGANISM
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VERSION
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SOURCE
ORGANISM
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                                                        RESULT 460
CN545945/c
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                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
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JOURNAL
COMMENT
                                                                                                                                                     ACCESSION
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39 bp mRNA linear EST 30-APR-2004 EST 18125 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00RL009C01 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="ripening stage"
Clone libe:Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
SfilA; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

1 (bases 1 to 39)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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ch 1.2%; Score 32.2; DB 1; Length 38; 1 Similarity 91.9%; Pred. No. 2.8e+02; 34; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                       2704 GTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 TTGGTTTAAAAAAAAAAAAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.2%; Score 32.2; DB 1; 91.9%; Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="vitis vinifera"
/mol type="mRNA"
/cultivar="Cabernet Sauvignon"
/db xref="taxon:29760"
/clone="B3CS00RL009C01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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SOURCE

AUTHORS

REPERENCE

RESULT 463 BQ591342/c

DEFINITION

ACCESSION

VERSION KEYWORDS

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Pain, A., Renauld, H., Berriman, M., Murphy, L., Yeats, C.A., Weir, M., Karhornou, A., Aslett, M., Bishop, R., Bouchier, C., Cochet, M., Coulson, R.M. R., Cronin, A., de Villiers, E., Fraser, A., Fosker, N., Gardner, M., Goble, A., Griffiths Jones, S., Harris, D.E., Katzer, F., Larke, M., Lord, A., Maser, P., McKellar, S., Marris, D.E., Katzer, F., Larke, M., Lord, A., Maser, P., McKellar, S., Mooney, P., Morton, F., Rawlings, N.D., Rutter, S., Saunders, D., Seeger, K., Shah, T., Squares, R., Star, S., Saunders, D., Seeger, K., Shah, T., Dobbelaere, D.A.E., Langsley, G., Rajandream, M.-A., McKeever, D., Shiels, B., Tait, A., Barrell, B. and Hall, M.
The genome of the host-cell transforming parasite Theileria annulata and a comparison with T. parva
Unpublished (2005)
Contact: Pain A
The Pathogen Sequencing Unit
The Wellcome Trust Sanger Institute
Genome Campus, CB10 18A, UNITED KINGDOM
Piroplasm cDNA library: Frank Katzer and Brian Shiels, Division of Veterinary Infection and Immunity, ICM, University of Glasgow, UK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 32)
Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S., Nikolaidou-Katsaridou, N., Quali, M.A., Wilson, R.A. and Ivens, A.C.
Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlCliel2.qif"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AM044529 achistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA clone SmlCllel2.qlk, mRNA sequence.
AM044529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="TAC31d08_plka"
/dev_stage="piroplasm"
/lab_host="Bos taurus (cow)"
/clone lib="Theileria annulata piroplasm"
/note="country: Turkey:Ankara"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 1; I
Pred. No. 2.6e+02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .32
/organism="Schistosoma mansoni"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Theileria annulata"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/isolate="Ankara (clone D7)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.2%; Score ... 2.6e
100.0%; Pred. No. 2.6e
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Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 ISA, UNITED KINGDOM.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:5874"
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Best Local Similarity 100.0
Matches 32; Conservative
                                                      (bases 1 to 32)
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AM044529/c
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                                                            REFERENCE
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KEYWORDS
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                                                                                      AUTHORS
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AJ923479
AJ923479
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db xref="GABI:188777"
/db xref="taxon:161934"
/clone="024-017-620"
/tissue_type="storage root"
/lab host="EMPIZ-ADIS-024-storage root"
/note="Vector: pGWVSPORT6; Site 1: Sal1; Site 2: Not1;
/note="yerper room sugar beet, ilbrary provided by KWS
Kleinwanzlebener Saarzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
                                                                             BQ591342 40 bp mRNA linear EST 06-DEC-2002 E012713-024-017-G20-T7 MPIZ-ADIS-024-storage root Beta vulgaris CONA clone 024-017-G20 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Gagermatophyta; Care eudicotyledons; Caryophylales; Amaranthaceae; Beta.

1 (bases 1 to 40)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radeloff, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             orientation:
SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organiem="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 40 Sld Error: 0.00
Plate: 17 row: G column: 20
Seq primer: T7; GTAATACGACTCACTATAGGGC.
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Theileria annulata
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Best Local Similarity 91.9
Matches 34; Conservative
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                                                                                                                                                                                                                                                       Beta vulgaris
                                                                                                                                                                                                                                                                                   Beta vulgaris
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source

FEATURES

PUBMED COMMENT

JOURNAL

TITLE

ORGANISM

DEFINITION

ACCESSION

VERSION KEYWORDS

RESULT 464

g ò

AJ923479

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Gaps

.; 0

EST 20-SEP-2005

RESULT 466

ò g AM044934

DEFINITION

ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

FEATURES

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Gaps

.. 0

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/organism="Uryza Bativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="teaxon: 3994"
/clone="14ROOT--02-F12"
/tissue_type="root"
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/lab host="E.coli DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF291773 32 bp mRNA linear EST 14-AUG-2003 14ROOT--02-F12.bl Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-F12, mRNA
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongln, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (Gases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                /organism="Schistosoma mansoni"
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/clone lib="Schistosoma mansoni lung schistosomulum"
/note="Country: Puerto Rico"
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100.0%; Pred. No. 2.6e+02;
ive 0; Mismatches 0; Indels
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CF291773.1 GI:33660806
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Best Local Similarity 100.1
Matches 32; Conservative
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Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S., Nikolaidou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C. the lung schistosomulum of Schistosoma mansoni unpublished (2005)
                                                                                                                                      Gaps
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100.0%; Pred. No. 2.6e+02;
ative 0; Mismatches 0;
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/note="country: Puerto Rico"
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Pathogen Microarrays Group
Wellcome Trust Sanger Institute
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                Oryza sativa (japonica cultivar-group)
Mkaryota, Viridiplancae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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/note="Wector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Nahm B.H.
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
YongJi, Kyeonggi, Korea
YongJi, Kyeonggi, Korea
Fear: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongln, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
7LEAF--03-G07.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-G07, mRNA
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Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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100.0%; Pred. No. 2.6e+02;
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Location/Qualifiers
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                                                                                              CF299386.1 GI:33671147
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32 bp mRNA linear EST 15-AUG-2003 ABF--03-103.bl ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--03-103, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida; Poales, Poaceae, BEP
clade, Ehrhartoideae; Oryzeae, Oryza.
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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
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Yonglin, KyeongJi, Korea
Yenglin, KyeongJi, Korea
Fax: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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| Drark (ABF) | hoverexpressing transgenic rice plasmid
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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/mol_typs="mRNA"
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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0;
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Location/Qualifiers
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
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/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Spermatophyta; Vildiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

1 (bases 1 to 32)
1 (bases 1 to 32)
1 (kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., xim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Nahm B.H.
Contact: Nahm B.H.
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Yorgin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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1.68, Fred. No. 2.6

Best Local Similarity 100.0%; Fred. No. 2.6
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaae; Oryza.
1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                  Contact: Nahm B.H.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongln, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
      1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/organism="Oryza sativa (japonica cultivar-group)"

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Ehrhartoideae; Oryzeae; Oryza.
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Location/Qualifiers
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CV724815
14Salt--01-J14.91 Salt treated rice leaf lambda phage CDNA library (14Salt) Oryza sativa (japonica cultivar-group) CDNA clone 14Salt--01-J14, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTE
                                                                                                                                                                                                           Hominidae; Homo.

Is I (bases I to 32)

In (bublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capbs-remail.nih.gov
Tissue Procurement: ATC

CONA Library Preparation: Edge BioSystems

CDNA Library Preparation: Edge BioSystems

CONSTITUT (LINL)

DA Sequencing by: NH Intramural Sequencing Center (NISC)

Cloe distribution: MGC clone distribution information can be found through the I.M. AG.E. Consortium/LLNL at:

www-bio.lnl.lnl.gov/bbrp/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/image/im
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                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
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/clone="IMAGE:2846628"
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CV724815.1 GI:55412439
   AW327277.1 GI:6797772
                                                                           Homo sapiens (human)
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                                                                                                                    Homo sapiens
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.
E l (bases 1 to 32)
S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Lupublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/mol type="mRNA"
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/clone="NACL--07-F08"
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/lab_host="E.col DH108"
/clone lib="Rice callus plasmid cDNA library (NACL)"
/nore="Vector: pCR4-TOPO; Site_1: EcoR1; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF331270 132 bp mRNA linear EST 18-AUG-2003 NACL--07-F08.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--07-F08, mRNA
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                          /dev stage="proliferated callus on 2N6 media for 30 days" /lab_host="E.coli DH10B" /clone lib="Rice callus plasmid cDNA library (NACL)" /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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    Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.66
Matches 32; Conservative 0; Mismatches
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       tissue_type="callus"
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CF331270.1 GI:33810751
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnaliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

El (Bases I to 32)
El (Bases I to 32)
El (Masses I to 32)
Congaes scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongdi University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                   14Salt--02-L16.bl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--02-L16, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
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library (145alt)
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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
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/dev_stage="14 days after gernimation"
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library (14Salt)
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XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
CDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yogin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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100.0%; Pred. No. 2.6e+02;
tive 0; Mismatches 0;
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DEFINITION
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JOURNAL
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Oryza sativa (japonica cultívar-group)
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                                               Query Match
                                                                    Best Local
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CV728625/c
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Yongin, KyeongJi, Korea
Yongin, KyeongJi, Korea
Fax: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 (360uM/m-2sec-1) for Zhrs. CDNA was inserted into landa Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
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                                                                                                                                                                  Organism="Oryza sativa (japonica cultivar-group)"
mol type="mRNA"
cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Oryza sativa (japonica cultivar-group)"
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/db xref="taxon:39947"

/clone="14Salt--03-P17"

/fissue_type="1eaf"

/dev_stage="14 days after gernimation"

/lab_host="E.coli SOLR"
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/clone="14Salt--03-G20"
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/cultivar="Nackdong"
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Best Local Similarity
Matches 32; Conserva
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32 bp mRNA linear EST 04-NOV-2004 14Salt--05-014.bl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone CV727659
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Oryza sativa (japonica cultivar-group)
Gryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Enrhattoideae; Oryzae; Oryza.

(bases I to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
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Contact: Nahm B.H.

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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: ANOI; Leaf was incubated at 4 C(360uM/m-2aec-1) for 2Drg. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
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FLO--01-A24.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-A24, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="leaf"
/dev_stage="14 days after gernimation"
/lab_host="E.coli SOLR"
/clone lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
                                                                                                               Gaps
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/mol type="mRNA"
/cultivar="Nackdong"
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                                                   Length 32;
with EcoRI and 3' end with XhoI site."
                                                   1.2%; Score 32; DB 1; L4
100.0%; Pred. No. 2.6e+02;
tive 0; Mismatches 0;
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100.0%; Pred. No. 2.6e+02;
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/clone="14Salt--05-014"
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sequence.
CV732586
CV732586.1 GI:55438578
EST.
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                                                                                                                                                               Best Local Similarity
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                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                  RESULT 485
CV732146/c
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Cryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopaida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Orizeae; Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)

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Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

El (Dases 1 to 32)

SKim, J.S., Jun, K.M., Cheong, V.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTB

Unpublished (2003)

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/clone="FLO--01-A24"
/tissue_trype="flower"
/lab host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xhol; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with Xhol site."
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FLO--01-P21.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-P21, mRNA
                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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.00.0%; Pred. No. 2.6e+02;
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Location/Qualifiers
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cultivar="Nackdong"
/db_xref="taxon:39947"
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Best Local Similarity
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JOURNAL
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AUTHORS
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Cryza sativa (japonica cultivar-group)

EMALYOCA: Virtidiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryoca; Virtidiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryoca; Virtidiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryzea.

Exim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-escale Sequencing Analysis of Rice ESTs

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6155

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CV732146 32 bp mRNA linear EST 05-NOV-2004 FLO--06-H23.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--06-H23, mRNA
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XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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/lab_host="E.coli SOLR"
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/note=""Vector: pBluescript SK(+); Site_1: BcoRI; Site_2:
Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with BcoRI and 3' end with XhoI site."
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1.2%; Score 32; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0;
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                             FEATURES
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clad; Ehrhartoideae; Oryzaa.

El (Basea I to 32)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Murinae; Mus.

E 1 (Dases 1 to 32)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

L Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

Mail 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol type="mkNa"
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XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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100.0%; Pred. No. 2.6e+02;
ive 0; Mismatches 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: M column: 16
Seg primer: cGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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nes 32; Conservative
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Fax: 801 585 7177
Email: ddunn@genet
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Best Local 8
                           ORGANISM
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    SOURCE
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWaPAZ (gilfylaplAPI2977.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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1M0285F14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic Cone UUGC1M0285F14 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                    /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note=""vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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Pred. No. 2.6e+02;
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Insert Length: 10000 Std Error: 0.00
Plate: 0285 row: F column: 14
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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Best Local Similarity 100.0%; Pred. No. 2.6
Matches 32; Conservative 0; Mismatches
                                                                                                 organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                                                                                /mol_type="genomic DNA"
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Location/Qualifiers
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                                                                                                                                                                                                                                                         /sex="Male"
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Unpublished (2000)
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Fax: 801 585 7177
   High quality
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High quality sequence stop: 32.
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                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orlifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwap42 (gql 4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0438E02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murcidea; Muridae; Musinae; Mus.

1 (bases 1 to 32)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Ralam, M., Longacres, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R.
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Fax: 801 585 7177
Bazil: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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1.2%; Score 32; UB.
Best Local Similarity 100.0%; Pred. No. 2.6.
Matches 32; Conservative 0; Mismatches
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                            organism="Mus musculus"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                     /mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC1M0285F14"
High quality sequence stop: 32.
Location/Qualifiers
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GSS.
                                                                                                                                                                                                             /sex="Male
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84112, USA
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AZ611890/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high malar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoreais. Vector DNA was prepared from a derivative of pWD42 (gi|473214|qb|A123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
T-E1: 801 S85 566
Fax: 801 S85 7177
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Role, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R..
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
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2M0012O20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0012O20 R, genomic survey sequence.
AZ778018
                                                                                                                                                                                                                                            /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse lokb plasmid UUGCIM library"
/note="Wetcor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/65 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Pred. No. 2.6e+02;
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Insert Length: 10000 Std Error: 0.00
Plate: 0012 row: O column: 20
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                            /organism="Mus musculus"
                                                                                             /mol_type="genomic DNA"
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                                                                                                                                                  /db_xref="taxon:10090"
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Location/Qualifiers
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                                                                                                                                                                                                                        /sex="Male"
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Best Local Similarity
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'organism="Brassica rapa subsp. pekinensis"
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1.2%; Score 32; DB
Best Local Similarity 100.0%; Pred. No. 2.6
Matches 32; Conservative 0; Mismatches
                                                                 /sub_species="pekinensis"
/db_xref="taxon:51351"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol type="genomic DNA"
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/clone="DKEY-85121"
                  /mol_type="genomic DNA"
/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Danio rerio"
                                                                                                                /clone="KBrS016J03'
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Danio rerio
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                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gil #4732114|gbl=R212972.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
                                                                                                                                                                                                    /lab. host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Twetcor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/64 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
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                                                                                               mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                       db_xref="taxon:10090"
clone="UUGC2M0012020"
       High quality sequence stop: 32.
Location/Qualifiers
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DU835386.1 GI:83871982
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Class: BAC ends.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinifones; Cyprinidae; Danio.

1 (bases 1 to 32)

Humphray,S.J., Huckle,E. and Hunt,S.E.

Direct Submission

Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail contact: hunquery@sanger.ac. uk Unpublished

This sequence was generated from the T7 end of BAC 85L21. 85L21 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
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Gallus gallus
Gukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
/lab_host="E. coli DH10B"
/clone lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="vector: pCUGIBACI; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
                                                                                                                                                                                                                                      Gaps
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Danio rerio genomic clone DKEY-85L21, genomic survey sequence.
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
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1.2%; Score 32; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0;
                                                                                                                                                                            1.2%; Score 32; DB 1; L. 100.0%; Pred. No. 2.6e+02;
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/note="vector pIndigoBAC-536"
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AZ345610
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                                                                                                                                                                                                                                                                                                                        BU431798 33 bp mRNA linear EST 09-SEP-2002 60165890R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855694 3', MRNA sequence.
BU431798
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                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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1 (bases 1 to 33)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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100.0%; Pred. No. 2.7e+02;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                              1. .33
/organism="Gallus gallus"
/mol_type="mKNA"
/db_xref="taxon:9031"
                                                                          Contact: Frazer Murray Dept. Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 31.
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                                           BP Chicken Brain Library
Unpublished (2001)
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Homo sapiens
Phasianinae; Gallus.
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Best Local Similarity 100.C
Matches 32, Conservative
                (bases 1 to 33)
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University of Utah

Residual Sender B. Weiss

University of Utah

Rem. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                       /tissue_type="adenocarcinoma"
/lab host="hHi0B (phage-resistant)"
/clone_lib="NHMGC_66"
/note=Torgan: ovary; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ345610 34 bp DNA linear GSS 29-SEP-200
1M0080C24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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//note="Wector: PWD42In', Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: C column: 24
Seq primer: GGTGTAAAACGACGGCCAGT
Class: plaamid ends
High quality sequence stop: 34.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   / organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/64"
/db_xref="taxon:10090"
/clone="UUGC1M0080C24"
/clone="IMAGE:3855694"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
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Page 190

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electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XIII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tlasue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM9501 row: j column: 08
High quality sequence stop: 30.
Location/Qualifiers
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/db xref="taxon 9606"
/clone="IMAGE:4184167"
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/lab_hogt="glioblastoma with EGFR amplification"
/lab_hogt="DH108 (T1 phage-resistant)"
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/note=logan: brain; Vector: pCWV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 35)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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.00.0%; Pred. No. 2.7e+02;
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100.0%; Pred. No. 2.7e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
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DR073823 35 bp mRNA linear EST 08-JUN-2005 ik86e02.gl Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA

LOCUS DEFINITION

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

E 1 (bases 1 to 35)
S Erener, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mccombie@cshl.org
Original 3 prime EST has been reverse completed to be in 5 prime
direction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /notes-Torgan: leaf; Vector: :pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Stratagene ZAP Express CDNA Synthesis The library was size-fractionated to enrich for large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.2%; Score 32; DB 1; Lt. 00.0%; Pred. No. 2.7e+02;
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|mol_type="mkNA"
|db_xref="taxon:6183"
|clone="SmlC21f11.q1k"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
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Best Local Similarity 100.0%; Pred. No. 2...
Matches 32; Conservative 0; Mismatches
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Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers

    .35
    /organism="Ginkgo biloba"

                                                                                              Ginkgo biloba (maidenhair tree)
Ginkgo biloba
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/db_xref="taxon:3311"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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DR073823.1 GI:67051746
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Schistosoma mansoni
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Oryza sativa (japonica cultivar-group)
Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Supermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.

El (Dases 1 to 40)
S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
U Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University
YongIn, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 8 231 231 6355
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S013312-024-018-B02-T7 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-018-B02 3-PRIME, mRNA sequence.
BQ590703.1 GI:26120286
EST.
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                                                                                                                                                                                                                                                                         EST 04-NOV-2004
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                                                                                                                                                                                                                                                                     CV723737 Linear EST 04-NOV-20 root--04-J23.gl Rice root lambda phage cDNA library (root) Oryza sativa (japonica cultivar-group) cDNA clone root--04-J23, mRNA
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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/mol type="mRNA"
/cultivar="mackdong"
/db xref="taxon:39947"
/clone="root--04-J23"
/fissue_type="root"
/dev stagge="14 days after germination"
/lab_nost="E.coli SOLR"
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Location/Qualifiers
                                                                       Length 39
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2.9e+02;
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                                                                     1.2%; Score 32; DB 1; L. 100.0%; Pred. No. 2.9e+02;
                                                                                                                                           2709 ААААААААААААААААААААААААААААА
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                                                                                      Local Similarity 100.
1es 32; Conservative
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Beta vulgaris
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Matches 32; Conserv
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35 bp mRNA linear EST 04-NOV-2004 [145alt--01-H08.gl Salt treated rice leaf lambda phage cDNA library [145alt) Oryza sativa (japonica cultivar-group) cDNA clone cV724720 [CV724720.] GI:55412344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="storage root"
/lab_host="EMDH108"
/clone lib="MPIZ-ADIS-024-storage root"
/note="vector: pomySPORT6; Site_1: Sal1; Site_2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophylales; Amaranthaceae; Beta.

1 (bases 1 to 35)

1 (bases 1 to 35)

Berwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             orientation:
SP6-Sall-CCA/GCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local P1: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 35)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Nahm B.H. GreenGene Biotech Inc.; Division Genomics and Genetics Institute, GreenGene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. 35
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                         Contact: Weisshaar B
ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: Weisshaa@mpiz-koeln.mpg.de
Insert Length: 35 Std Error: 0.00
Plate: 18 row: B column: 02
Seq primer: T7; GTAATACGACTCACTATAGGGC.
Location/Qualifiers
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/db_xref="taxon:161934"
/clone="024-018-B02"
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Tue Nov

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
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2M0207B13F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0207B13 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                    /db xref="taxon:39947"
/clone="14Salt--01-H08"
/tissue type="leaf"
/dev_stage="14 days after gernimation"
/lab_host="E.oli SOLR"
/clone lib="Salt treated rice leaf lambda phage cDNA
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|mol_type="mRNA"
|cultivar="Nackdong"
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of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                     Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0207 row: B column: 13
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/mt.zein="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0207B13"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 36.
Location/Qualifiers
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GSS.
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AZ945733/c
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/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Wouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resources
(http://www.jax.org/resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt enda-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 bp DNA linear GSS 08-AUG-2005 402101F02.2EL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic CZ919025
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( (Dasses 1 to 36)
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Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleages.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021011 row: F column: 02
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/lab_host="DH10B"
/clone_lib=="4021 - RescueMu Grid V"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHi; Site_2: BgIII; RescueMu is a 4.9 kb, moddified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
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/culTivar="mixed background W23/A188/B73/K55"
/tisue_trype="leaf"
/tisue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31.8; DB 1; Length 36;
Pred. No. 2.9e+02;
0; Mismatches 2; Indels
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/organism="Zea mays"
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ZEBRA_2F_2-II_03_ZEBRA_2F_2-II_03_G05.ab1, mRNA sequence.
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/mol_type="mRNA"
/cultivar="Nackdong"
/cultivar="Nackdong"
/clone="TAEAR--03-809"
/tissue_type="leaf"
/de_stage="7 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web stet "http://www.murransposon.org/project/RescueMu/". Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and Bill, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 37)
1 (bases 1 to 37)
1 (kim,J.K., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yonglin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers
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CF299167.1 GI:33670928
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/db xref="taxon:28909"
/clone="ZEBRA_2F_2-II_03_ZEBRA_2F_2-II_03_G05.abl"
/tissue_type="Crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass line Zebra subtracted cold acclimated cDNA library"
/note="Vector: Qiagen's pDrive; Messenger RNA was extracted from control and cold acclimated bermudagrass extracted from control and cold acclimated bermudagrass crown tissue at 2 and 28 days after acclimation and cDNA library was constructed following Clontech FCR- select cDNA subtraction procedure."
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AL462533
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                                                                                      Cynodon dactylon (Streptophyta; Embryophyta; Tracheophyta; Bubrayota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Chloridoideae; Cynodonteae; Cynodon.

I (bases 1 to 38)

Melmaise, K., Elavarthi, S. and Guenzi, A.C.
Identification of differentially expressed genes associated with and cDNA microarrays
Unpublished (2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Guenzi AC
Dep. of Plant and Soil Sciences
Oklahoma State University
368 Agriculture Hall, Stillwater, OK 74078-6028, USA
Pat: 405-744-6028
Pax: 405 744 6039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 38;
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1 Similarity 94.3%; Pred. No. 2.9e+02;
33; Conservative 0; Mismatches 2
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                                                                  Cynodon dactylon (Bermuda grass)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: acg@mail.pss.okstate.edu
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/cultivar="Zebra"
DN988546.1 GI:66248373
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BACKWARD: M13 Reverse
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CF278363.1 GI:33655749
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Best Local Similarity 97.0
Matches 32; Conservative
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AUTHORS
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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution in to give a tight size distribution is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing projects. In Genome Sequencing projects. In Barrell, Oxford University Press, 1999).
Email: nelsayed@etigr.oxg
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /uganzen_sca myz / mol type="genomic DNA" / mol type="genomic DNA" / cullivar="mixed background W23/A188/B73/K55" / db xref="taxon:4577" / td bxref="taxon:4577" / tsue_type="leaf" / dev_erage="adult" / dev_erage="adult" / lab_host="DH108" / clone_lib="4018 - RescueMu (engineered from fore="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Sire_l: BamHI; Sire_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web
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4018005H03.2EL x1 4018 - RescueMu Grid X Zea mays genomic, genomic
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Walbor V
Department of Biological Sciences
Stanford University
Stanfornia Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbor@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Trypanosoma brucei"
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                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:5691"
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Matches 33; Conservat
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Zea mays
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CZ908819
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TITLE
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site 'http://www.mutransposon.org/project/RescueMu/'. Grid X was grown at UCSD in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DHIOB cells were transformed and then screened on LB plates with ampicillin."
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14ETL--04-D24.gl Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-D24,
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7LEAF--01-G07.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-G07, mRNA
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Oryza sativa (japonica cultivar-group)
Dryza sativa (japonica cultivar-group)
Dryza sativa (japonica cultivar-group)
Dryza sativa (japonica cultivar-group)
Dryza, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Glade; Ehrharcoideae; Oryzeae; Oryza,
I (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Yongin, KyeongJi, Korea
Yongin, KyeongJi, Korea
Far: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/db.ref="TLEAF--01-G07"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Wettor: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and Then used as templates for
                                                                                                                                                                                                                                                                                Gaps
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/mol type="mRNA"
/cultivar="Nackdong"
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1.1%; Score 31.4; DB 1; Length 33;
Best Local Similarity 97.0%; Pred. No. 2.9e+02;
Matches 32; Conservative 0; Mismatches 1; Indels
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Pred. No. 3e+02;
0; Mismatches 1; Indels
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39 bp mRNA linear EST 01-AUG-2003
B09A01.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
CA853500
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Alkharouf,N., Khan,R. and Matthews,B.
Analyais of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Genome 47 (2), 380-388 (2004)
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                                         Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; Liliopaida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza,
1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gpio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/lab_host="B.coli DH10B"
/lab_host="B.coli DH10B"
/lab_host="B.coli DH10B"
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Location/Qualifiers
1. .39
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Fax: 301 504 5728
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Best Local Similarity
Matches 32; Conserv
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E 1 (bases 1 to 38)

S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH108"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
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Mkaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida, Poales, Poaceae; BEP
clade, Ehrhartoideae; Oryzeae, Oryza.
                                                                                              /tissue_type="Roots"
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/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 12hr SCN3"
/note="lib="cDNA Peking library 12hr SCN3"
/note="lib="cDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HD--13-D01.gl OsHDACI-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--13-D01, mRNA sequence.
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/mol_type="mRNA"
/cultivar="Nackdong"
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94.1%; Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                         Score 31.2; DB 1;
Pred. No. 3.2e+02;
0; Mismatches 3;
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organism="Glycine max"
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/clone="HD--13-D01"
          /mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
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                                                                              /clone="B09A01"
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Genomics and Bioinformatics
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Matches 31; Conserv
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                                                                          ABF--01-018.bl ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--01-018, mRNA sequence.
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Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantea, Streptrophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza,
I (basea: I to 39)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yogian, Kyeonggi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/db_xrel=taxon:39947"
/clone="ABE-taxon:39947"
/tissue_type="leaf"
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/dev_stage="leaf"
/dev_stage="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA_library (ABF)
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nes 33; Conserv
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Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Sitel: EcoRI
R. Site2: Smal 5' Seq Primer T3 Normalised library constructed from
bovine ovary. Clones available from UK Centre for Functional
Genomics in Farm Animals. Roslin Institite, Roslin, Midlothian, UK,
EH25 9PS, www.axkgenomics.crg.
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Sitel: EcoRI
R. Site2: NotI S' Seq Primer M13F Normalised library constructed
from pooled early embryos, from 8- cell stage to blastocysts.
Clones available from UK Centre for Functional Genomics in Farm
Animals, Roslin institute, Roslin, Midlothian, UK, EH25 9PS,
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Development of CDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
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mRNA sequence.
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/note="Vector: pBlueScriptII(SK+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled early embryos, from 8-cell stage
to blastocysts."
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/tissue type="ovary"
/clone lib="KN261"
/note="vector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2: SmaI; Single pass sequencing. Normalised library constructed from bovine ovary."
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 31)
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2.9e+02;
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100.0%; Pred. No....
0; Mismatches
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/tissue_type="embryo"
/clone_lib="KN277"
                                                                                                                                                                                                                                                                                                                                                                            /organism="Sus scrofa"
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/mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                   www.arkgenomics.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (cattle)
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mRNA sequence.
CF278807
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CF278807
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                                                                                                                                                                                                                                                                                                                                   Schistosoma manson:
Eukaryota: Metazoa; Platyhelminthes; Trematoda; Digenea;
Eukaryota: Metazoa; Platyhelminthes; Trematoda; Digenea;
Erigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
El (bases 1 to 31)

Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaidou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni
U Unpublished (2005)
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CBIO 1SA, UNITED KINGDOM.
                                                                                                                                                                                                         AM044121 Schistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                            Gaps
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/db xref="taxon:6183"
/clone="SmlCl1f01.q1k"
/clone="lung schistosomulum"
/clone lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"
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Glossina morsitans morsitans
Glossina morsitans
Glossina morsitans
Glossina morsitans
Glossina, Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.

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1 (base 1 to 31)
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100.0%; Pred. No. 2.9e+02;
ative 0; Mismatches 0;
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/organism="Schistosoma mansoni"
                                                                         2709 АААААААААААААААААААААААААААА
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                                                                                               100.0%; Prec. ....
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Genome Biol. 4 (10), R63 (2003)
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AM044121.1 GI:72293459
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BX569502.1 GI:33437420
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1es 31; Conservative
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Query Match
Best Local Similarity
Matches 31; Conserv
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/note="country: Zimbabwe; EST from adult gut infected with
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                  /organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tee903" plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans adult infected
The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J.Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix q1c are reverse primer reads starting at the 3' end.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Location/Qualifiers
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/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
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1.1%; Score 31; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0;
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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--04-N15"
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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RESULT 518 CF300345/c

8 셤 DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb12 (gil #4732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Mus maculus
Mus musculus
Muscaryotas, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Nm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse lokb plasmid UUGCIM libraty"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
1 (bases 1 to 31)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 506
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: A column: 21
Seg primer: CGTTGTAAAACGACGACCAGT
Class: plasmid ends
High quality sequence stop: 31.
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/strain="C57BL/6J"
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/clone="UUGC1M0062A21"
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/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:39947"
/clone="7LEAR--04-L08"
/tissue_type="leaf"
/dev stage="7 days after germination"
/dow stage="7 days after germination"
/done="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF300345
7LEAF--04-L08.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-L08, mRNA
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Oryza sativa (japonica cultivar-group)
Coryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spernatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Ory
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Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
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Yongin, KyeongJi, Korea
1330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                     DB 1; Length 31;
2.9e+02;
                                                                                                                              0; Indels
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                                                     1.1%; Score 31; DB: 100.0%; Pred. No. 2.9ctive 0; Mismatches
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AZ333315.1 GI:10397811
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                                                     Query Match
Best Local Similarity 100.0
Matches 31; Conservative
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FEATURES

GSS 02-OCT-2000

VERSION KEYWORDS SOURCE ORGANISM

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RESULT 519 AZ333315/c

Best Loca Matches

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                              AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gil-4732114 [gb]-AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0354P14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0354P14 F, genomic survey sequence.
AZ510092
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus.
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/clone lib="Mouse 10kb plasmid UNGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G77BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                         Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
1 (bases 1 to 31)
Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC1M0129D08"
                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
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GSS.
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                                                                                                                                                                      Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gilfyl732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                          Unpublished (2000)
Contact: Robert B. Weiss
Contversity of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/close_lib="Mouse_10kb plasmid UUGCIM library"
/note="Wector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Dunn, D., Aoyago, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Waiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0354 row: P column: 14
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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Location/Qualifiers
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MAG69CO9R MOUSE 10kb plasmid UUGC1M library Mus musculus genomic
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
l (bases 1 to 31)

Dunn,D., Aoyagi,A., Barber,W., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Nouse, whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunm@gonetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0461 row: G column: 21
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Seg primer: CGTTGTAAAACGACGGCCAGT
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Location/Qualifiers
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Mus musculus
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AUTHORS
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                                                                                  TITLE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of public 4732114 [pd] AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xillo-Gold (stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                           Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
1 (bases 1 to 31)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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100.0%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0469 row: C column: 09

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                              plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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Location/Qualifiers
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Mus musculus (house mouse)
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            (bases 1 to 31)
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Best Local Similarity
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2M0093F21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab host="E. Coli strain XLIO-Gold, TI-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.musculus G57BL/65 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                              E., SLC,
1 (bases 1 to 31)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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University of Utah Genome Center
University of Utah
Win. 308, Biomedical Polymers Research Bldg., 20 S. 2030
84112, USA
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                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0014 row: O column: 02
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
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Best Local Similarity 100.0%; Pred. No. 2.3
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0014002"
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Location/Qualifiers
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DEFINITION
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AUTHORS
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(http://www.dax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gilfa732114 [gb] AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
Loades 1 to 31)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD421v; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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100.0%; Pred. No. 2.9e+02;
7ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0093 row: F column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC2M0093F21"
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REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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/ vuganizume ...cea wayb."
/wol_type="genomic DNA"
/cul_ivar="mixed background W23/A188/B73/K55"
/dispue="genomic DNA"
/tissue_type="leaf"
/tissue_type="leaf"
/tissue_type="leaf"
/lab_host="DH10B"
/clone_lb="dogan: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamH1; Site_2: Bg1II;
/RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/'. Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHI
and Bg1II, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."
                                             Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                         Department of Biological Sciences
Stanford University
Stanford University
Stanford University
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uuwssoll SSS 22-DEC-20
KBrS015N15F KBrS, Brassica rapa SaulAl BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS015N15, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            End sequence of Brassica rapa Sau3AI (KBrS) BAC clone Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 31;
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Fax: +82-31-299-1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31; DB 1; Le
Pred. No. 2.9e+02;
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V 100.0%; Pred. No. ...
'--- 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                              Class: transposon-tagged.
Location/Qualifiers
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     (bases 1 to 31)
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/ clone lib="mouse 10kb plasmid UUGCIM library"
/ clone lib="wouse 10kb plasmid UUGCIM library"
/ note="Vector: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114]gb|APL29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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4021004C05.1EL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 31)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Nouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center
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.00.0%; Pred. No. 2.9e+02;
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84112, USA
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                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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tive 0; Mismatches

    .31
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: CGTTGTAAAACGACGGCCAGT
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: plasmid ends
High quality sequence stop: 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:10090"
clone="UUGC2M0102C19"
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E.coli DH10B"
/clone lib="KBrB, Brassica rapa BamHI BAC library"
/clone lib="KBrcor: pcuGlabCl; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                               ö
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS015N15
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 31)
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
End sequence of Brassica rapa BamHI (KBrB) BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Beom-Scok Park
Brassica Genomics Team
Brational Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Brasi: +82-31-299-1672
Brail: pbeom@ads.go.kr
                                                                                                                                                  /mol type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="caxon:51351"
/clone="KBrS015N15"
/lab_host="E. coli DH10B"
/clone lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."
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/organism="Brassica rapa subsp. pekinensis"
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/mol_type="genomic DNA"
/cultivar="Chiifu"
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/db_xref="taxon:51351"
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                                                                                                Location/Qualifiers
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nes 31; Conservative
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KBrB071A09
Seq primer: T7
Class: BAC ends.
                                                        Seq primer: T7
Class: BAC ends
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AV674152 Nori Satoh unpublished cDNA library Ciona intestinalis CDNA clone citb14122 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Pulebobranchia; Cionidae; Ciona.
1 (bases 1 to 34)
Satch,N., Satcu,Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satch
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 31-JAN-2000
                                                Gaps
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Pneumocystis carinii
Bukaryota; Pungi; Ascomycota; Pneumocystidomycetes;
Bukaryota; Pungi; Ascomycota; Pneumocystidaceae;
1 (bases 1 to 34)
Smullan,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C., Edman,J.C., Kovacs,J. and Cushion,M.
Expressed sequence tags from Pneumocystis carinii
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Staben C
School of Biological Sciences
University of Kentucky
University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library"
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    Length 31;
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                                              Indels
1.1%; Score 31; DB 1; L. 100.0%; Pred. No. 2.9e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Ciona intestinalis"
/mol_type="mkn4"
/db_xref="taxon:719"
/clone="citb14i22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                          2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
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AV674152.1 GI:10112151
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Query Match
Best Local Similarity 100.
Matches 31; Conservative
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BQ587432
BQ587432.1 GI:26117014
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Query Match
Beet Local Similarity 100...
"Thes 31; Conservative
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E 1 (bases 1 to 36)
S Alis, Holloway, B. and Taylor, W.C.
Normalisation of creal endosperm EST libraries for structural and functional genomic analysis.

Plant Mol. Biol. Rep. 18, 123-132 (2000)
Contect: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry.

CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia Tel: 61 2 6246 5203
Fax: 61 2, 6246 5203
                                                                                                                                        /mol type="mkna".
/db Xref="taxon.4754"
/db Xref="taxon.4754"
/db Aref="E.coli"
/clone lib="Ag21"
/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6, ascrificed on 3/17/9) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard conditions described by vendor, Stratagene. Further details see www.uky.edu/Project/Pheumocystis/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    post anthesis) "Life Technology)" "Close in the host" DH108 (Life Technology)" "Close in the host "DH108 (Life Technology)" "Close in the west EST endosperm library" (note—"Vector: ZipLox; Site I: Sal I; Site 2: Not I; mRNA was prepared from endosperm Lissues of the wheat cultivar Hartog. CDNA was synthesized from pooled 6, 8, and 10 dpa endosperm using Not I-oligo (dT)18 primer/adapter (Pharmacia Biotech), and then ligated to the Sal I-Not I saite of ZipLox vector (Life Technology) after adding a Sal I-Xho I adapter (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CV066718 ST endosperm library Triticum aestivum cDNA clone WNEL7d3 Wheat EST endosperm library Triticum aestivum cDNA clone WNEL7d3 5' similar to Unknown Function, mRNA sequence.
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/dev_stage="developing endosperm tissue 6,
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.1%; Score 31; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 31; Conservative 0; Mismatches 0; Indels
                                                                                                                          organism="Pneumocystis carinii"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol type="mRNA"
/cullivar="Hartog"
/db xref="taxon:4565"
/clone="WNEL7d3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Bill.Taylor@csiro.au
Seq primer: Ml3 reverse primer
High quality sequence stop: 36
Location/Qualifiers
                          Fax: 606 257 1717
Email: staben@pop.uky.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CV066718
CV066718.1 GI:51529895
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/note="Vector: pcMvSPORT6; Site 1: Sall; Site 2: Not1; CDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schullz@kws.de; cloning sites Sall-Not1, primer sites and
                                                         ö
                                                                                                                                                                                                                                                                                                               BQS87432
S013303-024-010-B02-T7 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta vilgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 34)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
and Radelof,U.
Construction of a 'uniqene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
plant J. 32 (5), 845-857 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/culTivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
     DB 1; Le
. 3.2e+02;
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/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: weisshad@mpiz-koeln.mpg.de
Insert Length: 34 Std Error: 0.00
Plate: 10 row: B column: 02.5
Seq primer: T7; GTAATACGACTCACTATAGGGC.
Location/Qualifiers
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/clone="024-010-B02"
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Query Match
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CV848473/c
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              GSS 22-DEC-2005
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KBrB051B15F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB051B15, genomic survey sequence.
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                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
J4 bp DNA linear GSS 22-DEC-2(KBrS011B02F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS011B02, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. coli DH10B"
/clone lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBACI; Site 1: Sau3AI, Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
                                                                                                                                                                                                                                                                       Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J. H. and Park,B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'organism="Brassica rapa subsp. pekinensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       National Institute of Agricultural Biotechnology 225 Seodun-Dong, Suwon, 441-707, Korea Tel: +82-31-299-1670
Fax: +82-31-299-1672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30.8; DB 1;
Pred. No. 3.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS011B02"
                                                                                                                                                      Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA/
/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: T7
Class: BAC ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               Contact: Beom-Seok Park
Brassica Genomics Team
                                                                                                                DU832879.1 GI:83869475
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Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KBrS011B02
                                                                                               DU832879
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/clome_lib="KBrB, Brassica rapa BamHI BAC library"
hote="Vector: pCUGIBAC1; Site_l: BamHI; Brassica rapa spp
pekinensis var. Chilfu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CV848473 37 bp mRNA linear EST 17-NOV-2004 IIOAAEBSCH01RM1 IDOAEBS ACYTCHOSiphon pisum cDNA clone IDOAEBSCH01 5.7, mRNA sequence.
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Acyrthosiphon pisum
Acyrthosiphon pisum
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases I to 37)
Sabater-Munoz, B., Legeai, F., Bonhomme, J., Dang, P., Dossat, C.,
Duclert, A., Gauthier, J.P., Hunter, W., Martinez-Torres, D., Moya, A.,
Simon, J.C., Stern, D., Wincker, P. and Tagu, D., Shigenobu, S.,
Annotated ESTs of the pea aphid
Unpublished (2004)
National Institute of Agricultural Biotechnology
225 Seedun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB051B15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBS-SKminus; Site_1: EcoRI; Site_2: XhoI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                 /organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/cultivar="chiifu"
/sub are="chiifu"
/db xref="taxon:5131"
/clone="KBrB051B15"
/lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 34;
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INRA Rennes
HWR BioJP, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30.8; DB 1;
Pred. No. 3.2e+02;
0; Mismatches 2;
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    .37
    /organism="Acyrthosiphon pisum"

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/clone="ID0AEE5CH01"
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/lab_host="XL1-Blue"
                                                                                                                                                                                                                                                       Location/Qualifiers
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FORWARD: CAGGAAACAGCTATGACC
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/cultivar="yr2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CV848473.1 GI:55814156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%;
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                                                                                                                                                                                                    Seq primer: T7
Class: BAC ends.
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Query Match
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JOURNAL
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                                                                           REFERENCE
AUTHORS
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Sample name: IDOAEE; Plant growth place: INRA Rennes, UMR BiO3P, 35327, 35653 Le Rheu Cedax France; Soil conditions: Soil; Sowing date: 15/04/2004; Harvesting date: 15/04/2004; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. Appisum YRZ is holocyclic, i.e. able to change its reproductive mode under short photoperiods (sexual) versus long photoperiods (clonal). experimental condition: long photoperiod (16-hr light/8-hr dark at 18 degc)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CF302459
32 bp mRNA linear EST 15-AUG-2003 7LEAF--08-A01.gl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--08-A01, mRNA
                                                                                                                                                                                                                                                                                                                                                                      AJ791147 Antirrhinum majus whole plant Antirrhinum majus cDNA clone AJ791147 A1147—01, mRNA sequence.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiids, Lamiales, Plantaginaceae, Antirrhineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 32)
Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
Saedler,H. and Zachgo,S.
Characterization of Antirrhium Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
                                                                                                                                                                                                                             Gaps
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0
                                                                                                                                                                                     1.1%; Score 30.6; DB 1; Length 37; 89.2%; Pred. No. 3.4e+02; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="texon:4151"
/db_cref="texon:4151"
/tissue="1018_2 07 001"
/tissue="type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                              37 AATAAAAAAAAAAGAAAAATAAAGAAAAAAAAAA 1
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Pred. No. 3.3e+02;
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MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antirrhinum majus (snapdragon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Schwarz-Sommer Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ791147.1 GI:51061240
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                                                                                                                                                                                                          Best Local Similarity 89.2
Matches 33; Conservative
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tes 31; Conservative
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Best Local S:
Matches 31
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AJ791147/c
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7Î, Avenúe Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
                                                                                                                                                                                                                          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="leaf"
/dev_stage="7 days after germination"
/dev_stage="7 days after germination"
/lab host=="8.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza,
1 (bases 1 to 32)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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    .32
/organism="Oryza sativa (japonica cultivar-group)"

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96.9%; Pred. No. 3.3e+02;
tive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: 9.hamdi@bordeaux.inra.fr
Seq primer: 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:39947"
/clone="7LEAF--08-A01"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="Nackdong"
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Query Match
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        AZ314322/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                          DV083947 1:0 H15 KS Nematostella vectensis normalized cDNA library 327 Nematostella vectensis cDNA clone 327-384-10 H15 KS, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="whole embryos"
/dev_stage="mixed stages from unfertilized eggs to primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
/mol_type="mRNA"

cultivar="cabernet Sauvignon"

/do xref="taxon:29760"

/do xref="Ba3CS128016C02"

/dev stage="green stage"

/dev stage="green stage"

/do stage="green stage"

/note="Organ: Fruit without seeds; Vector: Lambda

TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Nematostella vectensis normalized cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Technau, U., Rudd, S., Maxwell, P., Gordon, P.M.K., Saina, M., Grasso, U.C., Hayward, D.C., Sensen, C.W., Saint, R., Holstein, T.W., Ball, E. E. and Miller, D.J. Maintenance of ancestral complexity and non-metazoan genes in two basal cnidarians

Trends Genet. (2005) In press Contact: Ulrich Technau Sars Centre for Marine Molecular Biology Sars Centre for Marine Molecular Biology High Technology Building, Thormohlensgt. 5 5008 Bergen, Norway Tel: 447-55584340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nematostella vectensis
Eukaryota; Metazoa; Cnidaria; Anthozoa; Hexacorallia; Actiniaria;
Edwardsiidae; Nematostella.
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96.9%; Pred. No. 3.3e+02;
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/organism="Nematostella vectensis"
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/sex="hermaphrodite"
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/db_xref="taxon:45351"
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                                                                                                                                                                              Query Match
Best Local Similarity 96.99
Marches 31; Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwbM2 (giffa)2114 [gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
AZ314322 329-SEP-2000 1M0031N05F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0031N05 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                       Euteleostomi;
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//lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
//lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
//clone lib="Mouse 10kb plasmid UUGCIM library"
//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                            Sciurognathi, Murcidea; Muridae; Muzinae; Musinae; Lougacie; Lougacie; Mahmoud; M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Kose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weises, R.
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                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut.
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 031 row: N column: 05
Seq primer: CGTTGTAAACGACGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="UUGC1M0031N05"
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Location/Qualifiers
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AZ314322.1 GI:10360096
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Page 208

AZ579652/c LOCUS ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL COMMENT

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Location/Qualifiers
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Class: BAC ends
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                                                                                                                                                                                                    Mus musculus (note) modes, Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muscidea; Murinae; Mus. Rosentia; Losses 1 to 32) S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. ingey, A., von Niederhausern, A. and Wright, D., Weiss, R. ingey, A., von Dupulished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Genome Center University of Utah
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                        AZ579652 32 bp DNA linear GSS 13-DEC-2000
1M0367C12R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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                                                                            clone UUGC1M0367C12 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
Fax: 801 585 7177
Insert Length: 10000 Std Error: 0.00
Plate: 0367 row: C column: 12
Seq primer: CARACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 32.
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="UUGC1M0367C12"
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                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                       AZ579652
AZ579652.1 GI:11694081
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Matches 31; Conserv
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FEATURES

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Jabp DNA linear GSS 10-JAN-2006 KBrB031B19R KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB031B19, genomic survey sequence.
                          GSS 22-DEC-2005
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases I to 32)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
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Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
J2 bp DNA linear GSS 22-DEC-20 KBrS014013F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS014013, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab host="E. coli DH10B"
/clome_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="vector: pCtGIBAC1; Site_l: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
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Xang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.1%; Score 30.4; DB 1; Length 32; 96.9%; Pred. No. 3.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Beom-Seck Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seedun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sub_species="pekinensis"
/db_xref="taxon:51351"
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Oryza sativa (japonica cultivar-group)

Gryza sativa (japonica cultivar-group)

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatcphyta; Magnollophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 33)

Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,

Song, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H.

Large-Grale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B. H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Bmail: bhnahm@ggblo.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverses transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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                                                                                    EST 18-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
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/clone="JMT--04-F19"
/tissue_type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
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Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
I (basea I to 34)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                    JMT--04-F19.gl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--04-F19, mRNA sequence. CF334899
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1.1%; Score 30.4; DB 1;
Best Local Similarity 96.9%; Pred. No. 3.38+02;
Matches 31; Conservative 0; Mismatches 1;
                                                                                    mRNA
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AZ307192.1 GI:10345947
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                                                                                    CF334899
                                 RESULT 546
CF334899/c
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                                                                                                                                                                                                                                                                                                                                                                                               / gub_species="pekinensis"

/ db_xref="texon:51351"

/ clone="KBrB031B19"

/ lab_host="B.coli DH10B"

/ clone_lib="KBrB, Brassica rapa BamHI BAC library"

/ note="Vector: pUCGIBAC1; Site_1: BamHI; Brassica rapa spp

pekinensis var. Chiffu BAC library (KBrB BAC) is provided

by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 32)

Humphray, S. J., Huckle, E. and Hunt, S. E.

Direct Submission

Direct Submission

Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: hunguery@sanger.ac.uk Unpublished

This sequence was generated from the SP6 end of BAC 1F7. 1F7 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
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Contact: Beom-Seok Park
Brassica Genomics Team
Brassica Genomics Team
Brassica Genomics Team
Brain Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Brail: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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Danio rerio genomic clone DKEY-1F7, genomic survey sequence.
AL735323
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Location/Qualifiers
1. .32
/organism="Danio rerio"
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1 .32
/organism="Brassica rapa subsp. pekinensis"
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1.1%; Score 30.4; DB 1;
Best Local Similarity 96.9%; Pred. No. 3.3e+02;
Matches 31; Conservative 0; Mismatches 1;
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/note="vector pindigoBAC-536"
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                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/cultivar="Chiifu"
                                                                                                                                                                                                                          Seq primer: M13 Reverse
Class: BAC ends.
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Best Local Similarity 96.9
Matches 31, Conservative
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Gaps

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CN546158.1 GI:46910783
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Contact: Hamdi S.
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Matches 31; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab host="E" Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus (C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
/nttp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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SET 17850 Ripe Grape Skin Triplex2 Library Vitis vinifera CDNA clone B3CS00RL006C01 3', mRNA sequence.
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1 (bases I to 36)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps .
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                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0008 row: B column: 07
Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AAAAAAAAAGAAAAAAAAAAAAAAAA 34
                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
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Location/Qualifiers
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clone="UUGC1M0008B07"
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CN545906.1 GI:46910531
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Vitis vinifera
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                       COMMENT
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/mol type="mRNA"
/mol type="mRNA"
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SfilA; Site_2: SfilB; Oriented library"
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                                                             71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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France
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Wataryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons,
rosids, Vitaceae, Vitis.
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Abbal, P., Agases A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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Universite de Bordeaux I, Institut National de la Recherche
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                                                                                                                                                                                                                                                                                                     /organism="Vitis vinifera"
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/cultivar="Cabernet Sauvignon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                  Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seg primer: T7
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Vitis vinifera
Vitis vinifera
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bermacophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermacophyta, Magnoliophyta, eudicotyledons,
rosids, Vitaceae, Vitis.
1 (bases, 1 to 36)
Abball, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
Or seeds) at Various Developmental Stages
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Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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KBrS014E10R KBrS, Brassica rapa Sau3Al BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS014E10, genomic survey
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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      Length 36;
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    Score 30.4; DB 1;
Pred. No. 3.5e+02;
0; Mismatches 1;
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1.1%; Score 30.4; DB 1;
Best Local Similarity 96.9%; Pred. No. 3.5e+02;
Matches 31; Conservative 0; Mismatches 1;
                                                                                 2709 ААААААААААААААААААААААААААААА
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Fax: 00-33-(0)5-57-12-25-48
Email: 8.hamdi@bordeaux.inra.fr
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ilarity 96.9%;
Conservative 0
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Brassica Genomics Team
Mational Institute of Agricultural Biotechnology
225 Seodun-Dong; Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Fmail: pbecom@rda.go.kr
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Vitis vinifera
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 37)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / sub_species="pokinensis"

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rosids, eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 36)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J. H. and Park, B.S. End sequence of Brassica rapa Sau3AI (KBrS) BAC clone Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNS45897 30-APR-EST 17841 Ripe Grape Skin Triplex2 Library Vitis vinifera CDNA clone B3CS00RL006804 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 36
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: 77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Seg primer: M13 Reverse
Class: BAC ends.
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Query Match Best Local 9

Matches

ઠ g VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

AUTHORS TITLE

REFERENCE

JOURNAL

COMMENT

LOCUS DEFINITION

RESULT 553 DN988462/c

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38 bp mRNA linear EST 30-APR-2004 EST 18695 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera CDNA clone B3CS58RB008C04 3', mRNA sequence.
                                                                                                                          CNS46437
EST 18581 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera CDNA clone B3CS57RB007A02 3', mRNA sequence.
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Vitis vinifera
Vitis vinifera
Vitis vinifera
Vitis vinifera
Vitis vinifera
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases I to 38)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Handi, S., Romieu, C. and Terrier, N.
Handis, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

1 (bases 1 to 38)
Abbal, P., Agases, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Handli, S., Komieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
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TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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/cultivar="Cabernet Sauvignon"
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CTGAAAAAAAAAAAAAAAAAAAAAAAA
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/clone="B3CS57RB007A02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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                                                                                                                                                                                                                                      CN546437.1 GI:46911062
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Vitis vinifera
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Best Local Simi
Matches 31;
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LOCUS
DEFINITION
                                                                           RESULT 554
CN546437/c
LOCUS
DEFINITION
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SOURCE
ORGANISM
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DN988462 2F.2-II 03 ZEBRA_2F 2-II 03 B04.abl Bermudagrass line Zebra subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone ZEBRA_2F_2-II_03_B04.abl, mRNA sequence.

DN988462
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SfiIA; Site_2: SfiIB; Oriented library"
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Cynodon dactylon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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( Dases i to 3).

Melmise, K., Elavarthi, S. and Guenzi, A.C.

Identification of differentially expressed genes associated with cold acclimation using suppression subtraction hybridization (SSH)
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Contact: Guenzi AC
Copt of Plant and Soil Sciences
Oklahoma State University
368 Agriculture Hall, Stillwater, OK 74078-6028, USA
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                                                                                                                                                                                                                                                                  / Match 1.1%; Score 30.4; DB 1; Length 37; Local Similarity 96.9%; Pred. No. 3.5e+02; Heat 31; Conservative 0; Mismatches 1; Indels
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Seg primer: M13 Forward.
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Fax: 405 744 6039
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                    Query Match
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                  Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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Triplex2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons,
rosids, Vitaceae, Vitis.
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Abbal, P., Agases, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaidechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
Unpublished (2002)
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TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Fax: 00-33-(0)5-57-12-25-48
Email: 8.hamdi@bordeaux.inra.fr
                                                                                                                                                                                                 Seq primer: T7.
Location/Qualifiers.
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Best Local Similarity 96.99
Matches 31, Conservative
  Unpublished (2002)
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401301SCO8.1EL x1 4013 - RescueMu Grid O Zea mays genomic, genomic
CZ916174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea. (bases 1 to 36)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Very probable ligation site of ends cut by single endonuclease. Reverse complemented post-ligation sequence from source sequence. Plate: 4013015 row: C column: 08
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/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="leaf"
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/db xref="leaf"
/db xref="leaf"
/db xref="DH10B"
/lobe lib="4013 - RescueMu Grid O"
/note="Organ: leaf; Vector: RescueMu (engineered from
                                                                 Gaps
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Score 30.4; DB 1;
Pred. No. 3.6e+02;
0; Mismatches 1;
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Stanford University
855 California Ave, Palo Alto, CA 94304,
121 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
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KEYWORDS
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Eukaryota, Metazoa, Platyhelminthes; Trematoda; Digenea;
Eukaryota, Metazoa, Platyhelminthes; Trematoda; Digenea;
Extragaldia, Schistosomatoidea; Schistosoma.

E 1 (bases 1 to 30)
E 1 (bases 1 to 30)
S Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaidou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni
L Unpublished (2005)
Context: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
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                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 30)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
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/db_xref="taxon:6183"
/clone="smlCl3a04.q1k"
/dev_stage="lung schistosomulum"
/clone lib="Schistosoma mansoni lung schistosomulum"
/clone lib="Schistosoma mansoni lung schistosomulum"
DKFZp56611846 r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp56611846, mRNA sequence.
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/lab_host="Xl-2blue"
/clone_lib="566 (8ynonym: hfkd2)"
/note="Vector: pAMPl; Site_1: NotI; Site_2: Sall"
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Location/Qualifiers
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/organism="Schistosoma mansoni"
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/organism="Homo sapiens"
/nol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKF2p56611846"
/tissue_type="kidney"
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EST (Ottenwaelder, et al.)
Unpublished (1999)
                                                            AL038650.1 GI:49682176
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                                                                                                     Homo sapiens (human)
Homo sapiens
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Best Local Similarity 100.0
Matches 30; Conservative
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BG666435 30-APR-2001
DRACKCO2 Rat DRG Library Rattus norvegicus cDNA clone DRACKCO2 5',
mRNA sequence.
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Laboratory of Sensory System
Institute of Neurosocience
10stitute of Neurosocience
2020 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
Fax: 86-21-6471346
Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
Pudong New Area, P.R.China: Please contact with Zhang Xu
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 30)
Xiao, H.S., Huang, Q.H., Zhang, F.X., Bao, L., Lu, Y.J., Guo, C.,
Yang, L., Huang, W.J., Fu, G., Xu, S.H., Cheng, X.P., Yan, Q., Zhu, Z.D.,
Zhang, X., Chen, Z., Han, Z.G. and Zhang, X.
Identification of gene expression profile of dorsal root ganglion in the rat peripheral axotomy model of neuropathic pain
Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
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/dev_stage="adult"
/clone_lib="Rat DRG Library"
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/mol_type="mRNA"
/strain="Sprague-Dawley"
/db xref="taxon:10116"
/clone="DRACRC02"
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2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
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Best Local Similarity 100.0%; Pred. No. 3.3
Matches 30; Conservative 0; Mismatches
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CF280699
CF280699.1 GI:33658085
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                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
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POLYA=No.
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30 bp mRNA linear EST 14-AUG-2003 14ROOT--02-M10.gl Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-M10, mRNA
                Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sparavota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhattoideae; Oryzeae; Oryza.
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Eukaryota; Viridiplantae; Strebtcoup)

Eukaryota; Viridiplantae; Streptcophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lilioppida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 30)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Sang,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeongqi, Korea 131 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yogin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/mol_type="mRNA"
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100.0%; Pred. No. 3.3e+02;
tive 0; Mismatches 0;
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/organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
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/db xxef="traxon:39947"
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with oligoribonucleotides and then used as templates for
RT-PCR."
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Kim, V.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Location/Qualifiers
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1 Similarity 100.0%; Pred. No. 3.3e+02;
30; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.3e+02;
ive 0; Mismatches 0;
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com,
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Best Local Similarity 100.º
Matches 30, Conservative
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
ABF--08-C19.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--08-C19, mRNA sequence. CF312417
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/mol type="mRNA"
/cultivar="Nackdong"
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Location/Qualifiers
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CF322226.1 GI:33693987
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CF322226/c
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
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/note="vector: pCR4-TOPO; Site 1: EcoR1; Callus was treated with ABA(20um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Fax: 82 31 321 6355
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                                                                                        'organism="Oryza sativa (japonica cultivar-group)"
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bhnahm@bio.myongji.ac.kr.
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
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100.0%; Pred. No. 3.3e+02;
trive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.3e+02;
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/clone="HD--13-M02"
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/cultivar="Nackdong"
                                                                                                                      /mol_type="mRNA"
/cultivar="Nackdong"
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Location/Qualifiers
                             Location/Qualifiers
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Vitis vinifera
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     ó,
                                                                                                                                                                  EST 18-AUG-2003
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Vitis vinifera
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, Vitaceae, Vitis.
1 (bases 1 to 30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="NackOng"
/db_xref="txen:39947"
/clone="JMT--06-K13"
/tissue_type="leaf"
/dev_stage="leaf"
/dev_stage="leaf"
/dev_stage="leaf"
/dev_stage="coli DH10B"
/clone lib="E.coli DH10B"
/clone lib="AtJWT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, MyongJi University
Yogin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                       30 bp mRNA linear BST 18-AUG-20 JMT--06-K13.gl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone CP3.45cc
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CF336555.1 GI:33821487
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CNS45913.1 GI:46910538
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Best Local Similarity 100.
Matches 30; Conservative
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France
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, M. Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
Onpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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1 (bass 1 to 30)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Handi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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Pred. No. 3.3e+0
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Fax: 00-33-(0)5-57-12-25-48
Email: 8.hamdi@bordeaux.inra.fr
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Location/Qualifiers
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CV728764 1inear EST 05-NOV-2004 FLO--01-E06.gl Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-E06, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                   71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
                                                                          Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

1 (bases 1 to 30)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
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Clone lib="Turning Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantas Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bloinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Vitis vinifera"
/mol_type="mRNA"
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/clone="B3CS38TB008G04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Location/Qualifiers
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                        Vitis vinifera
Vitis vinifera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         CN546474 30 bp mRNA linear EST 30-APR-2004 EST 18618 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera cDNA clone B3CS57RB007D06 3', mRNA sequence.
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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/mol_type="mRNA"
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Triplex2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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Vitis viniters

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Viteaceae; Vitis.

(bases 1 to 30)

Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,

Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,

Hamdi,S., Romieu,C. and Terrier,N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

or seeds) at Various Developmental Stages
                           /dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                    Gaps
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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     /clone="B3CS57RB007C01"
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Fax: 00-33-(0)5-57-12-25-48
Email: 9.hamdi@bordeaux.inra.fr
Seg primer: T7.
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CN546474.1 GI:46911099
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FEATURES

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Page 219

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Enkaryota; Ginkgoaceae; Ginkgo.

Spermatophyta; Ginkgophyta; Ginkgoaceae; Ginkgo.

El (Abases I to 30)

Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,

Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo female leaf (NYBG).

Unpublished (2005)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8894

Fax: 516 367 8894

Email: mccombiedeshl.org
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1 (bases 1 to 30)

2 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

L Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ357603 30 bp DNA linear GSS 02-OCT-2000 IM0099H17F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0099H17 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Ginkgo female leaf (NYBG)"
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Site_2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
ik85b01.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
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100.0%; Pred. No. 3.3e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Ginkgo biloba"
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/db_xref="taxon:3311"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 AAAAAAAAAAAAAAAAAAAAAAAAAA 1
                                                                                                                  Ginkgo biloba (maidenhair tree)
Ginkgo biloba
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seg primer: -21M13UnivRev.
Location/Qualifiers
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Mus musculus
                                                                             GI:67050908
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AZ357603.1 GI:10471303
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Fax: 801 585 7177
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Matches 30; Conserval
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/db_xref="taxon:39947"
/tissue_type="flower"
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/lab_host="E.ofl Solk"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
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Xhol; DNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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/lab_host="XL10 Gold"
/lab_host="XL10 Gold"
/clone_lib="Whole Heart Library (DOGESTS)"
/note="Organ: Heart; Vector: pBluescript II SK; Site_1:
ECORI; Site_2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"
                                                                                                                                                                                                                                                                                                                                       ö
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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Balija,V.S., Nascimento,L.U. and McCombie,W.R.
ESTS from Canis familiaris whole heart (dog)
Unpublished (2004)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
                                                                                                                                                                                                                                                                               DB 1; Le
3.3e+02;
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    .30
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/db_xref="taxon:9615"

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1.1%; Score 30; DB 1
Best Local Similarity 100.0%; Pred. No. 3.3e
Matches 30; Conservative 0; Mismatches
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Location/Qualifiers
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CX014987.1 GI:56397398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (dog)
Canis familiaris
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Best Local Similarity 100.0
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

AUTHORS TITLE JOURNAL COMMENT

FEATURES

REFERENCE

CX014987/c DEFINITION

RESULT LOCUS

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Gaps ö 5

RESULT 574 DR073060/c LOCUS

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Email: ddunn@genetics.utah.edu
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84112, USA
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AZ481739/c
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                                                                                                                                                                                                                                                                                                                                                             /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse lokb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse sun annealed to
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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        Std Error: 0.00
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                                                                                                                                                                                             /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6"
/db xref="taxon:10090"
/clone="UUGC1M0099H17"
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Insert Length: 10000 Std Error:
plate: 0099 row: H column: 17
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                 High quality sequence stop: 30.
Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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DEFINITION
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                                                                                                                                                 FEATURES
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Laboratory Mouse DNA Resource Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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E 1 (bases 1 to 30)
S Dunn, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Railly,M., Rose,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Dasmid inserts
Unpublished (2000)
L. Contact: Robert B. Weiss
University of Utah Genome Center
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1M0306N12F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0306N12 F, genomic survey sequence.
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/clone llb="Mouse 10kb plasmid UUGCNM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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3.3e+02;
          Std Error: 0.00
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100.0%; Pred. No. 5...
0; Mismatches
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Insert Length: 10000 Std Error:
Plate: 0258 row: D column: 16
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0258D16"
                                                                                                 Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male
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Fax: 801 585 7177
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Location/Qualifiers
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               Insert Length: 10000
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Matches 30; Conserv
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CZ917652
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732114 |gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; muridea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                 /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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ilarity 100.0%; Pred. No. 3.38+02;
Conservative 0; Mismatches 0;
       Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error:
Plate: 0306 row: N column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                     /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="UUGC1M0306N12"
                                                                                               High quality sequence stop: 30.
Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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AZ582114.1 GI:11700674
                                                                                                                                                                                                                                                                                                /sex="Male"
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Best Local Similarity
Matches 30; Conserv
                                                                                                                                                   source
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VERSION
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwDM22 (gi|4732114|gb|AF129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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4021006E03.2EL_Y1 4021 - RescueMu Grid V Zea mays genomic, genomic
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Unpublished (2001)
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Fax: 650 725 8221
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021006 row: E column: 03
Class: transposon.tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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100.0%; Pred. No. 3.3e+02;
tive 0; Mismatches 0; Indels
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Std Error: 0.00
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                                 Plate: 0374 row: J column: 17
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
                                                                                                                                                                                                                                              /organism="Mus musculus"
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Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0374J17"
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Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: +390815790919
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Matches 30; Conserv
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Best Local Simil
Matches 30; (
                                                                                                                                                                                                               Query Match
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PUBMED
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                                                                                                                               /dev gtage="adilt"
//lab_host="DH10B"
//lab_host="DH10B"
//clone_lib="4021 - RescueMu Grid V"
//clone_lib="4021 - RescueMu Grid V"
//note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamH1; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu', Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
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4021014H02.2EL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic
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Unpublished (2001)
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    (bases 1 to 30)

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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 8221
85ail: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Reverse complemented post-ligation sequence from source sequence.
Class: transposon-tagged.
Location/Qualifiers
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/tissue_type="leaf"
/dev_grage="ault"
/dev_grage="ault"
/lab host="19110B"
/clone_lib="4021 - RescueMu Grid V"
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RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
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                                          /mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/tiswe_traxon.4577"
/tiswe_type="leaf"
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/cultivar="mixed background W23/A188/B73/K55"
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100.0%; Pred. No. 3.3e+02;
ive 0; Mismatches 0; Indels
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/organism≃"Zea mays"
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Best Local Similarity 100.0
Marches 30; Conservative
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Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BgII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
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Sequence tag generated by 5' RACE of total RNA from gene trap BS
Sequence tag generated by shoring insertion mutation of target
Gene are available upon request from TIGEM. Annotation information
available from TIGEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Cobellis, G., Nicolaus, G., Iovino, M., Romito, A., Marra, E.,
Barbarisi, M., Sardiello, M., Di Giorgio, F.P., Iovino, N., Zollo, M.,
Ballabio, A. and Cortese, R.
Tagging genes with casette-exchange sites
Nucleic Acids Res. 33 (4), e44 (2005)
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/cell_line="El4"
/clone_lib="TIGEM gene trap library"
/note="Vector: pPLIP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Via P. Castellino, 111, 80131 NAPOLI, ITALY
Tel: +390816132205
                                                                                                                                                                                                                                                             1.1%; Score 30; DB 1; Le
llarity 100.0%; Pred. No. 3.3e+02;
Conservative 0; Mismatches 0;
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Pred. No. 3.3e+02;
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/mol_type="mRNA"
/strain="129 ola"
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/clone="A015.C10"
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Mus musculus (house mouse)
Mus musculus
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/culfivar="Chilfu"
/culfivar="Chilfu"
/sub species="pekinensis"
/db xref="teaxon:51351"
/clone="KBrS016N21"
/lab host="KBrS. Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa species pekinensis var. Chilfu BAC library (KBrS BAC) is available at NIAB."
    JUB35531 30 bp DNA linear GSS 22-DEC-2005 KBrS016N21F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS016N21, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                      Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
125 Seedun-Dong, Suwon, 441-707, Korea
1281: +82-31-299-1670
Fax: +82-31-299-1670
Email: pbeom@rda.go.kr
BAC cond sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
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                                                                                                                                                  Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Fosids; eurosids II; Brassicales; Brassicaceae; Brassica.

I to 30,
Yang, T. J. Kwon, S. J. Kim, J. A., Kim, J. S., Lim, K. B., Jin, M.,
Park, J. Y., Lim, M. H., Kim, H. I., Choi, B. S., Seol, Y. J., Park, D. S.,
Hahn, J. H. and Park, B. S.

Bnd sequence of Brassica rapa Sau3AI (KBrS) BAC clone
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
BAC end sequences of Library RP-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 30)
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AG191161 30 bp DNA linear GSS 06. Pan troglodytes DNA, clone: RP43-066P20.T7, genomic survey sequence.
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Pan troglodytes
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DU835531.1 GI:83872127
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AGI91161.1 GI:45223337
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Class: BAC ends.
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AG191161/c
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AUTHORS
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Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. Direct Submission
Submitted (107-JAN-2002) Hong-Seog Park, Korea Research Institute of Submitted (107-JAN-2002) Hong-Seog Park, Korea Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the RkD process and may have higher chance of clone tracking errors.
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602389549F1 NIH_MGC_94 Mus musculus CDNA clone IMAGE:4501164 5',
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1 (bases 1 to 31)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I. M. A.G. B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M. A.G. E. Consortium/LLNL at:
http://mage.llnl.gov
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/lab_host="lund (phage-resistant)"
/clone lib="NIH MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1%; Score 30; DB 1; Length 30;
100.0%; Pred. No. 3.38+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/clone="RP43-066P20.T7"
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Location/Qualifiers
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/db_xref="taxon:10090"
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RESULT 585 CN545579/c

ð g DEFINITION

ACCESSION

VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL COMMENT

TITLE

FEATURES

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Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Vitaceae; Vitis.

I (basea 1 to 31)

S Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,

Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,

Hamdi, S., Romieuu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

AL Unpublished (2002)

Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne
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Vitis vinifera

Witis vinifera

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Vitaceae; Vitis.

I (bases 1 to 31)

S Abbal, P., Agasse, A., Atanassova, R., Barrieu, F.,

Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,

Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

or seeds) at Various Developmental Stages

L Unpublished (2002)
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Coganism="vitis vinifera"

/mol type="mkNA"

/culTivar="Cabernet Sauvignon"

/db xxef="teaxon:2976"

/cloine="BaCS00Rb002609"

/dev_stage="ripening stage"

/cone lib="Ripe Grape Skin Triplex2 Library"

/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:

SfilA; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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Universite de Bordeaux I, Institut National de la Recherche
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100.0%; Pred. No. 3.40+02;
ative 0; Mismatches 0;
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: s.hamdi@bordeaux.inra.fr
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Fax: 00-33-(0)5-57-12-25-48
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CNS45867
EST 146910492
EST.
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Clone lib="Ripe Grape Skin Triplex2 Library"
/noce="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
Sfilk; Site_2: Sfilk; Oriented library"
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
           Site_2: Sall; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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Universite de Bordeaux I, Institut National de la Recherche
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iive 0; Mismatches 0;
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/culfivar="Cabernet Sauvignon"
/db_xref="texon:29760"
/clone="B3CS00RL003F11"
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Fax: 00-33-(0)5-57-12-25-48
Email: B.hamdi@bordeaux.inra.fr
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Vitis vinifera
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Matches 30; Conserva
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RESULT 586 CN545867/c

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatorphyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

I (bases I to 31)

Abbal, P., Agaese, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Handi, S., Romieu, C. and Terrier, N. Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

Unpublished (2002)

Contact: Hamdi S.

UNR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
                             CNS46130 31 bp mRNA linear EST 30-APR-2004 EST 18082 Ripe Grape Skin Triplex2 Library Vitis vinifera CDNA clone B3CS00RL008G05 3', mRNA sequence.
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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                                        /organism="vitis vinifera"
/mol type="mRNA"
/mol type="mRNA"
/cultivar="Cabernet Sauvignon"
/db xref="taxon:29760"
/clone="B3CS00RL006b06"
/clone="B3CS00RL006b06"
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/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_l: Sfil8; Site_l: Sfil8; Oriented library"
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/mol type="mRNA"
/uuliye="abernet Sauvignon"
/db xref="taxon:29760"
/clone="B3CS00RL007F01"
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons,
rosids, Vitaceae, Vitis.
1 (bases, 1 to 31)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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100.0%; Pred. No. 3.4e+02;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.4e+02;
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Fax: 00-33-(0)5-57-12-25-48
Email: 8.hamdi@bordeaux.inra.fr
    Location/Qualifiers
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AZS97046

31 bp DNA linear GSS 13-DEC-2000
1M0410K08R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0410K08 R, genomic survey sequence.
AZS97046.1 GI:11719236
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/organism="Vitis vinifera"
/mol type="mRNA"
/cultivar="Cabernet Sauvignon"
/db xref="taxon:29760"
/clone="B3CS00RL008G05"
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University of Utah Genome Center
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
                                                                                                          Location/Qualifiers
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Mus musculus
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RESULT 589

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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/clone llb="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated for sheared DNA
was blunt end-repaired with T4 DNA polymerses and T4
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarces get of plasmid R1. The vector was ligated
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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4021007E11.2EL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                             E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                        Polymers Research Bldg., 20 S. 2030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1%; Score 30; DB 1; Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 2227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.4e+02;
                                                        Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0410 row: K column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2709 AAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                               High quality sequence stop: 31.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC1M0410K08"
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CZ917966
CZ917966.1 GI:71937128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
University of Utah
Rm. 308, Biomedical
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 30; Conservative
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 591
CZ917966
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TITLE
JOURNAL
COMMENT
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/uriant Lype="genomic DNA"

/ cultivar="mixed background W23/A188/B73/K55"

/ cultivar="mixed background W23/A188/B73/K55"

/ tissue type="leaf"

/ dev stage="adult"

/ lab host="DH10B"

/ clone lib="4011 - RescueMu Grid V"

/ note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamH1; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from rotal agenomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web site "http://www.mutransposon.org/project/RescueMu/. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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1 (bases 1 to 3)

1 (bases 2)

1 (bases 3)

1 (bases 3)

2 (bases 4)

2 (bases 4)

2 (bases 4)

3 (bases 4)

3 (bases 4)

4 (bases 4)

5 (bases 4)

5 (bases 4)

6 (bases 4)
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1M0166C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021007 row: E column: 11
Class: transposon-tagged.
Location/Qualifiers
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Pred. No. 3.4e+02;
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Insert Length: 10000 Std Error: 0.00
Plate: 0166 row: C column: 14
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.1%; Scor.
100.0%; Pred. No. 5...
... 0; Mismatches
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 32.
Location/Qualifiers
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Best Local Similarity 100.
Matches 30, Conservative
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Fax: 801 585 7177
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84112, USA
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ымуьзббэ 33 bp mRNA linear EST 04-MAY-2005
it91c01.gl Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brenner, B. D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Banidey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8884
Email: mccombiecshl.org
Seq primer: -21M13UnivRev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryoča; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetophyta; Gnetopsida; Gnetales; Gnetaceae; Gnetum.
1 (bases 1 to 33)
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/note="Organ: mature, unfertilized reproductive strobili;
/note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site_l: XhoI; Site_2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"
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Triticum aestivum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
                          (URL, http://www.nirs.go.jp)
                                                                      Query Match 1.1%; Score 30; DB 1; Length 33; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Matches 30; Conservative 0; Mismatches 0; Indels
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/organism="Gnetum gnemon"
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/db_xref="taxon:3382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Best Local Similarity
Matches 30; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                               DN955605
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CV066327
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KEYWORDS
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                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xii0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the Smal site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 03-AUG-1998
                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse lokb plasmid UGGCNM library"
/note="Vector: PWB4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 33)
Morimyo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUO13658 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc08464, mRNA sequence.
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National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
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Schizosaccharomyces pombe
Eukaryota, Pungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaces;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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/mol_type="mRNA"
/strain="972"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 1; Le
Pred. No. 3.4e+02;
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v 100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                      /db_xref="taxon:10090"
/clone="UUGC1M0166C14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:4896"
/clone="spc08464"
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Email: morimyo@nirs.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mitsuoki Morimyo
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AU013658.1 GI:3368449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
                                                                                                                            /sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1998)
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Best Local Similarity
Matches 30; Conserv
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TITLE
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Gaps

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2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Email: s.hamdi@bordeaux.inra.fr
                     Seq primer: T7.
Location/Qualifiers
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Best Local Similarity 93.9'
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                             Similarity
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Best Local Simi]
Matches 31; (
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DEFINITION
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                E 1 (bases 1 to 35)

S Ali, S, Holloway, B. and Taylor, W.C.

Normalisation of cereal endosperm EST libraries for structural and functional genomic analysis.

L Plant Mol. Biol. Rep. 18, 123-132 (2000)

Contect: Bill Taylor

Commonwealth Scientific and Industrial Research Organisation

Division of Plant Industry.

CSIRO Plant Industry.

CSIRO Plant Industry.

Tel: 61 2 6246 5000

Email: Bill.Taylor@csiro.au

Seq primer: Mil reverse primer

High quality sequence scop: 35.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="endosperm"
/dev_stage="developing endosperm tissue 6, 8, 10 dpa (days
post_anthesis)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab host="DH10B (Life Technology)"
/clone_lib="Wheat EST endosperm library"
/clone_lib="Wheat EST endosperm library"
/note="Vector: ZipLox; Site_l: Sal I; Site_2: Not I; mRNA was prepared from endosperm tissues of the wheat cultivar Hartog. cDNA was synchesised from pooled 6, 8, and 10 dpa endosperm using Not I-oligo(dT)18 primer/adapter
(Pharmacia Biotech), and then ligated to the Sal I-Not I site of ZipLox vector (Life Technology) after adding a Sal I-Xho I adapter (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNS45607 133 bp mRNA linear EST 30-APR-2004 EST 17551 Ripe Grape Skin Triplex2 Library Vitis vinifera CDNA clone B3CS00RL004A03 3', mRNA sequence.
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Vitis vinifera
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 33)
Abbal, P., Agases, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
Or seeds) at Various Developmental Stages
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Universite de Bordeaux I, Institut National de la Recherche
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                                                                                                                                                                                                                                                                                                                                                                       1. .35
/organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1%; Scor.
100.0%; Pred. No. 3...
0; Mismatches
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Pooldeae; Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                                           /mol type="mRNA"
/cultivar="Hartog"
/db_xref="taxon:4565"
/clone="WNEL32e2"
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Fax: 00-33-(0)5-57-12-25-48
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CN545607.1 GI:46910232
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Best Local Similarity 100.(
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Hamdi S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agronomique
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ORGANISM
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CN545607/c
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                                                                       TITLE
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/dev_stage="ripening stage"
/clone lib="Ripe Grape Skin Triplex2 Library"
/noce="Organ: Fruit skin; Vector: Lamba TriplEx2; Site_1:
SfilA, Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DXO50853 10-JAN-2006 SERBO53024R KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB053024, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI, Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005) Contact: Beom-Seok Park Brassica Genomics Team
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/cultivar="Chiffu"
                                                                                                                                                                                                                                                               Length 33;
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                                                                                                                                                                                                                                                             Score 29.8; DB 1;
Pred. No. 3.6e+02;
0; Mismatches 2;
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Pred. No. 3.6e+02;
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/organism="Vitis vinifera"
/mol type="mRNA"
/culfivar="Cabernet Sauvignon"
/db xref="taxon:29760"
/clone="B3CS00RL004A03"
                                                                                                                                                                                                                                                                                                                                                                                                                          CTTACAAAAAAAAAAAAAAAAAAAAAAAA 1
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/db_xref="taxon:51351"
/clone="KBrB053024"
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                                                                                                                                                                                                                                                             1.1%;
illarity 93.9%;
Conservative (
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clone="ROS064A03"
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Unpublished (2001)
Contact: Frazer Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL587823.1 GI:13192857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (chicken)
Gallus gallus
      Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murray, F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa (japonica cultivar-group)"
/organism="Noryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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                                                                                                                         CF301193 37 bp mRNA linear EST 15-AUG-2003 7LEAF--05-P05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-P05, mRNA
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Enrhartoideae; Oryzeae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-goale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitacaee; Vitis.

1 (bases 1 to 36)
Abbal, P., Agases, A., Ageorges, A., Atanassova, R., Barrieu, F., Gouture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University
Yogin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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33 GTATTTAAAAAAAAAAAAAAAAAAAAAA 1
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Best Local Similarity 93.93
Matches 31; Conservative
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/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
SfilA; Site_2: SfilB; Oriented library"
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/dab_nost="DH10B"
/clone lib="BPC Chicken Brain Library"
/clone lib="BPC Chicken Brain Library"
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                                                                                  Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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GCGGCCGCTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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1.1%; Score 29.6; DB 1;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 32; Conservative 0; Mismatches 4;
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Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
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/mol_type="mRNA"
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                                                                                                                                                                 Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
                                                                                                                                                                                                                                                         Seg primer: T7.
Location/Qualifiers
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/note:
                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ591372 31 bp mRNA linear EST 06-DEC-2002 E012712-024-017-I15-T7 MPIZ-ADIS-024-8torage root Beta vulgaris CDNA clone 024-017-I15 3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Egermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 11)
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                         Gaps
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0
                                                               1.1%; Score 29.6; DB 1; Length 37; 88.9%; Pred. No. 3.9e+02;
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-won-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: Weisshaa@mpiz-koeln.mpg.de
Insert Length: 31 Std Error: 0.00
Plate: 17 row: 1 column: 15
Seq primer: T7; GTAARAGGACTCACTATAGGGC.
                                                                                                                                      Indels
                                                                                                                                                                                                         2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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Pred. No. 3.7e+02;
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   Clonetech (*6854-1)"
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EST.
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                                                                                               Best Local Similarity
Matches 32; Conserv
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ö CNS45785 Sipe Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00RL005H07 3', mRNA sequence. EST 15-JUN-2004 Vitis vinifera

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

| (bases 1 to 31)
| Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
| Hamdi, P., Romieu, C. and Terrier, N.
| Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
| Contact: Hamdi S. Agronomique 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, These sequences may be of either nuclear or mitochondrial origin. Location/Qualifiers ŏ /db_xref="taxon:62324" /sex="male and female" /dev_stage="embryo, larvae, pupae, and adult" /clone lib="ESTs from wild-caught Anopheles funestus populations" Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; Anophelinae; Anopheles.

Besanaky, N. J., Serazin, A. C. and Dana, A.
Towards the transcriptome of Anopheles funestus: a molecular Center for Tropical Disease Research and Training, University Gaps UMR 619 - Equipe Biologie de la Vigne Universite de Bordeaux I, Institut National de la Recherche CD577356

1gor3_E10_Q2_081 ESTs from wild-caught Anopheles funestus populations Anopheles funestus cDNA 5', mRNA sequence. ö Length 31; 317 Galvin Life Science, Notre Dame, IN 46556, USA Tel: 5746319321 Email: nbesansk@nd.edu Indels 1.1%; Score 29.4; DB 1; 96.8%; Pred. No. 3.7e+02; /organism="Anopheles funestus" /mol_type="mRNA" /strain="West African" /note="Vector: LambdaTriplEx2" 2706 ACTAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736 1 AGTAAAAAAAAAAAAAAAAAAAAAAAAA 31 0; Mismatches Unpublished (2003) Contact: Andrew Serazin Collins/Besansky Lab CD577356 CD577356.1 GI:48718371 CN545785.1 GI:46910410 Anopheles funestus Anopheles funestus Conservative Vitis vinifera Similarity Notre Dame snapshot CN545785 France Query Match Best Local Simi Matches 30; JOURNAL

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31 AAAAAAAAAAGAAAAAAAAAAAAAAA 1

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|qb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murcidea; Murinae; Mus.

E 1 (bases 1 to 31)

E 1 (bases 1 to 31)

S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Really, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Diamid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                               AZ486763 31 bp DNA linear GSS 05-OCT-2000 1M0315A11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0315A11 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (Male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 31;
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Best Local Similarity 96.8%; Pred. No. 3.7e+02;
Matches 30; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
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           31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC1M0315A11"
                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                              AZ486763.1 GI:10653856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
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/organism="Vitis vinifera"
/organism="Vitis vinifera"
/organism="Vitis vinifera"
/orlivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CSORLOOSH07"
/dev_stage="ripening stage"
/clone lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
SfilA; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CN546374 31-APR-2004 EST 18327 Green Grape Berry Lambda Triplex2 Library Vitis vinifera CDNA clone B3CS1XGB016C11 3', mRNA sequence.
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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/organism="Vitis vinifera"
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/db_xref="taxon:29760"
/do_stage="green stage"
/dev_stage="green stage"
/clone_lib="Creen Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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1 (bases 1 to 31)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Universite de Bordeaux I, Institut National de la Recherche
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16.8%; Pred. No. 3.7e+02;
ve 0; Mismatches 1; Indels
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Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
                                                                                                                  Location/Qualifiers
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                                                                                       Seq primer: T7
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CN546374/c
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GSS 22-DEC-2005

AZ785111/c LOCUS

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DEFINITION ACCESSION

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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DX013882 310-JAN-2006 KBrB031I01R KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB031I01, genomic survey sequence.
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaese; Brassica.
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Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 31)
Yang T.J. Kwon, S.J. Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Bahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
                                                                                                              J1 bp DNA linear GSS 22-DEC-2C KBrS016D03R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS016D03, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / fub species="pekinensis"
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//db_aref="KarSo16003"
//db_host="E. coli DH10B"
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//note="locator: pcugnated arapa Sau3AI BAC library"
spekinensis var. Chiifu BAC library (KBrS BAC)
available at NIAB."
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/organism="Brassica rapa subsp. pekinensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            National Institute of Agricultural Biotechnology 225 Seodun-Dong, Suwon, 441-707, Korea Fat: +82-31-299-1670
Fax: +82-31-299-1670
Email: pbeom@rda.go.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.1%; Score 29.4; DB 1;
ilarity 96.8%; Pred. No. 3.7e+02;
Conservative 0; Mismatches 1;
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/mol_type="genomic DNA"/cultivar="Chiifu"
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Brassica Genomics Team
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                                                                                                                                                                                                                                                                                  DU835198.1 GI:83871794
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Matches 30; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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                                                                                                                                         GSS 16-FEB-2001
                                                                                                                                      AZ785111
2M0028B14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0028B14 R, genomic survey sequence.
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1 (bases 1 to 31)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Really, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Diasmid inserts
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0028 row: B column: 14
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/63"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus
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AZ785111.1 GI:12921525
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Fax: 801 585 7177
Email: ddunn@genet
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Matches 30; Conserv
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Query Match

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Length 31; Indels ö

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/cultivar="Cabernet_Sauvignon"
                                      2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
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       0; Mismatches
                                                                        0; Mismatches
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/organism="Vitis vinifera"
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/clone="B3CS00RL002F10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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CN546360.1 GI:46910985
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CN546360/c
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DKFZp566J0246_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
AL038680
                                                                                                                                                                                                                                                                                                                                                                                                         /lab_nost="E.coli_DH10B"
/clone lib="KBrB, Brassica rapa BamH1 BAC library"
/clone lib="KBrB, Brassica rapa BamH1, Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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                                                           Contact: Beom-Seck Park
Brassica Genomics Team
Mational Institute of Agricultural Biotechnology
22 Seedun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Bmail: pbeom@cue of Brassica rapa ssp. pekinensis BamHI BAC clone
Seg primer: M13 Reverse
Class: BAC ends.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="bKPZp56610246"
/tissue_type="kidney"
/dev stage="fetal"
/lab_host="X1_2blue"
/lab_host="X1_2blue"
/clone=lib="566 (8ynonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: SalI"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                  /organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
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                                                                                                                                                                                                                                                                                                                                                       /sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB031101"
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Unpublished (1999)
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Homo sapiens
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Best Local Similarity 96.8
Matches 30; Conservative
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1 (bases 1 to 32)
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Best Local Similarity
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AL038680
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CNS45857 30-APR-2004 EST 17801 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00RL002F10 3', mRNA sequence.
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Clone_lib==Ripe Grape Skin Triplex2 Library"
/note="Organ = Fruit skin; Vector: Lambda TriplEx2; Site_1:
SfilA; Site_2: SfilB; Oriented library"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis;

Losaes 1 to 34)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
Unpublished (2002)
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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1 (bases 1 to 34)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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Query Match
Best Local Similarity 96.8
Matches 30; Conservative
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Matches 30; Conservative
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Vitis vinifera"
/mol_type="mRNA"
/mol_type="mRNA"
/doultivar="cabernet Sauvignon"
/db xref="taxon:29760"
/clone="B3CS1XGB016B08"
/dev gtage="green stage"
/clone=lib="Green Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS37TB007D03"
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Location/Qualifiers
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Best Local Similarity 96.8
Matches 30, Conservative
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Vitis vinifera
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CN546734 30-APR-2004 BST 18505 Turning Grape Berry Lambda Triplex2 Library Vitis vinifera cDNA clone B3CS38TB008B09 3', mRNA sequence.
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Coone libe-Ripe Grappe Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
Sfilk; Site_2: Sfilk; Oriented library"
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Virial plantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

1 (bases 1 to 35)
Abball, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
/clone lib="Turning Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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Pred. No. 3.9e+02;
0; Mismatches 1;
                                                                                                        DB 1;
                                                                                                     1.1%; Score 29.4; DB 1; 96.8%; Pred. No. 3.9e+02; Itive 0; Mismatches 1.

    .35
    forganism="vitis vinifera"
/mol type="mRNA"
/cultivar="Cabernet Sauvignon"

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/clone="B3CS00RL007B06"
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Query Match
Best Local Similarity 96.8'
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                                                                                                                                                                                                                                                                                                           7\bar{1}, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
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                                    Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitecaes, Vitis.

1 (bases 1 to 35)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Vitis vinifera"
/organism="Vitis vinifera"
/mol type="mRNA"
/culcivar="Caberne Sauvignon"
/db xref="taxon:29760"
/clone="B3CS38TB008B09"
/dev stage="veraison stage"
/dcone_lib="Turning Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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                                                                                                                                                                                                                                      Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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Location/Qualifiers
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/organism="Homo sapiens"
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/clone="DKF2pS64F0564"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="X1-2blue"
                                                                                                                                                                                                                                                                                                                                                      Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Location/Qualifiers
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EST (Duesterhoeft, et al.)
Unpublished (1999)
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Matches 30; Conserv
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UND#23//
EST 17321 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
Clone B3CS00GL007D11 3', mRNA sequence.
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/cone lib="Green Grape Skin Triplex2 Library"

/note="Grgan: Fruit skin; Vector: Lambda TriplEx2; Site_1:

SfilA; Site_2: SfilB; Oriented library"
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Vitis vinifera
Vitis vinifera

Vitis vinifera

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

1 (bases I to 36)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,

Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,

Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

Unpublished (2002)
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
                                                                                                                                  Gaps
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
/clone_lib="564 (synonym: hfbr2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: Sal1"
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                                                                            Length 36;
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                                                                         1.1%; Score 29.4; DB 1;
96.8%; Pred. No. 4e+02;
tive 0; Mismatches 1;
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/cultivar="Cabernet Sauvignon"
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Best Local Similarity 96.8%; Pred. No. 4e+0.
Matches 30; Conservative 0; Mismatches
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/clone="B3CS00GL007D11"
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Fax: 00-33-(0)5-57-12-25-48
Email: 8.hamdi@bordeaux.inra.fr
Seg primer: 77.
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CN546215.1 GI:46910840
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CV091545.1 GI:51570884
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Fax: 301-504-5653
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Local b. 30;
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KEYWORDS
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AL038356
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta; eudicotyledons; core eudicotyledons; rosida; Vitaceae; Vitis.

E 1 (bases 1 to 36)
S Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N. Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
L. Unpublished (2002)
Contact: Hamdi S.
Universite de Bologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 bp mRNA linear EST 30-APR-2004 EST 18456 Turning Grape Berry Lambda Triplex2 Library Vitis vinifera cDNA clone B3CS37TB007F08 3', mRNA sequence. CN546685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev stage="ripening stage"
/clone lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Ti, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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Vitis vinifera
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases I to 36)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
Unpublished (2002)
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
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/clone="B3CS00RL009F07"
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
                                                                                                                                                                                                                                                                                                                        Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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nes 30, Conservative
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/db xref="taxon:6926"
/tisue_type="Flower buds including bud scales"
/dev_stage="Mature plants"
/clone lib="cDNA non acclimated Bluecrop library"
/note="Vector: pBluescript SK-; cDNA clones from Vaccinium corymbosum cv. Bluecrop, RNA for preparation of library was extracted from flower buds collected in the fall from
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                                                                                                                                        /dev_stage="veraison stage"

/clone_lib="Turning Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda

TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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Monitoring gene expression changes during cold acclimation oblueberry (Vaccinium corymbosum L.) using a cDNA microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US Department of Agriculture (USDA), ARS, FSI
Bldg 010A, 10300 Baltimore avenue, BARC West, Beltsville,
20705-2350, USA
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/organism="vitis vinifera"
/mol_type="mRNA"
/culfivar="Cabernet Sauvignon"
/db_xref="teaxon:29760"
/clone="B3CS37TB007F08"
                                                                                                                                                                                                                                                                            1.1%; Score 29.4; DB 1
ilarity 96.8%; Pred. No. 4e+02;
Conservative 0; Mismatches
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Pred. No. 4e+02;
0; Mismatches
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Location/Qualifiers
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/cultivar="Bluecrop"
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="UUGC1M0089K13"
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Mus musculus
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Best Local Similarity 88.6%;
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Fax: 801 585 7177
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DEFINITION
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AZ351309
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yb16g12.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA
clone IMAGE:71398 3' similar to similar to gb:L19437 TRANSALDOLASE
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I (bases 1 to 35)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Lewkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rikkin, L., Rohlfing, T., Schallenberg, K., Soares, M. B., Tan, F., Thierry-Weg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,
                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                              Hominidae; Homo.
1 (bases 1 to 34)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
DKFZp566L152_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566L152, mRNA sequence.
AL038356
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="DKRZDSSGLI52"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="S66 (symonym: hfkd2)"
/note="Vector: pAMPI; Site_1: NotI; Site_2: SalI"
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                          Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 29.2; DB 1; Length 34; 91.2%; Pred. No. 4e+02; tive 0; Mismatches 3; Indels
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                           Wiemann,S.
EST (Ottenwaelder, et al.)
Unpublished (1999)
                                                             AL038356.1 GI:49682097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMAN), mRNA sequence
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Contact: Wilson RK
                                                                                                    Homo sapiens (human)
Homo sapiens
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T50295.1 GI:652155
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Best Local Similarity 91.23
Matches 31; Conservative
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/tissue_type="fetal spleen"
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/dev_stage="fetal"
/db_host="SOLR cells (Kanamycin resistant)"
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/lab_host="SOLR cells (Kanamycin resistant)"
/clone="Ilb="Stratagene fetal spleen (#937205)"
/note="Organ: spleen; Vector: pBluescript SK-; Site_1:
/note="Organ: spleen; Vector: pBluescript SK-; Site_1:
/note="Organ: spleen; Vector in the spleen 
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1M0089K13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0089K13 F, genomic survey sequence.
AZ351309
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rolly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace consider overall poor quality
Seq primer: -21ml3
High quality sequence stop: 1.
Location/Qualifiers
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8.6%; Pred. No. 4e+02;
ve 0; Mismatches 4; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: K column: 13
Seg primer: CGTTGTAAAACGACGGCCAGT
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/organism="Mus musculus"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Query Match
Best Local Similarity
Matches 31; Conserv
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Matches 29;
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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Weator: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The Jackson
(http://www.jax.org/resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymersas and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gil | 4732114 | gb| AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xiii0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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4013007D07.2EL_x1 4013 - RescueMu Grid O Zea mays genomic, genomic
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1 (bases 1 to 35)
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Unpublished (2001)
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Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 401307 row: D column: 07
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/cust_cree="genomic DNA"
/cust_cree="genomic DNA"
/cust_cree="genomic DNA"
/cust_cree="cason 4577"
/tissue_type="leaf"
/dov stage="leaf"
/dov stage="adult"
/dov stage="adult"
/dob host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/note="Organ: leaf; Vector: RescueMu (engineered from pBDlueScript backbone); Site 1: RemHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 4e+02;
0; Mismatches 3; Indels
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Fax: 650 725 8221
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1.1%; Score 29.2; DE
Best Local Similarity 91.2%; Pred. No. 4e+05
Matches 31; Conservative 0; Mismatches
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Department of Biological Sciences
Stanford University
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Location/Qualifiers
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JOURNAL
COMMENT
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SOURCE
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CZ914519

ઠે а REFERENCE

FEATURES

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designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
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Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 29)
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Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 29)
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/clone="smlc32907.glx"
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/clone lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"
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100.0%; Pred. No. 3.8e+02;
iive 0; Mismatches 0;
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Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
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2709
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Best Local 9
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhatroideae; Oryzeae; Oryza.

(bases 1 to 29)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S., Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C. Mikrozarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni Unpublished (2005)
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                                                                                                                                                                                                        /.organism="Schistosoma mansoni"
/organism="Schistosoma mansoni"
/dob_xref="texon:6183"
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/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"
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| mol type="mRNA"
| cultivar="Nackdong" |
| db xref="taxon:39947"
| clone="14ETL--05-N22"
| clssue type="lad" |
| clssue type="14 days after germination" |
| clab_host="8.coli DH108"
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Genomics and Genetics Institute, GreenGene Biotech In
Genomics and Genetics Institute, GreenGene Biotech In
Of Bioscience and Bioinformatics, MyongJi University
Yolsin, Kyeonggi, Korea
Tel: 82 31 321 6155
Fax: 82 31 321 6155
Email: bhahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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100.0%; Pred. No. 3.8e+02;
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                                                                                              Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 ISA, UNITED KINGDOM.
Location/Qualifiers
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Matches 29; Conserv
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CF299920
29 bp mRNA linear EST 15-AUG-2003
7LEAF--04-C02.gl Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-C02, mRNA
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaea; Oryza.

1 (bases 1 to 29)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza,
1 (bases 1 to 29)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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/note="Vector: pCR4-TOPO; Site 1: ECORI; mRNA was capped with oligoribonucleotides and Then used as templates for RT-PCR."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongQi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/cultivar="Nackdong"
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Location/Qualifiers
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100.0%; Pred. No. 3.8e+02;
ive 0; Mismatches 0;
| 100 | | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 10
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CF299920.1 GI:33671681
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CF312601.1 GI:33684362
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Vitis vinifera
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; Vitaceae; Vitis.
I (bases 1 to 29)
Abbal P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
Or seeds) at Various Developmental Stages
Large-Bcale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Fat: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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// clasue_type="leaf"
// dev stage="leaf"
// lab_host="E.coli DH10B"
// lab_host="E.coli DH10B"
// clone lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
// note="Yector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and fibra used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
                                                                                                                                                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/cultivar="Cabernet Sauvignon"
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/clone="B3CS00GL004G11"
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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CNS46382 29 bp mRNA linear EST 30-APR-2004 EST 18335 Green Grape Berry Lambda Triplex2 Library Vitis vinifera cDNA clone B3CS1XGB016D07 3', mRNA sequence. CNS46382 GIS46382.1 GI:46911007 EST.
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/dev_stage="green grape Skin Triplex2 Library"

/note="Organ: Fruit shin; Vector: Lambda TriplEx2; Site_1:

SfilR; Site_2: SfilB; Oriented library"
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SfilA; Site_2: SfilB; Oriented library"
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France
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1 (bases 1 to 29)
Abbal, P., Agases, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Handi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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/mol type="mRNA"
/cultivar="Cabernet Sauvignon"
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/clone="B3CS00RL009D04"
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; 1 (bases, Vitis.

1 (bases 1 to 29)
Abbal, P., Agase, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N. Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Vitis vinifera"
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/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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1 (bases 1 to 29)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                        Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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100.0%; Pred. No. 3.8e+02;
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                                                                                                                                                                                                                                                                                                                                        France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: 8.hamdi@bordeaux.inra.fr
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seg primer: T7.
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EST.
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Matches 29; Conserv
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
                                                                                                                             /dev stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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/clone="ipe stage"
/clone lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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EST 18701 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
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Abbal, P., Agases, A., Agoorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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100.0%; Pred. No. 3.8e+02;
tive 0; Mismatches 0;
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/cullivar="Cabernet Sauvignon"
/db xref="taxon:29760"
/clone="B3CS57RB007A03"
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/cultivar="Cabernet Sauvignon"
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organism="Vitis vinifera"
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Location/Qualifiers
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E 1 (bases 1 to 29)

S Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Ballia, V. Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor Laboratory

Tel: 516 367 8884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Cardiac muscle"
/dev stage="3 month old normal canine"
/dev stage="3 month old normal canine"
/lab_host="XLIO Gold"
/lab_host="Lab."
/clone lib="Right Cardiac Ventricle (DOGEST6)"
/clone lib="Right Cardiac Ventricle using pBluescript II SK; Site 1:
/note="Corgan: Heart; Vector: pBluescript II SK; Site 1:
/note="Torgan: Heart; Vector: pBluescript II SK; Site 2:
/note="Torgan: Heart; Vector: pBluescript II SK; Site 2:
/note="Torgan: Heart; Vector: pBluescript SK kit from Stratagene. Cloned CDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"
                    CV999708 1.00 29 bp mRNA linear EST 03-DEC-2004 iv52f08.bl Right Cardiac Ventricle (DOGEST6) Canis familiaris cDNA,
                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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ik86f04.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
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Balija, V.S., Nascimento, L.U. and McCombie, W.R.
ESTS from Canis familiaris right cardiac ventricle (dog)
Unpublished (2004)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Pax: 516 367 8874
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.00.0%; Pred. No. 3.8e+02;
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Ginkgo biloba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9615"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mccombie@cshl.org.
Location/Qualifiers
                                                                    mRNA sequence.
CV999708
CV999708.1 GI:56271125
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                                                                                                                                                                     Canis familiaris (dog)
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DR073120/c
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AUTHORS
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/lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
musculus C57BL/6J (male) was obtained from the Jackson
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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                                                                                                                                                                                                                                      /clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: :pBK-CMV; Site_1: XhoI;
Site_2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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0
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100.0%; Pred. No. 3.8e+02;
tive 0; Mismatches 0;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: D column: 21
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2709 ААААААААААААААААААААААААААА
                                                                                                                      1. .29
/organism="Ginkgo biloba"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
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Mus musculus
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GSS.
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Best Local Similarity 100.0
Matches 29, Conservative
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL110-GG1d (Stratagene) cells and selected for ampicillin resistance." ö GSS 03-OCT-2000 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a AZ414283
1M0188G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0188G12 R, genomic survey sequence. Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Mus. /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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/note="Vector: PWD42nv; Purified_genomic_DNA_from M.
musculus C57BL/6J (male) was obtained from the Jackson 1 (bases it cold)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000) Gaps ; 0 Length 29; 0; Indels Score 29; DB 1; Le Pred. No. 3.8e+02; Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Laboratory Mouse DNA Resource 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737 100.0%; Preu. ... Insert Length: 10000 Std Error: (Plate: Olds row: G column: 12 Seq primer: CACAGGAAACAGCTATGACCClass: plasmid ends organism="Mus musculus" Contact: Robert B. Weiss University of Utah Genome Center University of Utah /mol_type="genomic DNA" /strain="C57BL/6J" 1.1%; Score 29; /db_xref="taxon:10090" /clone="UUGC1M0188G12" High quality sequence stop: 29. Location/Qualifiers Mus musculus (house mouse) AZ414283.1 GI:10538296 GSS. /sex="Male Query Match Best Local Similarity 100. Matches 29; Conservative Tel: 801 585 5606 Fax: 801 585 7177 Mus musculus VERSION KEYWORDS SOURCE ORGANISM RESULT 637 AZ414283/c DEFINITION

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0251E05R Mouse 10kb plasmid UUGCIM library Mus musculus genomic Cone UUGCIM0251E05 R, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone lib="Mouse lokb plasmid UUGCNM library"
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musculus C57BL/6J (male) was obtained from the Jackson
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Kose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20:84112, USA
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Pred. No. 3.8e+02;
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Pax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0251 row: E column: 05
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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100.0%; Pred. No. J...
'... 0; Mismatches
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Location/Qualifiers
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Mus musculus
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Best Local Similarity
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Murcidae; Muridae; Muridae; Rodentia;

Sciurognathi; Murcidae; Muridae; Mus.

1 (bases 1 to 29)

Sunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Nidedribusern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

#4112, Onta
0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xili0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0281G24F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0281G24 F, genomic survey sequence.
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musculus C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0281 row: G column: 24
Seg primer: CGTTCTAAAACGACGCCAGT
Class: plasmid ends
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Location/Qualifiers
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ORGANISM KEYWORDS SOURCE

REFERENCE AUTHORS JOURNAL

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TITLE

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RESULT 639 AZ468402/c DEFINITION ACCESSION VERSION

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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymcrases and T6 polymcrases. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarese gel electrophorasis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 29)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/note="Vector: PWDATN; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: N column: 21
Seq primer: CGTTGTAAAACGACGCCAGT
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100.0%; Pred. No. ...
... 0; Mismatches
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High quality sequence stop: 29.
Location/Qualifiers
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Matches 29, Conservative
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Fax: 801 585 7177
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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was hydrodynamically sheared by repeated passage through a
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1M0540K20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0540K20 F, genomic survey sequence.
AZ661709
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/clone_lib="Mouse lokb plasmid UUGClM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Waiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Insert Length: 10000 Std Error: 0.00
Plate: 0540 row: K column: 20
Seg primer: CGTTGTAAAACGACGGCCAGT
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100.0%; Pred. No. 3.8
ative 0; Mismatches
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Best Local Similarity 100.0
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Fax: 801 585 7177
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was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides ware ligated to the blunt ends in high molar excess. The adaptored blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transfermed into chemically-competent E. coli XI10-GG1d (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 29)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rally, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Dlasmid inserts

Unpublished (2000)
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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100.0%; Pred. No. 3.8e+02;
tive 0; Mismatches 0;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: I column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC2M0026113"
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Mus musculus
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Clone lib="Mouse 10kb plasmid UNGCIM library"
/note="Vector: PMD42vry: Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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1 (Dasea 1 to 29)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Distand inserts
Unpublished (2000)
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nsert Length: 10000 Std Brror: 0.00
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/sex="Male"
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Matches 29; Conservative
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Fax: 801 585 7177
Email: ddunn@qenet
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REFERENCE

AZ806470

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AUTHORS

JOURNAL

TITLE

FEATURES

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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymcrase and T4 polymcrase and T4 polymcrated kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 k range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pushila (P12902.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0078J15R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0078J15 R, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
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/clone lib="Mouse 10kb plasmid UGCIM library."
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 29;
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100.0%; Pred. No. 3.8e+02;
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Insert Length: 10000 Std Error: 0.00
Plate: 0078 row: J column: 15
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC2M0078J15"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
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Matches 29; Conservative
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Fax: 801 585 7177
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0180L02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0180L02 R, genomic survey sequence.
AZB68731
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 29)
1 John Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Pred. No. 3.8e+02;
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Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0180L02"
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Mus musculus
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Best Local Similarity 100.0
Matches 29; Conservative
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Fax: 801 585 7177
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KEYWORDS
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AZ868731
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TITLE

COMMENT

FEATURES

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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides ware ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2001)
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stanform diversity
855 California Ave, Palo Alto, CA 94304, USA
855 California Ave, Palo Alto, CA 94304, USA
858 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 8221
Email: walbot@stanford.edu
Email: walbot@stanford.edu
Email: valbot@stanford.edu
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021012 row: F column: 10
Class: transposon-tagged.
Location/Qualifiers
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Pred. No. 3.8e+02;
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Best Local Similarity 100.
Matches 29; Conservative
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CZ919318
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Query Match

Best Local Matches 2

ð ద ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL

COMMENT

REFERENCE AUTHORS

LOCUS DEFINITION

647 DU833998/c

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Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Birect Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
[E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AG193759 29 bp DNA linear GSS 06-MAR-2004
Pan troglodytes DNA, clone: RP43-071B06.T7, genomic survey
                  Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="E. coli DH10B"
/clome_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
                                                                                                                                                                          Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S.; Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J., Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1%; Score 29; DB 1; Length 29;
100.0%; Pred. No. 3.8e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                        National Institute of Agricultural Biotechnology 225 Seodun-Dong, Suwon, 441-707, Korea Tel: +82-31-299-1670
Fax: +82-31-299-1672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS016B12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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AG193759.1 GI:45225935
                                                                                                                                                          1 (bases 1 to 29)
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Class: BAC ends
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LOCUS
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KBrS016B12F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS016B12, genomic survey
                                                                                                                                                                                                                                                                                                                                        GSS 22-DEC-2005
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Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Institute of Agricultural Biotechnology
25 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Email: pbeem@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
                                                                                                                                                                                                                                                                                                                   19 bp DNA linear GSS 22-DEC-20 KBrS013D17F KBrS, Brassica rapa Sau3A1 BAC library Brassica rapa subsp. pekinensis genomic clone KBrS013D17, genomic survey sequence.
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Xang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H. Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="KBrS013D17"
/lab_host="E. coli DH10B"
/clone lib="KBrS, Brassica rapa Sau3AI BAC library"
/slone="Vector: pcUGIBAC1; Site_1: Sau3AI, Brassica ra
/note="Vector: pcUGIBAC1; Site_1: Sau3AI, Brassica ra
spp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .29
/organism="Brassica_rapa subsp. pekinensis"
                                                  1.1%; Score 29; DB 1; Length 29; 100.0%; Pred. No. 3.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 29; 3.8e+02;
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                                                                                                                                                                                        1 AAAAAAAAAAAAAAAAAAAAAAAAAAA 29
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/db_xref="taxon:51351"
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/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Beom-Seok Park
Brassica Genomics Team
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DU833998.1 GI:83870594
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DU835145.1 GI:83871741
  ampicillin."
                                                                                                          29; Conservative
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Class: BAC ends.
                                                                                  Similarity
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source

FEATURES

59

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DU835145

DEFINITION

ACCESSION VERSION

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Gaps

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1 (Dages 1 to 29)

Whilingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb): The v + i method used for the library construction is
described in detail in Smith, H. and Vener, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelssyedGetigr.org

Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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T. brucei sheared genomic DNA clone 334g09, reverse sequence,
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Trypanosoma brucei
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae,
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0
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/clone_lib="RP-43 Chimpanzee Male BAC Library"
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100.0%; Pred. No. 3.8e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                       /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-071B06.T7"
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/strain="TREU927"
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/clone="334909"
                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                           : pBACe3.6
: EcoRI
: ECORI.
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                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
                                                                                                                Sequencing: T7
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1 (bases 1 to 29)
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Matches 29; Conservative
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R.Site 2
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TA334G09Q/c
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JOURNAL
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AUTHORS
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KEYWORDS
SOURCE
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        COMMENT
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Murinae; Mus.

E (bases 1 to 30)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L (Dapplished (1999)

L (Onbert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CONDA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://image.llnl.gov

Plate: LLAMINGS) row: e column: 12
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EST 17789 Ripe Grape Skin Triplex2 Library Vitis vinifera CDNA
clone B3CSOORL002E09 3', mRNA sequence.
                                                                                                                                                                      BG865511 30 bp mRNA linear EST 29-MAY-2001
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Vitis vinifera
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
Abbal, P., Agasse, A., Agoerges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
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/clone="rkAGE:4909811"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_SG2"
2709 AAAAAAAAAAAAAAAAAAAAAAAAA 2737
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                            29 AAAAAAAAAAAAAAAAAAAAAAA 1
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/mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 30.
Location/Qualifiers
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EST.
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                                                                                                                                                                                                                    mRNA sequence.
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/cultivar="cabernet Sauvignon"

/db_xref="taxon:2976"

/clone=193CSOMSL002E09"

/dev stage="ripening stage"

/clone lib="Ripe Grape Skin; Vector: Lambda Triplex2; Site_1:

/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:

SfilA; Site_2: SfilB; Oriented library"
                                                                     Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
Agronomique Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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Contact: Walbot V
Contact: Walbot V
Stanford University Sciences
Stanford University Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 725 8221
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1 (bases 1 to 31)
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4013006B10.2EL yl 4013 - RescueMu Grid O Zea mays genomic, genomic
survey sequence.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages Unpublished (2002)
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Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013006 row: B column: 10
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/mol type="genomic DNA"
/molltvar="mixed background W23/A188/B73/K55"
/db xref="taxon.4577"
/tissue_type="leaf"
/dev stage="adult"
/lab_host=="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/note="Organ: leaf; Vector: RescueMu (engineered from
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100.0%; Pred. No. 3.8e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                         Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: B.hamdi@bordeaux.inra.fr
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CZ914262.1 GI:71930750
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pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
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1 (bases 1 to 32)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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/clore_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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Universite de Bordeaux I, Institut National de la Recherche
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100.0%; Pred. No. 3.9e+02;
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/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
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/clone="B3CS57RB007H05"
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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UMR 619 - Equipe
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                            DN955775 32 bp mRNA linear EST 04-MAY-2005 it93f12.gl Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
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Spermatophyta; Gnetophyta; Gnetopsida; Gnetales; Gnetaceae; Gnetum.
1 (bases 1 to 32)
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Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 387 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gex="female"
/clone lib="Gnetum female cone (NYBG)"
/clone lib="Gnetum female cone (NYBG)"
/note="Corpan: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express ODNA Synthesis Kit. The
Library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"
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I (bases 1 to 34)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATC.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                   , mRNA
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100.0%; Pred. No. 4e+02;
ive 0; Mismatches 0; Indels
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/db_xref="taxon:3382"
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DN955775
DN955775.1 GI:63027913
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BU431802.1 GI:22770284
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Best Local Similarity 100.v
                                                                                                                                                               Gnetum gnemon
Gnetum gnemon
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/clobe=Invake:1839/42.
/tissue type="globlastoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NH1 MGC 57"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: Sfil (ggccgcctcgggcc); Site_2: Sfil (ggccattatggcc);
Sil (ggccgcctcgggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGACATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGACATTATGGCC-3' and 3' adaptor (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="endosperm"
/dev_stage="developing endosperm tissue 6, 8, 10 dpa (days
post_anthesis)"
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/clone_lib="Wheat EST endosperm library"
/note="Vector: _ZipLox; Site_l: Sal I; Site_2: Not I; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae, BEP clade; Pooldeae, Triticeae, Triticum.

1 (bases 1 to 35)
Ali,S, Holloway,B. and Taylor,W.C.
Normalisation of cereal endosperm EST libraries for structural and functional genomic analysis
Plant Mol. Biol. Rep. 18, 123-132 (2000)
Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
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CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia Tel: 61 2 6246 5223

Fax: 61 2 6246 5000

Email: Bill.Taylor@csiro.au
Seq primer: Mil reverse primer
High quality sequence stop: 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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/mol_type="mRNA"
/cultivar="Hartog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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                             0
                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 TAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                /clone="IMAGE:3839742"
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Triticum aestivum
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/clone="WNEL10h12"
                          Plate: LLCM528 row: k colum
High quality sequence stop: 3
Location/Qualifiers
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http://image.llnl.gov
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AZ627842.1 GI:11750128
GSS.
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Fax: 801 585 7177
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Best Local Similarity
Matches 30; Conserv
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AZ627842/c
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was prepared from endosperm tissues of the wheat cultivar Hartog. CDNA was synthesised from pooled 6, 8, and 10 dpa endosperm using Not I-oligo(dT)18 primer/adapter (Pharmacia Biotech), and then ligated to the Sal I-Not I ste of ZhpLox vector (Life Technology) after adding a Sal I-Xho I adapter (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HD--08-E17.bl OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--08-E17, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                            EST 11-AUG-2005
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Contact: Ivens AC
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 15A, UNITED KINGDOM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Platyhelminthes, Trematoda, Digenea,
Strigeidida, Schistosomatoidea, Schistosomatidae, Schistosoma.
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"
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4.2e+02;
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                                                                                                                                                                1.1%; Score 29; DB
100.0%; Pred. No. 4.1.
tive 0; Mismatches
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/db_xref="taxon:6183"
/clone="SmlC21b12.q1k"
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CF318239.1 GI:33690000
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AM044046.1 GI:72292514
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Schistosoma mansoni
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Best Local Similarity 100.0
Matches 29, Conservative
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CF318239/c
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coll DH10B"
/clone_lih="colpAcl-overexpressing transgenic rice plasmid
cDNA library (HD)_"
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Dunn, D., Aoyagi, A., Barber, M., Meenen, E., Pedersen, T.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.0%; Score 28.8; DB 1; Length 32; 93.8%; Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                    Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: G column: 03
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
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University of Utah Genome Center
University of Utah
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/clone="HD--08-E17"
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7 10:41:28 2006

Tue Nov

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Gaps

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Coulson, P.S.,

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Vitis vinifera

Subaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; cosids; Vitaceae; Vitis.

Tosids; Vitaceae; Vitis.

Tosids; Vitaceae; Vitis.

Tosids; Vitaceae; Vitis.

Abbal.P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,

Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,

Hamdi.S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

Lonpublished (2002)

Lonpublished (2002)

Contact: Hamdi.S.

Unk 619 - Equipe Biologie de la Vigne

Universite de Bordeaux I, Institut National de la Recherche
                                                                                                                                                                                                                                                                                     AM043639 Schistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA clone SmlC23b07.q1k, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNS46288 30 bp mRNA linear EST 30-APR-2004
EST 18240 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
CDNA clone B3CS1XGB015D07 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Schistosoma mansoni
Schistosoma mansoni
Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeldida; Schistosomatoidea; Schistosoma.

(bases 1 to 36)
Billon, G.F., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S., Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C. Microarray analysis identifies genes preferentially expressed in Unpublished (2005)
Contact: Ivens A.C.
Pathogen Microarrays Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Schistosoma mansoni"
/mol_type="mRNA"
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/clone="SmlC23b07.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"
        Length 34;
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1.0%; Score 28.8; DB 1;
93.8%; Pred. No. 4.2e+02;
tive 0; Mismatches 2;
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93.8%; Pred. No. 4.3e+02;
tive 0; Mismatches 2;
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Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
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Query Match 1.0
Best Local Similarity 93.8
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalv4 (gil 4732114[gb]AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Antirrhinum majus
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Lamiales; Plantaginaceae; Antirrhineae;
                                                                                                                                                                       /lab_host="B. Coli strain XLIO-Gold, TI-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/db_xref="taxon:4151"
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/tissue_type="whole plant"
/clone_lib="Antixrhinum majus whole plant"
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Pred. No. 4.1e+02;
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MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany
Location/Qualifiers
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/organism="Antirrhinum majus"
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                        organism="Mus musculus"
                                                                                                 /db_xref="taxon:10090"
/clone="UUGC1M0474G03"
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EST.
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ilarity 93.8%;
Conservative
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Best Local Similarity
Matches 30; Conserv
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AJ800678/c
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                 81, 33883 Villenave D'Ornon Cedex,
                                                                                                                                                                         / Organism="vitis vinifera"
/mol type="mRNA"
/mol type="mRNA"
/mol type="mRNA"
/doutiver="cabernet Sauvignon"
/db xref="taxon:29760"
/clone="B3CS1XGB015D07"
/dev stage="green stage"
/clone_lib="green grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ443322 30 bp DNA linear GSS 04-OCT-200 IM0237L20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic COOR UUGCIM0237L20 R, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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1 Unn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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96.7%; Pred. No. 4.2e+02;
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
          71, Avenue Edouard Bourleaux, BP
France
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
                                                   Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7
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Location/Qualifiers
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/clone="UUGC1M0237L20"
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AZ443322.1 GI:10591190
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Plate: 0237 row: L c
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Best Local Similarity 96.7'
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Agronomique
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musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resources (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAPL (gil 4732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0261124R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0261124 R, genomic survey sequence.
AZ458127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Enarchontoglires, Glires, Rodentia, Goiurognathi, Muroidea, Muridae, Murinae, Mus.

1 (bases 1 to 30)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rally, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Duval, B., Consein, E., Pedersen, T., Ponse M., Rose, M., Rose, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Nouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28.4; DB 1;
Pred. No. 4.2e+02;
0; Mismatches 1.
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Insert Length: 10000 Std Error: 0.00
Plate: 0261 row: I column: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC1M0261124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: plasmid ends
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Best Local Similarity 96.73
Matches 29; Conservative
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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Query Match
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musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMPA2 (gil 47321141gbl AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Kratagene) cells and selected for ampicillin resistance."
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/mol_type="genomic DNA"
/wol_type="genomic DNA"
/wol_type="genomic DNA"
/wol_type="genomic DNA"
/tissue_type="leaf"
/tissue_type="leaf"
/tissue_type="leaf"
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/dev_stage="adult"
/lab_host="DH10B"
/lab_host="DH10B"
/loone_lib="4021 - RescueMu Grid v"
/clone_lib="4021 - RescueMu Grid vm
/clone="Organ: leaf; Vector: RescueMu; Site_1: BamH1; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/. Grid
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4021005B07.2EL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic
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Zea mays
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021005 row: B column: 07
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Score 28.4; DB 1; Length 30; 96.7%; Pred. No. 4.2e+02;
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Fax: 650 725 8221
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Location/Qualifiers
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CZ917310
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les 29; Conserv
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AUTHORS
TITLE
JOURNAL
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V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and Bull, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@rda.90.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (Bases I to 30)
Yang T.J. Kwon, S.J. Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica rapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. coli DH10B"
/clone lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBACI; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                         Length 30;
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/organism="Brassica rapa subsp. pekinensis"
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/cultivar="Chiifu"
/sub species="pekinensis"
/db Xref="taxon:51351"
/clone="KBrS013015"
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                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                            1.0%; Score 28.4; DB 1;
96.7%; Pred. No. 4.2e+02;
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                                                                                                                                                                                                    Local Similarity 96.7 tes 29; Conservative
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Class: BAC ends.
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DEFINITION
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Gaps

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33 bp mRNA linear EST 04-NOV-2004 14Salt--02-F20.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone CV725332
                                                                                                                                       /organism="vitis vinifera"
/mol_type="mRNA"
/mol_type="mRNA"
/dollivar="cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS58RB008A08"
/clone="B3CS58RB008A08"
/dev stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_l: SfilA; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="vector: pBluescript SK(+); Site_1: EcoRI; Site_2: Aboi; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAB XR vector at 5' end with EcoRI and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 3330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 33)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
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/lab_host="B.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
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/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                                                     1.0%; Score 28.4; DB 1; Length 33;
llarity 96.7%; Pred. No. 4.4e+02;
Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:39947"
/clone="14Salt--02-F20"
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7
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                                                                                                 Location/Qualifiers
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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

roaids; Vitaceae; Vitis.

I (bases 1 to 32)

S Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,

Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,

Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

or seeds) at Various Developmental Stages

L Unpublished (2002)

L Conteact: Hamdi S.

Universite de Bordeaux I, Institut National de la Recherche
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/clone="B3CS00RL007D07"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit shin, Vector: Lambda TriplEx2; Site_l:
SfilA; Site_2: SfilB; Oriented library"
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1 (bases 1 to 33)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp Or seeds) at Various Developmental Stages
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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/cultivar="Cabernet Sauvignon"
     lone B3CS00RL007D07 3', mRNA sequence.
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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CN546161 35 bp mRNA linear EST 30-APR-2004 EST 18113 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00RL009B01 3', mRNA sequence.
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/lab host="DH10B (T1 phage-resistant)"
/clon="lab"NIH_MGC_6"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
/note="Organ: prostate; Vector: prostate; Vector (Clontech); Vector (Clontech);
/note="Organ: prostate; Vector (Clontech); Vector (Clontech); Vector (Clontech);
/note="Organ: prostate; Vector (Clontech); Vec
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Vitis vinifera

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons,
rosids, Vitaceae, Vitis.

1 (bases I to 35)
Abbal, P., Agases, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI610 row: o column: 06
High quality sequence stop: 34.
                                                                Hominidae, Homo.

1 (bases 1 to 34)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov

Tissue Procurement: DCTD/DTP
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Universite de Bordeaux I, Institut National de la Recherche
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96.7%; Pred. No. 4.4e+02;
tive 0; Mismatches 1;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:4739549"
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205139241 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4739549 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1526 row: e column: 12
High quality sequence stop: 34.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 34)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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BG531309.1 GI:13522846
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Best Local Similarity 96.7%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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Homo sapiens
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BG612023
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/clone lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
SfilA; Site_2: SfilB; Oriented library"
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EST 18369 Green Grape Berry Lambda Triplex2 Library Vitis vinifera cDNA clone B3CS1XGB016G05 3', mRNA sequence.
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1 (bases I to 35)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, P., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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/cloine lib="Green Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.0%; Score 28.4; DB 1; Length 35; Best Local Similarity 96.7%; Pred. No. 4.5e+02; Matches 29; Conservative 0; Mismatches 1; Indels
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/organism="Vitis vinifera"
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71, Avenue Edouard Bourleaux, BP
France
                                                     Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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                                                                                                                                                 Location/Qualifiers
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Location/Qualifiers
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Fax: 00-33-(0)5-57-12-25-48
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CN546416.1 GI:46911041
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Best Local Similarity 96.77
Matches 29; Conservative
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Vitis vinifera
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ST 18437 Turning Grape Berry Lambda Triplex2 Library Vitis Vinifera cDNA clone B3CS37TB007E01 3', mRNA sequence. CN54666 CN546666.1 GI:46911291
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Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis;
1 (bases 1 to 35)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
Unpublished (2002)
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Vitis vinifera
Vitis vinifera
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons,
rosids, Vitaceae, Vitis.

1 (bases 1 to 35)
Abbal, P., Agasse, A., Agasse, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
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TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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Universite de Bordeaux I, Institut National de la Recherche
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/culfivar="Cabernet Sauvignon"
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2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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                                                                                                                                                                                                                                                                                            Vitis vinifera
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CN546666/c
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                                                                                                                  RESULT 675
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CZ919845
                                                                                                                              CF335736/c
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JOURNAL
COMMENT
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TITLE
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Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UNR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
T. Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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                                                                                                                                                                                                                                                                                                              /mol type="mmNA"
/unclivar="Cabernet Sauvignon"
/cultivar="Cabernet Sauvignon"
/db xref="taxon:29760"
/clone="Basc337TB007E01"
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/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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Antirthinum majus
Antirthinum majus
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiales, Lamiales, Plantaginaceae, Antirrhineae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H., Saedler,H. and Zachgo,S. Characterization of Antirrhinum Petal Development and Identification of Target Genes of the Class B MADS Box Gene
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/clone_lib="Antirrhinum majus whole plant"
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Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
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/organism="Antirrhinum majus"
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                                                                                                                                                                                Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
                                                                                                                                                                                                                                                              Location/Qualifiers
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Best Local Similarity 96.73
Matches 29; Conservative
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverses transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
                                                                                                                                                                        EST 18-AUG-2003
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                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhattoideae; Oryzaee; Oryza.

1 (bases 1 to 33)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ALDMT-overexpressing transgenic rice plasmid
cDNA_library (JMT)"
                                                                                                                                                                                          JMT--05-112.bl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--05-112, mRNA sequence.
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/mol_type="mRNA"
/cultivar="Nackdong"
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2707 CTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
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90.9%; Pred. No. 4.5e+02;
tive 0; Mismatches 3
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/clone="JMT--05-112"
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CF335736.1 GI:33819839
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Matches 30; Conservative
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/note="vector pIndigoBAC-536"
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Best Local Similarity 90.9
Matches 30; Conservative
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Sus scrofa
                                                              Best Local Similarity
Matches 30; Conserv
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/dev_stage="adult"
/lab_host="bH10B"
/lab_host="bH10B"
/clone lib="4021 - RescueMu Grid V"
/note="Organ: leaf; Vector: RescueMu (engineered from pB1ueScript backbone); Site 1: BamH1; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DMA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamH1 and BglII, and ligated to form circular plasmids. DH10B capls were transformed and then screened on LB plates with ampicillin."
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Danio rerio genomic clone DKEY-85L9, genomic survey sequence.
AL983097
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1 (bases 1 to 33)

Humphray,S.J., Huckle,E. and Hunt,S.E.

Direct Submission

Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail contact: humquery@sanger.ac. uk Unpublished

This sequence was generated from the T7 end of BAC 85L9. 85L9 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
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                 Contact: Walbot V
Department of Biological Sciences
Stanford University
B55 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Tel: 650 725 8221
Email: walbot Gestanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021015 row: A column: 06
Class: transposon-tagged.
Location/Qualifiers
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                    /organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/b xref="taxon:4577"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28.2; DB 1; Length 33;
Pred. No. 4.5e+02;
0; Mismatches 3; Indels
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/mol_type="genomic DNA"
/db_rref="taxon:7955"
/clone="DKEY-8519"
/tissue_type="Testis"
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Best Local Similarity 90.9%;
Matches 30; Conservative
  Unpublished (2001)
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21181_111-43 Fundulus Heteroclitus Liver Fundulus heteroclitus cDNA, mRNA sequence.
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Conteat: Crawford, Douglas L.
Amarine Genomics - Crawford Lab
Rosenstiel School of Marine and Atmospheric Science - University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AJ746854 muscle - muscle minus alveolar macrophage Sus scrofa cDNA clone C0001822c_All, mRNA sequence.
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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Hopwood, P.A., Zhang, F., Lowden, S., Talbot, R., Burt, D., Archibald, A.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Metazoa, Chordata, Craniata, Euteleostei, Neoteleostei,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Cyprinodontiformes, Fundulidae, Fundulus, Atherinomorpha;
I (Bases I to 34)
Crawford, D.L., Oleksiak, M.F., Kolell, K.J., Paschall, J., VanWye, J.,
Roach, D.L. and Whitehead, J.A.
Fundulus Functional Genomics: EST Database for Teleost Fish
                                                         Gaps
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http://genomics.rsmas.miami.edu/funnybase/super_craw3/
Plate: 111 row: F column: 6.
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  Length 33;
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                                                      Indels
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/clone lib="Fundulus Heteroclitus Liver"
/note="Organ: Liver"
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90.9%; Pred. No. 4.6e+02;
1.0%; Score 28.2; DB 1;
llarity 90.9%; Pred. No. 4.5e+02;
Conservative 0; Mismatches 3;
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                                                                                                                                                              0; Mismatches
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Email: dcrawford@rsmas.Miami.edu
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/db_xref="taxon:8078"
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2709 AAAAAAAAAAAAAAAAAAAAAAAAAA
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AM043789.1 GI:72291602
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Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site.1:
ECORI R. Site 2: NotI Description: Normalised library constructed
Ifform pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institite,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
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Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
(Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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/clone lib="CSEQRAN09"
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."
                                                         Contact: Hopwood PA

Contact: Hopwood PA

Dept. of Preclinical Veterinary Sciences

Royal School for Veterinary Studies

Summarhall, Edinburgh, EH9 10H, UNITED KINGDOM

Sequencing was performed by ARK genomics. This clone is available from ARK- Genomics, Roslin Institute, Roslin, Midlothian EH25 9PS, UK. See www.ark- genomics.org or contact info@arkgenomics.org.
                                                                                                                                                                                                                                                                 /mol_type="mRNA"
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/tissue-sr000182c_All"
/tissue-sr000182c_All"
/cell_type="macrophage"
/clone_lib="muscle - muscle minus alveolar macrophage"
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AJ666435 CSEQRAN09 Sus scrofa cDNA clone C0000033_L21, mRNA
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Pred. No. 4.6e+02;
0; Mismatches 3;
and Dixon,L.
Development of a porcine cDNA microarray
Unpublished (2004)
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/mol_type="mRNA"
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/clone="C0000033_L21"
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Nikolaidou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.

Microarray analysis identifies genes. preferentially expressed in the lung schistosomulum of Schistosoma mansoni

Unpublished (2005)
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Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S. Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C. Marcoarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni
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/db_xref="taxon:6183"
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/clone liba-Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"
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Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 15A, UNITED KINGDOM.
Location/Qualifiers
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Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 iSA, UNITED KINGDOM.
Location/Qualifiers
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Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S., Nikolaidou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C. Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni
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Strigeidida, Schistosomatoidea, Schistosoma.
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/clone lila="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"
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AM044512.1 GI:75966804
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Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
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145TL--09-N05.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-N05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantea, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Nahm B.H. GreenGene Biotech Inc.; Division of Bioscience and Bloinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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                                                                                                                                    1...28
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100.0%; Pred. No. 4.2e+02;
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                                                                      Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
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Unpublished (2005)
Contact: Ivens AC
Pathogen Microarrays Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF282351.1 GI:33659738
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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CF282351
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Best Local Similarity
Matches 28; Conserv
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CF330938
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VERSION
KEYWORDS
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S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Min, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTS .

Unpublished (2003)

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YongJin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhahhm@gdpio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
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/mol type="mRNA"
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cDNA library (HD)"
                                                                                 EST 15-AUG-2003
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                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Wagnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (basea I to 28)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
                                                                                                 HD--13-E16.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--13-E16, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pGR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20un) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PGR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Matches 28; Conserv
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CF330748
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                                      RESULT 689
CF321885/c
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Torgin, KyeongJi, Korea
Tel: 82 31 330 6193
Pax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Rice callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, Y.K., Rim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
TongJi, Kyeongqi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa (japonica cultivar-group)"
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1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                               Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/cultivar="Nackdong"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Enkaryota; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

En (Lasses I to 28)

Shaughnessy, L. Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8874

Email: mccombie@cshl.org,
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/note="Organ: leaf; Vector: :pBK-CMV; Site_1: XhoI;
Site_2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
                                                                                                                                                                                                                                                  Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR073098 12005 28 bp mRNA linear EST 08-JUN-2005
ik86a05.gl Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol type="mana"
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/dev stage="veraison stage"
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/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
1 (bases 1 to 28)

Abbal,P., Agasec,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                       Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 4.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.0%; Score 28; DB 1;
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    .28
    /organism="Vitis vinifera"

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/mol_type="mRNA"
/db_xref="taxon:3311"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 AAAAAAAAAAAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                        Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ginkgo biloba (maidenhair tree)
Ginkgo biloba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -21M13UnivRev.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                Seg primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence
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DR073098/c
LOCUS
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AUTHORS
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AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta: Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

E (bases 1 to 28)

S Abbal, P., Agases, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

L Unpublished (2002)

Contact: Hamdi S.
UNK 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNE46703 28 bp mRNA linear EST 30-APR-2004 EST 18474 Turning Grape Berry Lambda Triplex2 Library Vitis vinifera cDNA clone B3CS37TB007H02 3', mRNA sequence.
                                                                                                                                                                                                                                                                         CN546364 128317 Green Grape Berry Lambda Triplex2 Library Vitis vinifera cDNA clone B3CS1XGB016C01 3', mRNA sequence.
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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/clone_lib="Green Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
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Vitis vinifera
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, Vitaceae, Vitis.
                                                   Gaps
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  DB 1; Length 28;
4.2e+02;
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                                                   Indels
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/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3C31XGB016C01"
Query Match
1.0%; Score 28; DB
Best Local Similarity 100.0%; Pred. No. 4.2
Matches 28; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 4.2 tive 0; Mismatches
                                                                                                  2709 AAAAAAAAAAAAAAAAAAAAAAAA 2736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Vitis vinifera"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: s.hamdi@bordeaux.inra.fr
Seg primer: T7.
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Fax: 00-33-(0)5-57-12-25-48
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Vitis vinifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 28; Conserv
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ACCESSION

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REFERENCE AUTHORS

JOURNAL

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TITLE

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Gaps

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AZ399637 1002 28 bp DNA linear GSS 03-OCT-2000 1M0165N04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0165N04 R, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sciurognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 28)

1 (bases 1 to 28)

1 (bases 2 to 28)

1 (bases 3 to 28)

1 (bases 3 to 28)

1 (bases 4 to 28)

1 (bases 5 to 28)

1 (bases 6 to 28)

1 (bases 7 to 28)

1 (bases 8 to 28)

1 (bases 8 to 28)
The library was size-fractionated to enrich for large inserts."
                                                                                                                                         Gaps
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                                                                                   Length 28;
                                                                                                                                         0; Indels
                                                                                1.0%; Score 28; DB 1; Le
100.0%; Pred. No. 4.2e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0165 row: N column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                       2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
                                                                                                                                                                                                                         28 AAAAAAAAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 28.
Location/Qualifiers
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Mus musculus
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                                                                                                                                      Conservative
                                                                          Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ399637
                                                                                                                                                                                                                                                                                                                        RESULT 695
AZ399637/c
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ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

LOCUS

ઠે g ACCESSION VERSION KEYWORDS SOURCE

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Laboratory Mouse DNR Resource
[http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor or oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil/4732114 gbl/AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Murcidea; Murinae; Mus.

1 (bases 1 to 28)

2 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

1 Unpublished (2000)

2 Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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chemically-competent B. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                            AZ401766 1085 03-OCT-200 AM linear GSS 03-OCT-200 AMO168008R Mouse 108b plasmid UUGCIM library Mus musculus genomic clone UUGCIM0168008 R, genomic survey sequence.
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                                                                                                                                                 Gaps
                                                                                                                                                 ö
                                                                                      Score 28; DB 1; Length 28;
                                                                                                                                                 0; Indels
                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0168 row: O column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ401766
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VERSION
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/ Gex="Male" | Jean | J

organism="Mus musculus"

source

FEATURES

/mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M0165N04"

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/lab hose="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G75BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gal
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognachi; Murcidea; Muridae; Mus.

E 1 (bases 1 to 28)

E 1 (bases 1 to 28)

S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Diamid inserts

L Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                  AZ471744 110286KOBR Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0286KOB R, genomic survey sequence.
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chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                     Gaps
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                                                                                       1.0%; Score 28; DB 1; Length 28;
100.0%; Pred. No. 4.2e+02;
                                                                                                                                               0; Indels
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Insert Length: 10000 Std Exror: 0.00
Plate: 0286 row: K column: 08
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
                                                                                                                   Local Similarity 100.0%; Pred. No. 4.2 nes 28; Conservative 0; Mismatches
                                                                                                                                                                                                          2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
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Mus musculus
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Fax: 801 585 7177
                                                                                                Query Match
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TITLE

COMMENT

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0327F02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0327F02 R, genomic survey sequence.
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(Loases 1 to 28)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Stokes, R., Stokes, R., Stokes, R., Stokes, R., Shokes, M., Moenen, E., Pedersen, T., Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Weiss Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/clone llb="Mouse 10kb plasmid UUGCN library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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0
                                                                                Length 28;
                                                                                                                                 0; Indels
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Pred. No. 4.2e+02;
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100.0%; Pred. No. 3...
'... 0; Mismatches
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Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
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fatrain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC1M0327F02"
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Insert Length: 10000 Std Erro
Plate: 0327 row: F column: 02
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                                                                                                                                   Conservative
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Fax: 801 585 7177
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/sex="Male" | Jecure 
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chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0527E02F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0527E02 F, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center
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0
                                                                                                             Length 28;
                                                                                                                                                                                     0; Indels
                                                                                                                                               4.2e+02;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0527 row: E column: 02
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Location/Qualifiers
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Best Local Similarity 100.0
Matches 28; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

2 (lucopathi; Muroidea; Murinae; Mus.

3 (lucopathi; Muroidea; Murinae; Mus.

4 (lucopathi; Muroidea; Murinae; Mus.

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chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                     Query Match 1.0%; Score 28; DB 1; Length 28; Best Local Similarity 100.0%; Pred. No. 4.2e+02; Matches 28; Conservative 0; Mismatches 0; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0028 row: J column: 01
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
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Mus musculus
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muscular cryburon (mare) was occarned from the caches. Laboratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor or oligonicleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114] gb|APL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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2M0099109F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0099109 F, genomic survey sequence.
chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/clone_lib="Mouse_10kb_plasmid_UGCIM_library"
/note="Vector: PWD42Iv; Purified genomic_DNA_from M.
musculus_C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 28)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Kose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                   Gaps
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0
                                                                                      1.0%; Score 28; DB 1; Length 28;
100.0%; Pred. No. 4.2e+02;
iive 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: I column: 09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0099109"
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Location/Qualifiers
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                                                                                                                       Local Similarity 100.
nes 28; Conservative
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Fax: 801 585 7177
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AZ824519/c
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TITLE

COMMENT

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

El (bases 1 to 28)

El (bases 1 to 28)

Bun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Conse to Benome scaffolding with paired end reads from 10kb plasmid inserts

L Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                           AZ833425 20-FEB-2001
2M0115D04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0115D04 R, genomic survey sequence.
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chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb plasmid UNGCNM library."
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                     Length 28;
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                                                                                     DB 1;
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Insert Length: 10000 Std Error: (
Jate: 0115 row: D column: 04
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
                                                                                        1.0%; Score 28;
100.0%; Pred. No.
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Location/Qualifiers
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/clone="UUGC2M0115D04"
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                                                                                        Query Match
Best Local Similarity 100.
Matches 28; Conservative
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Fax: 801 585 7177
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COMMENT
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AUTHORS
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/sex="Male" | Journal | Jo
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chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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ry Mus musculus genomic
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                         Length 28;
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1.0%; Score 28; DB 1; Ls
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0177 row: B column: 08
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0177B08"
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Location/Qualifiers
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AZ866569.1 GI:13068007
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AUTHORS
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/Woll type="genomic DNA"

/woll type="leavon:4577"

/tissue type="leavon:4577"

/dev stage="adult"

/dev stage="adult"

/dev stage="adult"

/lone lib="4012"

/clone lib="4012"

/clone lib="4012"

/clone lib="4012"

/clone lib="adult"

/worcor: RescueMu (engineered from pBlueScript backbone); Site il BamHi, Site 2: BglII;

RescueMu is a 4-9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid BB was grown at UC Berkeley in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII; and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                           4012010AA02.1EL_y1 4012 - RescueMu Grid BB Zea mays genomic, genomic CZ912316
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chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
Mais California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Very probable ligation site of ends cut by single endonuclease. Reverse complemented post-ligation sequence from source sequence. Plate: 4012010 row: A column: 02
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                                                                       Score 28; DB 1; Length 28;
                                                                                                                     0; Indels
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                                                                                            1 Similarity 100.0%; Pred. No. 4.2 28; Conservative 0; Mismatches
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Location/Qualifiers
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Fax: 650 725 8221
Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                         CZ912316.1 GI:71927550
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                                                                                                 Best Local Similarity
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CZ912316/c
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TITLE
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RESULT 705

LOCUS

CZ913960

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL COMMENT

AUTHORS REFERENCE

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Contract: Beam-Seok Park
Confract: Beam-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Swon, 441-707, Korea
7E1: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS003K05
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Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicacese, Brassica.
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BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
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/sub_ergel=utaxon:51351"
/db_xref="taxon:51351"
/clone="KBrS003X65"
/lab hosts="B. coli DH10B"
/clone=lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site_1: Sau3AI, Brassica rapa sap pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."
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KBrS016F07F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS016F07, genomic survey sequence.
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Bnd sequence of Brassica rapa Sau3AI (KBrS) BAC clone Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
          Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J. H. and Park,B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone Unpublished (2005)
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Pred. No. 4.2e+02;
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v 100.0%; Pred. No. ...
... 0; Mismatches
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/cultivar="Chiifu"
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Class: BAC ends.
Location/Qualifiers
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Matches 28; Conserv
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//dev stage="adult"
//dev stage="adult"
//deb_host="DH10B"
//clone_lib="dH10B"
//clone_lib="dH10B"
//clone_lib="dH10B"
//clone_lib="dH10B"
//clone_lib="dH10B"
//clone_lib="dH10B"
//clone_lib="descript"
//descript backbone); Site 1: BamH1; Site_2: BglII;
Rescuedwi is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
with a for more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu'.
O was grown at Stanfford in 2001. DNA was extracted from
leaf strips, double digested using BamH1 and BglII, and
ligated to form circular plasmids. DH10B cells were
transformed and then screened on LB plates with
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                           GSS 08-AUG-2005
                     C2913960 28 bp DNA linear GSS 08-AUG-2005 2013005A02.1EL_x1 4013 - RescueMu Grid O Zea mays genomic, genomic
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Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea. (bases 1 to 28)
                                                                                                                                                                                                                                                                                                                                                                  Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
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KBrS003K05R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS003K05, genomic survey
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/cultivar="mixed background W23/A188/B73/K55"
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.00.0%; Pred. No. 4.2e+02;
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organism="Zea mays"
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BAC end sequence
KBrB082B24
Seq primer: T7
Class: BAC ends.
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Brassica; Viridiplantae; Stredtophyta; Eudicotyledons; Core eudicotyledons;
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| clone="KBrS016F07" |
| lab host="KBrS016F07" |
| clone=| KBrS016F07" |
| clone=| TBr87 |
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BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
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/note="Vector: PCUGIBAC1; Site_1: Sau3AI, Brassica rapa
spp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
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/db_xref="taxon:51351"
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Seg primer: T7
Class: BAC ends.
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Best Local Similarity
Matches 28; Conserv
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DX072153 28 bp DNA linear GSS 10-JAN-2006 KBrB082B24F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB082B24, genomic survey
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/clone lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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T. brucei sheared genomic DNA clone 291a01, reverse sequence,
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Boermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases I to 28)
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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1 (bases 1 to 28)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
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/clone="KBrB082B24"
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AL486613.1 GI:11853602
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Best Local Similarity 100.0
Matches 28; Conservative
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TITLE

1 AAAAAAAAAAAAAAAAAAAAAAAAA 28

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Query Match
Best Local Similarity 100.0
Matches 28; Conservative
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CZ912823/c
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Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge GB10 18A, E-mail: barrell@sanger.ac.uk and

nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

betails of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridgé CB10 ISA, E-mail: barrell@eanger.ac.uk and nhl@sanger.ac.uk and nhl@sanger.ac.uk constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nalsayed@cigr.org

at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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Genomic survey sequence.
AL497637
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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.00.0%; Pred. No. 4.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
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/mol_type="genomic DNA"
/strain="TREU927"
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/clone="379d11"
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(bases 1 to 28)
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Matches 28; Conservative
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CZ912823 29 bp DNA linear GSS 08-AUG-2005 4012012A03.2EL_yl 4012 - RescueMu Grid BB Zea mays genomic, genomic survey sequence.
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/clone="B3CS00RL006A02"
/clone="B3CS00RL006A02"
/clone=lib="Ripe Grape Skin Triplex2 Library"
/clone lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
SfilR; Site_2: SfilB; Oriented library"
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Vitis vinifera
Vitis vinifera
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bokaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 29)
Abbal P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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Length 28;
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Pred. No. 4.3e+02;
                        4.2e+02;
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/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
1.0%; Score 28; DB 1;
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100.0%; Pred. No. ...
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             100.0%; Prec. ...
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Email: s.hamdi@bordeaux.inra.fr
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EST.
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/mol_type="genemics DNA"
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RescueMu is a 4:9 kb, modified maize Mu transpoon
pBlueScript backbone); Site 1: BamH1 Site 2: BglII;
RescueMu is a 4:9 kb, modified maize Mu transpoon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/. Grid
BB was grown at UC Barkeley in 2001. DNA was extracted
from leaf strips, double digested using BamH1 and BglII,
and ligated to form circular plasmids. DH10B cells were
transformed and then screened on LB plates with
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                                                                  Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V
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4013006B03.2EL_x1 4013 - RescueMu Grid O Zea mays genomic, genomic
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Unpublished (2001)
                                                                                                                             Department of Blological Sciences
Stanford University
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
1el: 650 723 2227
Fax: 650 725 8221
Fax: 650 125 8221
Fax: 650 post-ligation site of ends cut by 2 different endonucleases.
Possible ligation site of ends cut by 2 different endonucleases.
Plate: 4012012 row: A column: 03
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8155 California Ave, Palo Alto, CA 94304, USA
1e1: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
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clade; Panicoideae; Andropogoneae; Zea.
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Department of Biological Sciences
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CZ914240.1 GI:71930716
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Matches 28; Conservative
                          (bases 1 to 29)
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                                             Walbot, V.
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/clone_lib="4013 - RescueMu Grid O"
/clone_lib="4013 - RescueMu Grid O"
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RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/. Grid O was grown at Stanford in 2001. DNA was extracted from last strips, double digested using BamH1 and BgllI, and ligated to form circular plasmids. DH10B cells were
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Vitis vinifera

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

1 (bases 1 to 30)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,

Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,

Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

Unpublished (2002)
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Reverse complemented post-ligation sequence from source sequence. Plate: 4013006 row: B column: 03 Class: transposon-tagged.
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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0
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/culfivar="mixed background W23/Al88/B73/K55"
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100.0%; Pred. No. 4.3e+02;
ive 0; Mismatches 0; Indels
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
                                                                                                  Location/Qualifiers
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CN545968.1 GI:46910593
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Tue Nov

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/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
SfilA; Site_2: SfilB; Oriented library"
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Ti, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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Vitis vinifers

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; Vitaceae; Vitis,

(bases 1 to 30)

Abbal.P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,

Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,

Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

Unpublished (2002)
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/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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                                                                                Length 30;
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                                                                              1.0%; Score 28; DB 1; Le
Local Similarity 100.0%; Pred. No. 4.4e+02;
Nes 28; Conservative 0; Mismatches 0;
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Fax: 00-33-(0)5-57-12-25-48
Email: 8.hamdi@bordeaux.inra.fr
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Location/Qualifiers
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CN546523.1 GI:46911148
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                                                                                                                          Matches
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/ucganism="Zea mays"
/mol type="genomic DNA"
/cullivar="mixed background w23/A188/B73/K55"
/db xref="taxon:4577"
/tisue_type="leaf"
/dev stage="adult"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid V"
/lone="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site !! BamHl; Site_2: BglI;
/RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/' Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf stribs, double digested using BamHl
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
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2820044.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820044 3',
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

    (bases 1 to 30)

                                                                                                                                                       Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Malbot \mathbf V
                                                                                                                                                                                                                                                                                           Stanford University
855 California Ave, Palo Alto, CA 94304, USA
71: 650 723 2227
71: 650 725 8221
8mail: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021013 row: F column: 10
Class: transposon-tagged.
Location/Qualifiers
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2820044.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
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                                                                                                                                                                                                                                                                  Department of Biological Sciences
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1 (bases 1 to 31)
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Best Local Similarity 100.
Matches 28; Conservative
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AW245279
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organism="Hordeum vulgare subsp. vulgare"
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                                   /mol_type="mRNA"
/cultivar="Himalaya"
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Schistosoma mansoni
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Matches: 28; Conservative
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Best Local Similarity 96.6'
Matches 28; Conservative
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AM046790
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DEFINITION
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Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNLat:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washingtion Genome Center. Vector Trimming: cross match from University of Washingtion Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washingtion Genome Center: PHRED high quality bases following vector sequence: 0 contiguous PHRED high quality bases following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dlone="INAGE:280044"

/tissue_type="small cell carcinoma"

/tissue_type="small cell carcinoma"

/tissue_type="mall cell carcinoma"

/clone_lib="McG3"

/lab_host="DHJOB (phage-resistant)"

/clone_lib="NIH_MGC_7"

/note="Organ: lung; Vector: pOTB7; Site_1: Xho1; Site_2:

EcoR1; cDNA made by oligo-dr priming. Directionally

cloned into EcoR1/Xho1 sites using the following 5;

adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Hordeum vulgare subsp. vulgare
Bukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Clade; Pooideae; Triticeae; Hordeum.
I (bases 1 to 31)
Ali, S. Holloway, B. and Taylor, W.C.
Normalisation of cereal endosperm EST libraries for structural and functional genomic analysis
Plant Mol. Biol. Rep. 18, 123-132 (2000)
Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
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CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
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31 bp mRNA linear EST 24-AUG-20
BNEL32a8 Barley EST endosperm library Hordeum vulgare subsp.
vulgare cDNA clone BNEL32a8 5' similar to Unknown Function, mRNA
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: 4.5e+02;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Fax: 61 2 6246 5203
Email: Bill.Taylor@csiro.au
Seg primer: M13 reverse primer
High quality sequence stop: 31.
Location/Qualifiers
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90.3%; Pred. No.
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Best Local Similarity
Matches 28; Conserv
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AUTHORS
TITLE
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COMMENT

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/day_stage="developing endosperm tissue 10, 12, 15 dpa (days_stage="developing endosperm tissue 10, 12, 15 dpa (days_post_anthesis)"
/lab_hote="blublus (Life Technology)"
/clone lib="Barley EST endosperm library"
/clone lib="Barley EST endosperm Library"
/note="Vector: _ZipLox; Site_1: Sal I; Site_2: Not I; mRNA was prepared from endosperm tissues of the barley cultivar Himalaya. cDNA was synthesised from pooled 10, 12, and 15 dpa endosperm using Not I-oligo(dr)18 primer/adapter (Pharmacia Biotech), and then ligated to the Sal I-Not I site of _ZipLox vector (Life Technology) after adding a Sal I-Xho I adapter (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."
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Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S., Nikolaidou-Katsaridou, N., Quall, M.A., Wilson, R.A. and Ivens, A.C. Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC27e08.qlk"
/dev_stage="lung schistosomulum"
/clone lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB 1; Length 31;
Pred. No. 4.5e+02;
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100.0%; Pred. No. ...
'... 0; Mismatches
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Contact: Ivens AC
Achogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 15A, UNITED KINGDOM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAAAAAAAAAAAAAAAAAAAAAA 28
                                                                               tissue type="endosperm"
                         /db_xref="taxon:112509"
/clone="BNEL32a8"
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Query Match
Best Local Simi
Matches 28;
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AUTHORS
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E 1 (bases 1 to 32)
S Dum, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Ralla,M., Longacre,S., Mahmoud,M., Mesen,E., Pedersen,T., Rellam,H., Longacre,S., Mahmoud,M., Mesen,E., Pedersen,T., Niederhausern,A. and Wright,D., Weiss,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R., Tingey,A., von Dasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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1M0162P23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0162P23 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             These sequences may be of either nuclear or mitochondrial origin.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 Contact: Andrew Serazin
Collins/Besansky Lab
Center for Tropical Disease Research and Training, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         // sex="male and female"
//dev_stage="embryo, larvae, pupae, and adult"
//clone_lib="ESTs from wild-caught Anopheles funestus
                                                                                                                                                     Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera; Nematocera, Culicoidea; Culicidae, Anophelinae, Anopheles.

1 (bases 1 to 32)

Besanaky, N. J., Serazin, A.C. and Dana, A.

Towards the transcriptome of Anopheles funestus: a molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Igor1_A02_03_007 ESTs from wild-caught Anopheles funestus oppulations Anopheles funestus cDNA 5', mRNA sequence.
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317 Galvin Life Science, Notre Dame, IN 46556, USA
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1.0%; Score 28; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Anopheles funestus"
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/note="Vector: LambdaTriplEx2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strāin="West African"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
                                           CD577661
CD577661.1 GI:48718676
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 5746319321
Email: nbesansk@nd.edu
                                                                                                           Anopheles funestus
Anopheles funestus
                                                                                                                                                                                                                                                                                                              Unpublished (2003)
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwMD42 (gil4732114|gplAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector NNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 33)

Chang, C., Ye, M., Wu, X., Gu, J., Huang, Q., Zhou, J., Shen, Y., Han, Z.,
Chen, S., Mao, M. and Chen, Z.

Homo sapiens CB library cDNA clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone llb="Mouse 10kb plasmid UUGCNM lbrary"
/note="Vector: PWD42nv; Purlfied genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV743346 AHOMO SADIENS CDNA Clone CBMABD12 5', MRNA SEQUENCE. AV743346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
Location/Qualifiers
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Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
198: 86-21-64740490
Fax: 86-21-6474206
Email: mbshi@ms.stn.sh.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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Pred. No. 4.5e+02;
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            Std Error: 0.00
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100.0%; Pred. No. ...
'... 0; Mismatches
Insert Length: luuuu Complate: 0162 row: P column: 23
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
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                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC1M0162P23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV743346.1 GI:10860927
                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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8; Conservative
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7 10:41:28 2006

Tue Nov

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RESULT 726
CV727574/c
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TITLE
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1 (Dases 1 to 31)

8 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other_ESTS: 2821429.5prime
Contact: Robert Straubberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LiML) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washingtion Genome Center:
PHRAP suite. PoTy-T Identification: patMatch.pl from Berkeley Drosophila Genome washington edu Low Quality Sequence: 20
contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 31 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW249485 31 bp mRNA linear EST 07-JAN-2000 2821429.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821429 3',
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/tissue type="small cell carcinoma"
/cell_Ine="MGC3"
/lab host="HH10B (phage-resistant)"
/lab host="HH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average
/organism="Homo sapiens"
/mol type="mkNA"
/db xref="taxon:9606"
/clone="ChMABD12"
/tissue_type="cord blood"
/call type="CD34+ hematopoietic stem/progenitor cell"
/lab host="BMZ5.8"
                                                                                                                                                                                                /note="Vector: pBluescript; Site 1: EcoRI; The insert cloned randomly with the EcoRI digestion"
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                      1.0%; Score 28; DB 1; Lengua 2., 93.3%; Pred. No. 4.6e+02; Lindels
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/organism="Homo sapiens"
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High quality sequence stop: 20.
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/db_xref="taxon:9606"
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Homo sapiens
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Matches 28; Conservative
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AW249485
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CV727574

14Salt--05-M13.gl Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--05-M13, mRNA sequence.
                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                            CX014884 11 bp mRNA linear EST 06-DEC-2004 io77d03.gl Whole Heart Library (DGGEST5) Canis familiaris CDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                               Score 27.8; DB 1; Length 31;
Pred. No. 4.6e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 31)
Ballja,V.S., Nascimento,L.U. and McCombie,W.R.
ESTB from Canis familiaris whole heart (dog)
Unbublished (2004)
Contact: W. Richard McCombie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.6e+02;
                                                                                                                                                                                2709 ААВАВАВАВАВАВАВАВАВАВАВАВАВА 2739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organisme"Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.0%; Score 27.8; Di
Best Local Similarity 93.5%; Pred. No. 4.6e
Matches 29; Conservative 0; Mismatches
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EST.
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                                                                                                                    l Similarity 93.5%;
29; Conservative
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Matches 29; Conserv
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FEATURES

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|db_xref="GABI:192840"
|db_xref="taxon:161934"
|clone="024-025-L15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.0%;
Similarity 88.2%;
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Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
vo.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptil (SFA; R. Sitel: BcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pooled early embryos, from 8- cell stage to blastocysts.
Clones available from UK Centre for Functional Genomics in Farm
Animals, Roslin institite, Roslin, Midlothian, UK, EH25 9PS,
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1 (Dases 1 to 34)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Bevelopment of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AJ656734 Sus scrofa cDNA clone C0005194_F08, mRNA sequence. AJ656734
                    Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaae; Oryza.

1 (bases 1 to 33)
Kim.J.S., Jun.K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Exar: 82 31 321 6355
Email: bhnahm@gDio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: Xhol; Leaf was incubated at 4 C(360uM/m-28ec-1) for Zhre. CDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with Xhol site."
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/db_xref="taxon:19947"
/cione="145alt--05-M13"
/dev_stage="14 days after gernimation"
/dev_stage="14 days after gernimation"
/dev_stage="14 days after gernimation"
/dov_stage="14 days after 
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sativa (japonica cultivar-group)
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/cultivar="Nackdong"
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Sus scrofa
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AJ656734

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COMMENT

FEATURES

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/tissue_type="developing root"
| Tab host="EMDH10B" |
| Jab host="EMDH10B" |
| Clone lib="MPIZ-ADIS-024-developing root" |
| Index | Tab |
| I
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E012759-024-025-L15-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
CDNA clone 024-025-L15 5-PRIME, mRNA sequence.
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1 (baess 1 to 34)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005194 F08"
/tissue type="embryo"
/clone lib="KN277"
/note="Vector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."
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SP6-Sall-CCACGCGCTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
broject, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Construction of a 'unigene' CDNA clone set by oligonucleotide ingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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ADIS DNA core facility at MPIZ
MAX-Planck-Insetiute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 34 Std Error: 0.00
Plate: 25 row: L column: 15
Seg primer: SP6; CATACGATTTAGGTGACACTATAG.
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Pred. No. 4.9e+02;
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28; Conservative
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Vitis vinifera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="MPIZ-ADIS-024-storage root"
/clone lib="Wetcor: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
/note="Wetcor: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
cDNA library from sugar bett, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
                                                          ö
                                                                                                                                                                                                                                         EST 06-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, Caryophyllales, Amaranthaceae, Beta.
1 (bases 1 to 29)
1 (bases 1 to 29)
1 (bases 1 to 29)
2 Meisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H., and Radelof, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                           29 bp mRNA linear EST 06-DEC-2
E012643-024-019-C03-T7 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-019-C03 3-PRIME, mRNA sequence.
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/organism="Beta vulgaris"
/mol_type="mRNA"
/culTivar="KWS2320 (double haploid, monogerm breeding
                                                          Gaps
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                Length 34;
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 29 Std Error: 0.00
Plate: 19 row: C column: 03
Seg primer: T7; GTAATACGACTCACTATAGGGC.
Location/Qualifiers
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96.6%; Pred. No. 4.7e+02;
ve 0; Mismatches 1; Indels
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                Score 27.6; DB 1;
Pred. No. 4.9e+02;
                                                                                                                  |db_xref="GABI:189579"
|db_xref="taxon:161934"
|clone="024-019-C03"
|tissue_type="storage root"
|lab_host="EMDH10B"
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                                                        0; Mismatches
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                1.0%;
88.2%;
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Conservative
  Query Match
Best Local Similarity 88.29
Marches 30; Conservative
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Beta vulgaris
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Matches 28;
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AUTHORS
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RESULT 730

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CN545226 29 bp mRNA linear EST 30-APR-2004 EST 17170 Green Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00GL004F12 3', mRNA sequence.
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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/dev stage="green stage"
/clone_lib="Green Grape Skin Triplex2 Library"
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SfilA; Site_2: SfilB; Oriented library"
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1 (bases 1 to 29)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Handi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
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Vitis vinifera
Vitis vinifera

Vitis vinifera

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

1 (bases 1 to 29)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,

Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,

Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

Unpublished (2002)
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Universite de Bordeaux I, Institut National de la Recherche
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                     CNS45226
CNS45226.1 GI:46909681
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1 (bases 1 to 29)

S Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

L Unpublished (2002)

Contact: Hamdi S.

UNR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
                                                                                                                                                                                                                                                                                               /db_xref="texcor:29760"
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/clone_llb="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_l:
SfilR; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 bp mRNA linear EST 30-APR-2004 Lambda Triplex2 Library Vitis vinifera
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_I: SfiIA; Site_2: SfiIB; Oriented library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0%; Score 27.4; DB 1;
96.6%; Pred. No. 4.7e+02;
tive 0; Mismatches 1;
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/cultivar="Cabernet Sauvignon"
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                                                                                                                                                                                                                                 organism="Vitis vinifera"
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Fax: 00-33-(0)5-57-12-25-48
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Best Local Similarity 96.6
Matches 28; Conservative
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Vitis vinifera
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muscular collaboration (marie actorion) and paperatory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                            GSS 20-FEB-2001
                                                                                                                                                                                                      AZ825156
2M0100N08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0100N08 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse_10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/60 (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Insert Length: 10000 Std Brror: 0.00
Plate: 0100 Tow: N column: 08
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737

    .29
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/mol_type="genomic DNA"
/strain="C57BL/6J"

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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC2M0100N08"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                             AZ825156.1 GI:12995064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
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Best Local Similarity 96.6
Matches 28; Conservative
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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                                                                                                                                                                                   AZ825156
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LOCUS DEFINITION

CZ914157

8 셤 ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicacea; Brassica.

1 (bases 1 to 29)
S Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Hahn, J. H. and Park, B.S.
Brassica rapa Sau3AI (KBrS) BAC clone
(Ontact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 bp mRNA linear EST 06-JUL-2004
DKF2p566J1346 rl 566 (synonym: h£kd2) Homo sapiens cDNA clone
DKF2p566J1346, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3Al BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. coli DH10B"
/clone lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pcuGIBACI; Site 1: Sau3AI, Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/cultivar="Chifu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
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Pred. No. 4.7e+02;
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|db_xref="taxon:51351"
|clone="KBrS013N05"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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  JU834266.1 GI:83870862
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Best Local Similarity 96.6%;
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Homo sapiens
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EST (Ottenwaelder, e
Unpublished (1999)
Contact: MIPS
MIPS
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1 (bases 1 to 30)
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Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DU834266 29-DDA linear GSS 22-DEC-2005 KBrS013N05F KBrS, Brassica rapa Sau3A1 BAC library Brassica rapa subsp. pekinensis genomic clone KBrS013N05, genomic survey bu834266
                                                                                                                                                                           C2914157 28L_x1 4013 - RescueMu Grid O Zea mays genomic, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stanford University
855 California Ave, Palo Alto, CA 94304, USA
761: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Bossible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013005 row: G column: 04
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Best Local Similarity 96.6
Matches 28; Conservative
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CZ914157
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Zea mays
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AUTHORS

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RESULT 737

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cypriniformes; Cyprinidae; Danio.

(Spriniformes; Cyprinidae; Danio.

Humphray, S.J., Huckle, E. and Hunt, S.E.

Direct Submission

Submitted (14-NoV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambidgeshire, CBIO 1SA, UK. E-mail contact: humquery@sanger.ac.uk Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DR31A15T 30 bp DNA linear GSS 22-NOV-2002
Danio rerio genomic clone DKEY-31A15, genomic survey sequence.
                                                                                                                                                                                                                                                                  Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was generated from the 17 end of BAC 31A15. 31A15 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="green stage"
Coone libb="green Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
  l (bases 1 to 30)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
                                                                                                                                                                                                           UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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Location/Qualifiers
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Pred. No. 4.8e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="vitis vinifera"
/mol type="mRNA"
/culfivar="Cabernet Sauvignon"
/db xref="texon:29760"
/clone="B3CS1XGB015F11"
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/db_xref="taxon:7955"
/clone="DKEY-31A15"
/tissue type="Testis"
/note="vector pIndigoBAC-536"
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                                                                                                                                                                                                                                                                                                                                Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
rosids; Vitaceae; Vitis.
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Danio rerio
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l Similarity 93.3%;
28; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictyostelium discoideum
Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota, Wycetczoa, Dictyosteliida, Dictyostelium.
1 (bases 1 to 30)
Urushihara, H., Morio, T., Saito, T., Kohara, Y., Koriki, E., Ochiai, H., Maeda, M., Williams, J.G., Takeuchi, I. and Tanaka, Y.
Analyses of cDNAs from growth and slug stages of Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS46316 EST 10-2004 mRNA linear EST 30-APR-2004 EST 18268 Green Grape Berry Lambda Triplex2 Library Vitis vinifera CDNA clone B3CS1XGB015F11 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AU267300 AD at 11near EST 26-APR-2004 AU267300 VS Dictyostellum discoideum cDNA clone VSH345 5', mRNA
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Vitis vinifera
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons;
                                                                                                                                                                                                                   Gaps
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                      /tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: Sall"
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                                                                                                                                                                    Score 27.4; DB 1; Length 30;
Pred. No. 4.8e+02;
0; Mismatches 1; Indels
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Tel: 81-298-53-4664
Fax: 81-298-53-664
Email: hideko@biol.tsukuba.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels

    .30
    forganism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"

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Local Similarity 93.3%; Pred. No. 4.8e+02;
he 28; Conservative 0; Mismatches 2;
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University of Tsukuba
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/clone_lib="VS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:44689"
/clone="VSH345"
  clone="DKFZp566J1346"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AU267300.1 GI:20526098
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Best Local Similarity 96.6%;
Matches 28; Conservative
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RESULT 738

Matches

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DN988790.1 GI:66248617
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Best Local Similarity 96.6
Matches 28; Conservative
                                             plasmid inserts
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84112, USA
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DN988790/c
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                                                                                                                                                                                                                                                                 'Vitis vinifera'
'Vitis vinifera'
'Vitis vinifera

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

1. (Jasses I to 31)

2. (Jasses I to 31)

3. Abal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

L Unpublished (2002)

L Contact: Hamdi S.

UNIVERS 19 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
                                                                                                                     31 bp mRNA linear EST 30-APR-2004 EST 17860 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA calone B3CS00RL006D01 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .31
/organism="Vitis vinifera"
/mol_type="mRNA"
/mol_type="mRNA"
/cultivar="cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3GS00RL006D0!"
/dev stage="ripening stage"
/clone lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin, Vector: Lambda TriplEx2; Site_1:
SfilA; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 bp DNA linear GSS 16-FEB-200 IMO552E03R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIMO552E03 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
1 (Sase 1 to 33)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
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                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                              CN545916.1 GI:46910541
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GSS.
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Matches 28; Conservative
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DEFINITION
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                                                                                                      RESULT 740
CN545916/c
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AZ759642/c
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Meouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gfrom a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli X110-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (bases 1 to 34)
Melmaiee,K., Elavarthi,S. and Guenzi,A.C.
                                                                                                                                                                                                                                                                                    SIC,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                Ξ.
                                                                                                                               Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 108, Biomedical Polymers Research Bldg., 20 S. 2030
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                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
Fax: 8052 row: 8 column: 03
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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Cynodon dactylon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC1M0552E03"
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CF334956
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AW250841/c
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COMMENT
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                                                                                                                                                                                                                                                                                                                                             /organism="Cynodon dactylon"
/mol_type="mRNA"
/cullivar="22012"
/db_xref="taxon:28909"
/db_xref="taxon:28909"
/db_ref="taxon:28009"
/clone="YEBRA_ZR_2-II_02_ZEBRA_ZR_2-II_02_G01.abl"
/tissue_type="Crom"
/lab_hosf="E. coll"
/clone lib="Bermudagrass line Zebra subtracted cold acclimated cDNA library"
/note="Vector: Qlagen's pbrive; Messenger RNA was extracted from control and cold acclimated bermudagrass crom tissue at 2 and 28 days after acclimation and cDNA library was constructed following Clontech PCR- select cDNA subtraction procedure."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CF298526
7LEAF--01-P04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-P04, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
Identification of differentially expressed genes associated with cold acclimation using suppression subtraction hybridization (SSH) and cDNA microarrays
Unpublished (2005)
Contact: Guenzi AC
Dep. of Plant and Soil Sciences
Oklahoma State University
168 Agriculture Hall, Stillwater, OK 74078-6028, USA
Tel: 405-744-6028
Fax: 405 744 6039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.L., Xim,Y.K. Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongJi.ac.kr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27.4; DB 1; Length 34; Pred. No. 5.1e+02;
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                                                                                                                                                                                                    Email: acg@mail.pss.okstate.edu
PCR PRimers
FORWARD: M13 forward
BACKWARD: M13 Reverse
Seq primer: M13 Forward.
Location/Qualifiers
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les 28; Conservation
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                                                                    JOURNAL
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            TITLE
                                                                                        COMMENT
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhattoideae; Oryzeae; Oryza.

(bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongGi, Korea
Yel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
tissue type="leaf"

/dev Stage="leaf"
/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
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Organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="NackGong"
/db_xref="taxon:39947"
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llarity 90.6%; Pred. No. 5.1e+02;
Conservative 0; Mismatches 3; Indels
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10.6%; Pred. No. 5.1e+02;
.ve 0; Mismatches 3;
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AM048211.1 GI:75968183
EST.
Schistosoma mansoni
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AM048211/c
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/fmage/himage.html Base calling / Quality
Scores: PHRED from University of Washingtion Genome Center.
Trimming: cross_match from University of Washingtion Genome Center.
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 32
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 32 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this CDNA insert was
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/issue_type="most" |
/call line="MGG3"
/lab host="bull08 (phage-resistant)"
/clone lib="NHH MGC 7"
/note="organ: lung; Vector: pOTB7; Site 1: Xho1; Site 2:
ECOR1; cDNA made by oligo-dT priming. Directionally cloned into ECOR1/Xho1 size-selected >500bp for average adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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        2821274.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821274 3',
                                                                                                                                                                                          Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 bp DNA linear GSS 29-APR-2 co1856-3prime Exelixis piggyBac PB insertions Drosophila melanogaster genomic Sequence recovered from 3' end of piggyBac, CZ467504 CZ467504 GI:62961517 GI:SCZ657504 GI:SC
                                                                                                                                                                                                                                                                                                                                                       Hominidae, Homo.

1 (bases 1 to 32)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Notional institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821274.5prime
Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821274"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: LLCM6 row: G column: 3
High quality sequence stop: 32.
Location/Qualifiers
                                                                                                                            AW250841.1 GI:6593834
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                                                 nRNA sequence.
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Matches 29; Conserv
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AUTHORS
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/organism="Drosophila melanogaster"
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/clone lib="taxon:727"
/clone lib="taxon:raposaste PB GenBank accession number
/cl
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota, Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

I (bases I to 32)
Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L., Ryner, L., Cheung, L.M., Chong, A., Ericken, C., Fisher, W. W., Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Lauf, L., Ventura, R., Woo, A., Zakrajsek, I., Zahor, C., Swimmer, C., Kopczynski, C., Duyk, G., Winberg, M.L., and Margolis, J. A. complementary transposon tool kit for Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence orientation is forward strand relative to 5' end of piggyBac element.
The piggyBac insertion position is unspecified in the 32 bases.
This insertion position refers to the first base of the 4 base TTAA class: transposon insertion site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
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90.6%; Pred. No. 5.1e+02;
tive 0; Mismatches 3;
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Nat. Genet. 36 (3), 283-287 (2004)
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                                                                                              (bases 1 to 27)

Dillon,G.E., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S., Nikolaidou-Katearidou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C. Mixolaidou-Katearidou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C. Mixroarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni Unpublished (2005)
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida; Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzea, Oryza.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bloinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 27)
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/clone lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"
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100.0%; Pred. No. 4.8e+02;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
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-ive 0; Mismatches
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Schistosoma mansoni
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/dev stage="proliferated callus on 2N6 media for 30 days"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida; Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, YeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee, T.H., Shin, Y.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CF330557 19-AUG-NACL--06-F04.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--06-F04, mRNA
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NACL--05-C12.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-C12, mRNA
                                                       Gaps
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Length 27;
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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1.0%; Score 27; DB 1; I
.00.0%; Pred. No. 4.8e+02;
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                 100.0%; Prea. ....
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/cultivar="Nackdong"
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Location/Qualifiers
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  Query Match
Best Local Similarity 100.
Matches 27; Conservative
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Gaps

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/note="Vector: pCR4-TOPO, Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                       AW327923 28-JAN-2000 dr02g08.xl NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847159 5', mRNA
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S NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Emaal: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Edge BioSystems

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)

DNA Sequencing by: NIH Intramural Sequencing Center (NISC)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image/image/image.html

Plate: LLCM0029 row: M column: 16

Seq primer: -21M13 forward primer (ABI).
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/cell_line="MGC4"
/clone_lib="NIH MGC 3"
/note="Organ: Lymph; Vector: pOTB7a; Library prepared
                                                                                                                                               1.0%; Score 27; DB 1; Length 27;
100.0%; Pred. No. 4.8e+02;
Live 0; Mismatches 0; Indels
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Pred. No. 4.8e+02;
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                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2847159"
           CDNA library (JMT) "
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AW327923.1 GI:6798418
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Homo sapiens
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Best Local Similarity 100.
Matches 27; Conservative
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Vitis vinifera
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CNS45326/c
LOCUS
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AW327923
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TITLE
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP
Clade; Enrhartoideae; Oryzeae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Vim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:39947"
/db xref="taxon:39947"
/clone="NACL--06-F04"
/tissue_type="callus"
/dev stage="taxon:16erated callus on 2N6 media for 30 days"
/dab host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOP0; Site 1: BCORI; mRNA was capped
with_oligoribonucleotides and then used as templates for
                                                                                                           Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yorgin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggblo.com, bhnahm@bio.myongji.ac.kr.
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/clone="JMT--04-N08"
/tissue_type="ladas after germination"
/dev stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 bp mRNA linear EST 18-AUG-20 JMT--04-NO8.bl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--04-NO8, mRNA sequence. CF335229 (CF335229.1 GI:33818810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yonglin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
1 (bases 1 to 27)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/cultivar="Nackdong"
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/cultivar="Nackdong"
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Best Local Similarity
Matches 27; Conserv
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VERSION
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                          AUTHORS
  REFERENCE
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/organism="Vitis vinifera"
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Best Local Similarity 100.0
****hes 27; Conservative
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  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 755
CN545530/c
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CN545597/c
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             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosida; Vitaceae; Vitis.

E 1 (bases 1 to 27)

E Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Generation of Expressed Sequence Trag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

L Unpublished (2002)

Contact: Hamdi, S., Guibe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="green stage"
Clone_lib="green Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
SfilA; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNS45492 27 bp mRNA linear EST 30-APR-2004 EST 17436 Green Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00GL005G05 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                        Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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1 (bases 1 to 27)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp Or seeds) at Various Developmental Stages
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00GL006G12"
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                                                                                                                                                                                                                                                                                                                                                                   Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Location/Qualifiers
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CN545492.1 GI:46910117
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Best Local Similarity 100.
Matches 27; Conservative
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Vitis vinifera
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SfilA; Site_2: SfilB; Oriented library"
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// Organism="vitis vinifera"
// Organism="vitis vinifera"
// Organism="vitis vinifera"
// Organism="Cabernet Sauvignon"
// Ordar="etaxon:2970"
// Clone="BacScoRuc03809"
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// Ordar="stage="ripening stage"
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T., Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

rosids; Vitaceae; Vitis;

1 (bases 1 to 27)

Abbal, P., Agasse, A., Aganassova, R., Barrieu, F.,

Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,

Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

Or seeds) at Various Developmental Stages
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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100.0%; Pred. No. 4.8e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                             Score 27; DB 1; Le
Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                             Query Match 1.0%; Score 27; DB Best Local Similarity 100.0%; Pred. No. 4.8 Matches 27; Conservative 0; Mismatches
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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CN545962/c
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Vitis vinifera

Vitis vinifera

Vitis vinifera

SM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

E 1 (bases 1 to 27)

S Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, B., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="vitis vinifera"
/mol type="mRNA"
/mol type="mRNA"
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/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_l: SfilA; Site_1: SfilB; Oriented library"
  EST 30-APR-2004
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1 (bases 1 to 2)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Gameu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
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EST 17883 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL006F01 3', mRNA sequence.
CNS45938
CNS45938.1 GI:46910563
CNS45597 27 bp mRNA linear EST 30-APR.
EST 17541 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL003H05 3', mRNA sequence.
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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Universite de Bordeaux I, Institut National de la Recherche
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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                                                                                CN545597.1 GI:46910222
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                                                                                                                          Vitis vinifera
Vitis vinifera
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Matches 27; Conserv
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CN545938/c
LOCUS
DEFINITION
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KEYWORDS
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AUTHORS
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| 1...27 | Organism="Vitis vinifera" | Organism="Vitis vinifera" | Organism="Vitis vinifera" | Organism="RNA" | Organism="Cabernet Sauvignon" | Organism="Cabernet Sauvignon" | Organ="S100RL006F01" | Organ="ripening stage" | Organism="S100RL00F01" | Organism="Organism="Vinites" | Organism="Organism="Organism="Vinites" | Organism="Organism="Vinites" | Organism="Organism="Vinites" | Organism="Vinites" | Orga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNS45962 27 bp mRNA linear EST 30-APR-2004 EST 17910 Ripe Grape Skin Triplex2 Library Vitis vinifera CDNA clone B3CS00RL006H07 3', mRNA sequence.
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|note="Organ : Fruit shin; Vector: Lambda TriplEx2; Site_1:
|SfilA; Site_2: SfilB; Oriented library"
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Vitis viniters

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Viteaceae; Vitis.

1 (bases 1 to 27)
Mabbal.P., Agasse, A., Agoorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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Pred. No. 4.8e+02;
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/mol_type="mana"
/cultivar="Cabernet Sauvignon"
/db_xref="texon:29760"
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100.0%; Pred. No. 4.8e+
...ive 0; Mismatches
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                                                                                                Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Matches 27; Conservative
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Vitis vinifera
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CN546052/c DEFINITION

ઠે a ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

AUTHORS

REFERENCE

JOURNAL

COMMENT

TITLE

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CN546337 27-2004 EST 18289 Green Grape Berry Lambda Triplex2 Library Vitis vinifera cDNA clone B3CS1XGB015H08 3', mRNA sequence.
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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France
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Vitis vinifera
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Vitis vinifera
Vitis vinifera
Sukaryots, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases I to 27)
Abbal.P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Handis, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
Or seedal at Various Developmental Stages
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="green stage"
|Clone lib="green Grape Berry Lambda Triplex2 Library"
|note="Organ: Fruit without seeds; Vector: Lambda
|TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages Unpublished (2002)
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
                                                                                        Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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Pred. No. 4.8e+02;
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/mol type="mRNA"
/culfivar="Cabernet Sauvignon"
/db xref="taxon:29760"
/clone="B3CS1XGB015C02"
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llarity 100.0%; Pred. No. 4.8
Conservative 0; Mismatches
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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STT 18223 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
CDNA clone B3CS1XGB015C02 3', mRNA sequence.
CNS46271
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1 (bases 1 to 27)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; Vitaceae; Vitis:
1 (bases 1 to 27)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romleu,C. and Terrier,N.
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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1.0%; Score 27; DB 1; Le Best Local Similarity 100.0%; Pred. No. 4.8e+02; Matches 27; Conservative 0; Mismatches 0;
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/clone="B3CS00RL007H09"
             2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
                                            Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: 8.hamdi@bordeaux.inra.fr
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REFERENCE AUTHORS

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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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Eukaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

El (basea 1 to 27)

S Brenner, E. D. Twigg, R. W., Runko, S. J., Katari, M. S., Dedhia, N. N., O'Shaughnessy, A. L., Balija, V., Martienssen, R. A., McCombie, R. W., Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

L. Unpublished (2005)

L. Contact: W. Richard McCombie

Lita Annenberg hazen Genome Sequencing Center

Cold Spring Harbor Laboratory, PP Box 100, Cold Spring Harbor. NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids, Viteceae; Vitis.

1 (Dases 1 to 27)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N. Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

L. Unpublished (2002)

Contact: Hamdi S.

UNR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
                                                                                                                                                                                                                                                                                                                                                                                    Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
Fars 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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ik79h10.gl Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
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/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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1.0%; Score 27; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0;
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/cultivar="Cabernet Sauvignon"
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Location/Qualifiers
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Seg primer: -21M13UnivRev.
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E 1 (bases 1 to 2.7)

B Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couttre, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

L Unpublished (2002)

Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
                                                                                                                                                                                                                                                                                                                                                                                                          CNS46559 27 bp mRNA linear EST 30-APR-2004 EST 18703 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera CDNA clone B3CS58RB008C12 3', mRNA sequence.
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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// Organism="Vitis vinifera"
// mol type="mRNA"
// cultivar="Cabernet Sauvignon"
// db xref="taxon:29760"
// db xref="taxon:29760"
// dev stage="ripe stage"
// dev stage="ripe stage"
// clone lib="Ripe Grape Berry Lambda Triplex2 Library"
// note="Organ: Fruit without seeds; Vector: Lambda TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
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CNS46574 GI:46911199
EST.
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                                                                                          Length 27;
                                                                                                                                                    0; Indels
                                                                              Query Match
1.0%; Score 27; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0;
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Seq primer: T7.
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Fax: 00-33-(0)5-57-12-25-48
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CN546559.1 GI:46911184
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Vitis vinifera
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Vitis vinifera
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 763 CN546574/c

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DEFINITION

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Gaps

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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymoicacide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
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/clone_lib="Ginkgo female leaf (NYBG)" hote="Organ: leaf; Vector: :pBK-CMV; Site_l: Xhol; Site_2: Eco RK; Strategene ZAP Express CDNA Synthesis Kit. The library was size-fractionated to enrich for large
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Musinae, Mus.
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84112, USA
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Insert Length: 10000 Std Error: 0.00
Plate: 0778 row: H column: 15
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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1.0%; Score 27; DB
Best Local Similarity 100.0%; Pred. No. 4.8
Matches 27; Conservative 0; Mismatches
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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0078H15"
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Location/Qualifiers
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Fax: 801 585 7177
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TITLE

COMMENT

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Imporatory Mouse DNA Resource
[Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.05 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoreass. Vector DNA was prepared from a derivative
of pWD42 (gij473214]gb|AH22072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="B. Coli strain XL10-Gold, Iibrary"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nr, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                         Length 27;
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                                                                                                                                                                         1.0%; Score 27; DB 1;
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0168K04"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
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with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 27)
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musculus C57BL/6J (Male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                 Length 27;
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                                                                                                                                                                                                                                                                                                                                           1.0%; Score 27; DB 1; Le
100.0%; Pred. No. 4.8e+02;
tive 0; Mismatches 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: K column: 21
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
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/organism="Mus musculus"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                    /sex="Male"
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Fax: 801 585 7177
Email: ddunn@genet
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84112, USA
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoreasis. Vector DNA was prepared from a derivative of pWD42 (gi|473214|qb|At29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (Bally M., Aoyagi, A. Barber, M., Beacorn, T., Duval, B., Hamil, C.,

1 (Bally M., Rose, M., Rose, R., Stokes, R., Tingey, A., von.

1 (Miederhausern, A. and Wright, D., Weiss, R.)

1 (Mouse whole genome scaffolding with paired end reads from 10kb plasmid innerts

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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                    Score 27; DB 1; Length 27;
Pred. No. 4.8e+02;
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Insert Length: 10000 Std Error: 0.00
Plate: 0357 row: E column: 11
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Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
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Fax: 801 585 7177
                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                    Query Match
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/sex="Male"
/lab host="E. Coli strain XLIO-Gold, T1-resistant, F."
/lab host="E. Coli strain XLIO-Gold, T1-resistant, F."
/cloe lib="Mouse lokb plasmid UUGCIM library"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (qi|4732114|qib|AR29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
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E 1 (bases 1 to 27)

S Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Unpublished (2000)

L Unpublished (2000)

L Contact: Robert B. Weiss

University of Utah

University of Utah
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0369E24F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0369E24 F, genomic survey sequence.
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                                                                                                                                                                       1.0%; Score 27; DB 1; Length 27;
100.0%; Pred. No. 4.8e+02;
ive 0; Mismatches 0; Indels
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Fax: 801 585 7177
Email: ddunmgenetics.utah.edu
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Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 27.
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Best Local Similarity 100.0
Matches 27, Conservative
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84112, US
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TITLE

FEATURES

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SM Muss musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurcognathi; Muroidea; Muridae; Musinae; Mus.

1 (bases 1 to 27)
S Dunn, D., Ayogai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored wector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 4.8e+02;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0445 row: E column: 17
Seq primer: CACACAGGAAACAGCTAATGACC
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
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100.0%; Pred. No. ...
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GSS.
                                                                                                                                          Query Match
Best Local Similarity luv..
-hag 27; Conservative
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (4il 4732114 [gb]AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus.
Loases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Musc whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Uppublished (2000)
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27 bp DNA linear GSS 13-DEC-200
1M0460D12R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0460D12 R, genomic survey sequence.
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                             Length 27;
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100.0%; Pred. No. 4.8e+02;
ative 0; Mismatches 0;
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Insert Length: 10000 Std Brror: 0.00
Plate: 0460 Tow: D column: 12
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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farrain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0460D12"
/sex="Male"
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Best Local Similarity 100.0
Matches 27; Conservative
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Fax: 801 585 7177
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84112, US
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TITLE

COMMENT

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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomocleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|qb|h229072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islan, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Nouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

L Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, U 84112, USA
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Pred. No. 4.8e+02;
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Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: O column: 11
Seq primer: CGTGTAAAACGACGCCAGT
Class: plaamid ends
High quality sequence stop: 27.
Location/Qualifiers
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tive 0; Mismatches
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/organism="Mus musculus"
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/strain="C57BL/6J"
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/clone="UUGC1M0474011"
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Mus musculus
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1es 27; Conservative
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Fax: 801 585 7177
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Best Local S:
Matches 27
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/Bab. Mate. / Jab host="E. Coli strain XL10-Gold, T1-resistant, F-" / Clone lib="Mouse 10kb plasmid UUGCIM library" / Clone lib="Mouse 10kb plasmid UUGCIM library" / Clone lib="Mouse 10kb plasmid UUGCIM library" / Motele Wetcher: PWD42rv; Purified genomic DNA from M. musculus G57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114 gpl Hat129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0073B15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0073B15 F, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0;
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Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 zow: B column: 15
Seq primer: CGTTGTAAAACGACGGCCAGT
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="UUGC2M0073B15"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: plasmid ends
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84112, USA
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/clone libergia.
with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-GOId (Stratagene) cells and selected for ampicillin resistance."
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4021004B03.2EL_yl 4021 - RescueMu Grid V Zea mays genomic, genomic
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(bases 1 to 27)
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Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021004 row: B column: 03
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/db_xref="taxon:4577"
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Tel: 650 723 2227
Fax: 650 725 8221
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Pred. No. 4.8e+02;
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100.0%; Pred. No. ...
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Tue Nov

RESULT 775 DX046035

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ACCESSION VERSION KEYWORDS

ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

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/lab_host="E.coli_DH10B"
/loone_lib="KBYB, Brassica rapa BamHI BAC library"
/loote="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. chiifu BAC library (KBrB BAC) is provided
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Sus scrofa DNA, BAC clone L243P12, shotgun sequence of subclone
L243P12S001F01, read with M13Reverse primer, genomic survey
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Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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Uenishi, H., Tanaka, M. and Awata, T.
Direct Submission

Submitted (12-OCT-2004) Hirohide Uenishi, National Institute of
Agrobiological Sciences, Animal Genome Laboratory, Genome Research
Department; 2 Ikenodai, Tsukuba, Ibaraki, 305-8602, Japan

(E-mail:huenishi@affrc.go.jp, Tel:81-29-838-8627,
                                                             Contact: Beom-Seck Park
Brassica Genomics Team
Astional Institute of Agricultural Biotechnology
25 Seedun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1672
Emai: 192-91-672
Emai: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
Seq primer: T7
Class: BAC ends.
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Domukai,M., Eguchi-Ogawa,T., Shinkai,H., Awata,T. and Uenishi,H.
Genomic structure of the distal extended-class II region in swine
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2 Kenodai, Tsukuba, Ibaraki 305-8602, JAPAN
Tel: +81-29-838-8627
Fax: +81-29-838-8627
e-mail: huenishi@affrc.go.jp
Sequencing was carried out in Animal Genome Research Program
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/cultivar="chiftu"
/du species="pekinensis"
/db xref="taxon:51351"
/clone="KBrB060M12"
                         End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
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100.0%; Pred. No. 4.8e+02;
tive 0; Mismatches 0; Indels
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Hahn, J.H. and Park, B.S.
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Hirohide Uenishi
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1. 27
/ Organism="Barasica rapa subsp. pekinensis"
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/ mol_type="genomic DNA"
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/ note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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KBrB060M12F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB060M12, genomic survey
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Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosida II; Brassicales; Brassicaceae; Brassica.
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Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, andiolophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
121: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
Exat. ed. Sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                                           DNA linear GSS 10-JAN-2 KBrB047117R KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB047117, genomic survey
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Bind sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
Contact: Beom-Seok Park
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Yang.T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
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Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and

nl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTAt 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).
(Japan)

by National Institute of Agrobiological Sciences
and STAFF-Institute.
and STAFF-Institute.
Subclones of BAC clones were constructed with pUC18 vector.
Basecalling was performed by Phred 0.020425.c.
Vector sequences were eliminated by crossmatch version 0.990319.
Low quality bases were trimmed based on the quality values with the aid of the trim alt option of Phred.
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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Eukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae,
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                                                                                                                                                                                                                                /mol_type="genomic DNA"
/db xref="taxon:9823"
/clone="L243P12"
/sub clone="L243P128001F01"
/clone_lib="Sus scrofa shotgun BAC sequence"
                                                                                                                                                                                                                                                                                                                                                        1.0%; Score 27; DB 1; Length 27; 100.0%; Pred. No. 4.8e+02; Live 0; Mismatches 0; Indels
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llarity 100.0%; Pred. No. 4.8e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Trypanosoma brucei"
/mol type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="355b06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2709 AAAAAAAAAAAAAAAAAAAAAAAA 2735
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                                                                                                                                                                                                               /organism="Sus scrofa"
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Best Local Similarity 100.0
Marches 27; Conservative
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(bases 1 to 27)
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Best Local Simil
Matches 27; C
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2709 AAAAAAAAAAAAAAAAAAAAAAA 2735

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28 bp mRNA linear EST 15-AUG-2003
HD--13-I23.gl OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--13-I23, mRNA sequence.
ZBP-2003 DKFZp586I1924_rl 586 (synonym: hutel) Homo sapiens CDNA clone DKFZp586I1924, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoidae; Oryzeae; Oryza.

1 (bases 1 to 28)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yonglin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 28)
Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_cype="uterins"
/dev stage="adult"
/dev stage="adult"
/lab_host="DH10B"
/clone lib="s66 (synonym: hute1)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1/Mlu1"
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Location/Qualifiers
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Location/Qualifiers
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp58611924"
                                                                                                                                                                                                                                                                                                                                                               Wiemann,S.
EST (Duesterhoeft, et al.)
Unpublished (1999)
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                                                                                                               AL048439.1 GI:4727579
                                                                                                                                                                       Homo sapiens (human)
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Best Local Similarity 100.0
Matches 27; Conservative
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est.res

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TAAAAAAAAAAAAAAAAAAAAAA 28
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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                                                                                                                                                                               CN545498.1 GI:46910123
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Vitis vinifera
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CN545498/c
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a
                                                                                   /tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/dev_stage="proliferated"
/lab_nost="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished .v.o.,
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
Genomics and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 31 80 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/culcivar="NackGong"
/db xref="txxxon:3997"
/clone="JMT--07-N04"
/tissue type="ladf"
/dev stage="14 days after germination"
/lab_host="E.coli DH108"
/clone lib="AtUMT-overexpressing transgenic rice plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                           JBD mRNA linear EST 18-AUG-2C JMT--07-N04.gl AtJMT-Overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone CP3-7-N04, mRNA sequence.
                                                                                                                                                                      /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
                                                                                                                                                                                                                                                                                                                       Gaps
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/organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:39947"
/clone="HD--13-123"
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1.0%; Score 27; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 27; Conservative 0; Mismatches 0; Indels
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CF337400.1 GI:33823200
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Best Local Similarity 100.0
Matches 27; Conservative
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28 bp mRNA linear EST 30-APR-2004 clone B3CS00GL005G11 3', mRNA sequence.
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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Vitis vinifera
Vitis vinifera

Units vinifera

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Byermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids, Vitaceae, Vitis.

1 (bases I to 28)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
Or seeds) at Various Developmental Stages
Unpublished (2002)
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(bases 1 to 28)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Hamdi, S., Romieu, C. and Terrier, N. Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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/mol type="mRNA"
/cultivar="Caberne Sauvignon"
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/clone_lib="Green Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda TriplEx2 SfilA; Site_2: SfilB; Oriented library"
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TriplEx2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
                                                                                                      Conservative
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Best Local Similarity
Matches 27; Conserv
                                                                                 Similarity
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                                                                                                 27;
                                                                Query Match
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CZ918534/c
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DEFINITION
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SOURCE
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                                                                                                    Matches
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VERSION
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TITLE
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E 1 (bases 1 to 28)

S Abbal, P., Agasse, A., Agasse, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

L Unpublished (2002)

Contact: Hamdi S.

UNR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi 25
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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                                                                                                                                                                                                                                                                                               /organism="vitis vinifera"
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/mol_type="mRNA"
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/db xref="taxon:29760"
/clone="B3CS1XGB015D11"
/dev stage="green stage"
/clone=lib="Green Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="green stage"
/clone_lib="Green Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0%; Score 27; DB 1; Length 28; 000.0%; Pred. No. 4.9e+02; Ve 0; Mismatches 0; Indels
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/organism="Vitis vinifera"
/mol type="mRNA"
/cultivar="Cabernet Sauvignon"
/db xref="taxon:29760"
/clone="B3CSIXGB015E11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.00.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2709 AAAAAAAAAAAAAAAAAAAAAAAA 2735
                                                                                                                                                                               Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: 8.hamdi@bordeaux.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 AAAAAAAAAAAAAAAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: T7.
Location/Qualifiers
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Best Local Similarity 100.
Matches 27; Conservative
                                                                                                                                                                                                                                           Seq primer: T7.
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/db_xref="taxon:28909"
/clone="ZEBRA_2F_2-II_03_ZEBRA_2F_2-II_03_C05.abl"
/tisbue_type="Crown"
/lab host="E. coll"
/clone_lib="Bermudagrass line Zebra subtracted cold acclimated cDNA library"
/note="Vector: Qiagen's pDrive; Messanger RNA was extracted from control and cold acclimated bermudagrass crown tissue at 2 and 28 days after acclimation and cDNA library was constructed following Clontech PCR- select cDNA subtraction procedure."
                                                                                                                                                                                                                                                Z8 bp mRNA linear EST 17-MAY-2005 ZEBRA_ZF 2-II 03_C05.abl Bermudagrass line Zebra subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone ZEBRA_ZF 2-II_03_C05.abl, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                         Cynodon dactylon (Bermuda grass)
Cynodon dactylon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Chloridoideae; Cynodonteae; Cynodon.
1 (bases 1 to 28)
Melmaiee, K., Elavarthi, S. and Guenzi, A.C.
Identification of differentially expressed genes associated with
cold acclination using suppression subtraction hybridization (SSH)
Unpublished (2005)
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Fax: 405 744 6039
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Length 28;
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Pred. No. 4.9e+02;
1.0%; Score 27; DB 1; Le
100.0%; Pred. No. 4.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="Zebra"
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            100.0%; Pred. ...
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                                                                                                                                28 AAAAAAAAAAAAAAAAAAAAAAAA 2
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Dep. of Plant and Soil Sciences
Oklahoma State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 AAAAAAAAAAAAAAAAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: acg@mail.pss.okstate.edu
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                                                                                                                                                                                                                                                                                                                                                                                           DN988459.1 GI:66248286
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BACKWARD: M13 Reverse
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Page 301

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/organism="Homo sapiens"
      Genome 47 (2), 380-388 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
/wol type="genomic DNA"
/cullivar="mixed background W23/A188/B73/K55"
/db xref="taxon:4677"
/tissue_type="leaf"
/dev_stage="bH108"
/dloot="Dragn: leaf; Vector: RescueMu (engineered from DablueScript backbone); Site 1: BamH1; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B appicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine.
1 (bases 1 to 32)
Alkharouf,N., Khan,R. and Matthews,B.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
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                                                                                               Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Peparatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
(bases 1 to 28)
                                                                                                                                                                                                      Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                        Contact: Walbor V
Department of Biological Sciences
Stanford University
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOBEO6.seq CDNA Peking library 12hr SCN3 Glycine max CDNA clone BOBEO6 5', mRNA sequence.
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100.0%; Pred. No. 4.9e+02;
tive 0; Mismatches 0; Indels
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Location/Qualifiers
CZ918534.1 GI:71938162
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Best Local Similarity 100.C
Matches 27; Conservative
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                                                             Zea mays
                                                                                   Zea mays
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R16114

32 bp mRNA linear EST 13-APR-1995
ya5.1f03.s2 Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
IMAGE:66461 3' similar to gb:M93426 PROTEIN-TYROSINE PHOSPHATASE
ZETA PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                      Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="Seedlings"
/clone_lib="CDNA Peking library 12hr SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript SK- phagemid. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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1 (bases I to 32)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollan,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 32;
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1.0%; Score 27; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 27; Conservative 0; Mismatches 0;
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                                                                                                                                                                              Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
                                                                                                                                                                                                                                                                                                                                     /organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 AAAAAAAAAAAAAAAAAAAAAA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3847"
/clone="B08E06"
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High qality sequence stops: 1
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High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Roots"
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/cultivar="Peking"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-Merck EST Project
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15060591
Contact: Alkharouf, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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R16114.1 GI:767923
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Oryza sativa (japonica cultivar-group)
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                      1.0%;
ilarity 93.3%;
Conservative (
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                       Query Match
Best Local Simi
Matches 28;
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                                                                                                                                             CF332296/c
                                                                                                                                                                  DEFINITION
                                                                                                                                 RESULT 790
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JOURNAL
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SOURCE
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                                                                                                                                                                                                                                                                                                           CZ913832 30 bp DNA linear GSS 08-AUG-2005
4013004D04.2EL_x1 4013 - RescueMu Grid O Zea mays genomic, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Malbot V
Department of Biological Sciences
Stanford University
Tel: 650 723 2227
Fex: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence. Plate: 4013004 row: D column: 04 Class: transposon-tagged. Location/Qualifiers
                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                . 5.2e+02;
                                                                                                                                                                            1.0%; Score 27; DB 1; Length 32; 90.0%; Pred. No. 5.2e+02; tive 0; Mismatches 3; Indels
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clone="IMAGE:66461"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                        CZ913832.1 GI:71930085
GSS.
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                  survey sequence.
CZ913832
                                                                                                                                                                                         Best Local Similarity
Matches 27; Conserv
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Zea mays
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                               EST 18-AUG-2003
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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/cultivar="Nackdong"
/db xref="raxon:39947"
/clore="NACL-08-M01"
/tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coll DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongln, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                         CF332296
32 bp mRNA linear EST 18-AUG-NACL--08-M01.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--08-M01, mRNA
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ligated to form circular plasmids. DH10B cells v
transformed and then screened on LB plates with
ampicillin."
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Pred. No. 5.3e+02;
                                                                                                                 Length 30;
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                                                                                                                 Score 26.8; DB 1;
Pred. No. 5.2e+02;
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Location/Qualifiers
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CF307749.1 GI:33679510
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Best Local Similarity
Matches 29; Conserv
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="wackdong"
/cultivar="wackdong"
/db xref="taxon:39947"
/clone="FLO-06-M16"
/tissue_type="flower"
/lab_host="E.col; SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="wector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xho1; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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Oryza sativa (japonica cultivar-group)

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae, Oryza.

1 (bases 1 to 32)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group)

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza, Chram.

Chases I to 33)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Min,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of Bioscience and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongGi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Fax: 82 31 321 6355
                                                                                                                                                                                                                 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, KyeongJi, Korea 11 32 31 330 6193
Fax: 82 31 321 6555
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.0%; Score 26.8; DB 1; Length 32; 33.3%; Pred. No. 5.3e+02;
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cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="71EAF--04-115"
/tissue_type="leaf"
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Best Local Similarity
Matches 28; Conserv
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VERSION
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JOURNAL
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CF307749 28 bp mRNA linear EST 15-AUG-2003 ABF--01-E17.bl ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone CF307749
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 28)
Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for RT-PCR."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 310 6193
Fax: 82 31 321 6155
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
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/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                                                                            ch 1.0%; Score 26.6; DB 1; Length 33; 1 Similarity 87.9%; Pred. No. 5.6e+02; 29; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                           33 АААССАААААСААААСАААААААААААААА 1
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mkNA sequence.
CX001046
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Pneumocystis carinii"
/mol type="mRNA"
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/lab_host="E.coli"
/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6, 1712ol extracted RNA. Oligod T priming, strandard conditions described by vendor, Stratagene. Further details see www.uky.edu/Project/Pneumocystis/"
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France
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Tosids, Vitaceae, Vitis.

(bases 1 to 28)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNS45659 28 bp mRNA linear EST 30-APR. EST 17603 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00RL004E11 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                            Pneumocystis carinii
Bukaryota; Pungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
I (bases 1 to 28)
Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
Edman,J.C., Kovacs,J. and Cushion,M.
Expressed sequence tags from Pneumocystis carinii
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
                                                                                                                                                                                                                                        Contact: Staben C
School of Biological Sciences
University of Kentucky
Unl Morgan Building, University of Kentucky, Lexington, KY
40506-0255, USA
Tel: 606 257 1161
Fax: 606 257 1717
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1.0%; Score 26.4; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 5.3e+02;
Matches 27; Conservative 0; Mismatches 1; Indels
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Fax: 00-33-(0)5-57-12-25-48
Email: 8.hamdi@bordeaux.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                        Email: staben@pop.uky.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CN545659.1 GI:46910284
                     GI:6828800
                                                             Pneumocystis carinii
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Vitis vinifera
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                     AW332443.1
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CN545659/c
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/clone_lib="Left Cardiac Ventricle (BOGEST7)"
/clone_lib="Left Cardiac Ventricle (BOGEST7)"
/clone_lib="Left Cardiac Vector: plluescript II Site 2: Xho 1; Library Constructed using pBluescript XR kit from Stratagene. Cloned CDNA was size selected between 1-3 kb Tissue supplied by Mark Haskins VMD, Phb, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"
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                                                                                                                                                                                                 /dev_stage="ripening stage"
|Colone_libe.Ripe Grape Skin Triplex2 Library"
|note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
|SfilA; Site_2: SfilB; Oriented library"
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Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CX001046 13-DEC-2004 LINEAR LINEAR EST 03-DEC-2004 L124908.b7 Left Cardiac Ventricle (DOGEST7) Canis familiaris CDNA,
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                              Score 26.4; DB 1;
Pred. No. 5.3e+02;
0; Mismatches 1;
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    .28
    /organism="Canis familiaris"

                                                       'organism="Vitis vinifera"
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Location/Qualifiers
Location/Qualifiers
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EST.
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Canis familiaris
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Best Local Similarity 96.4%;
Matches 27; Conservative
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Best Local Similarity 96.4%;
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                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eyematophyta; Cycadophyta; Cycadales; Cycadaceae; Cycas.

Spermatophyta; Cycadophyta; Cycadales; Cycadaceae; Cycas.

E 1 (bases 1 to 28)

B renner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,

Expressed tag sequences from Cycas ovules (NYBG)

Lonpublished (2005)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8894

Email: mccombie@cshl.org
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E 1 (Dases 1 to 28)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R., Tingey,A., von Dasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah Genome Center
         DR062845 28 bp mRNA linear EST 06-JUN-2005
1922e09.gl Cycas ovule (NYBG) Cycas rumphii cDNA 3', mRNA sequence.
DR062845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Cycas ovule (NYBG)"
hote="Organ: Ovules; Vector: pBK-CMV; Site_1: XhoI;
Site_2: Bco RI; Stratagene ZAP Express CDNA_Synthesis Kit.
The library was size-fractionated to enrich for large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS 05-OCT-2000
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1.0%; Score 26.4; DB 1;
Best Local Similarity 96.4%; Pred. No. 5.3e+02;
Matches 27; Conservative 0; Mismatches 1;
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/organism="Cycas rumphii"
/mol_type="mRNA"
/db_xref="taxon:58031"
/sex="Female"
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Mus musculus
                                                                                       DR062845.1 GI:66986411
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Fax: 801 585 7177
                                                                                                                                      Cycas rumphii
Cycas rumphii
                                         DEFINITION
ACCESSION
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AZ514352/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gil-fa712114[gb]-RR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus.
1 (bases 1 to 28)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Nouse whoule genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                   /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0360 row: F column: 06
Seq primer: CACACAGGAAACAGCTATGACC
Class: plaemid ends
High quality sequence stop: 28.
Location/Qualifiers
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0360F06"
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                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Conservative
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Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
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Bource

FEATURES

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/dev stage="adult"
/lab_host="bH10B"
/clone lbb="d4021 - RescueMu Grid v"
/clone lbb="d4021 - RescueMu Grid v"
/clone lbb="d4021 - RescueMu Grid v"
/note="0rgan: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
unite. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu', Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHi
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma bruce; (TRY), GUTTAL 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
innsert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I (Dages I to 20)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1.8A, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: nelsayed@tigr.org
Details of T. brucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                 /mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
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llarity 96.4%; Pred. No. 5.3e+02;
Conservative 0; Mismatches 1; Indels
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/strain="TREU927"
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                                                             organism="Zea mays"
Location/Qualifiers
                                                                                                                                                                                     /tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL453073.1 GI:11854584
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                                                                                                                                                                                                                                                                                                                                                                                                                               /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42Nr; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bylorynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|Ar129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Unpublished (2001)
Contact: Walbot V
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Stanford University
Stanford University
Stanford University
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021003 row: D_column: 05
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Best Local Similarity 96.4%; Pred. No. 5.3e+02;
Matches 27; Conservative 0; Mismatches 1; Indels
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                                                             Plate: 0099 row: D column: 17
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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clone="UUGC2M0099D17"
                                                                                                                                                        High quality sequence stop: 28.
Location/Qualifiers
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
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CZ916890.1 GI:71935275
                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
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Zea mays
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RESULT 800 CZ916890

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ACCESSION

SOURCE ORGANISM

KEYWORDS

VERSION

TITLE JOURNAL COMMENT

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Gaps

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Page 307

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1.0%; Score 26.2;
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Matches 28; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/mol type="mRNA"
/cultivar="wackdong"
/db xref="taxon:3947"
/clone="NACL--03-G12"
/tissue type="roliferated callus on 2N6 media for 30 days"
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/clone=lib="Rice callus plasmid cDNA library (NACL)"
/noche="Vector: pCN4-TOPP; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                             CF328476 2903-2003 NACL--03-G12.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--03-G12, mRNA
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Dictyostelium discoideum
Bukaryota, Mycetozaa, Dictyosteliida, Dictyostelium.
1 (bases 1 to 31)
Urushihara,H., Morio,T., Saito,T., Kohara,Y., Koriki,E., Ochiai,H., Maeda,M., Williams,J.G., Takeuchi,I. and Tanaka,Y.
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                                                                                                                                                                                                                                                                                      Contact: Nature B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division Genomics and Genetics Institute, GreenGene Biotech Inc.; Division Volgin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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     Length 28;
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ch 1.0%; Score 26.4; DB 1;
1 Similarity 96.4%; Pred. No. 5.3e+02;
27; Conservative 0; Mismatches 1;
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                                                                                 28 AAAAAAAAAAAAAAAAAATAAAAAAAA 1
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AUZ68044.1 GI:20526842
                                                                                                                                                                                                                                                            CF328476.1 GI:33805199
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96.4%;
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Best Local Similarity
Matches 27; Conserv
Query Match
Best Local Similarity
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CF328476
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.

El (bases 1 to 31)
SKim,J.S., Jun,K.M., Cheong, D.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K., and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Lupublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/cultivar="mckAong"
/cultivar="mckdong"
/db xref="taxon:3994"
/clone="7LEAF--01-B17"
/clone="7LEAF--01-B17"
/dev_stage="7.7 days after germination"
/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Analyses of cDNAs from growth and slug stages of Dictyostelium
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                                                                              15010511
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
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    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            /organism="Dictyostelium discoideum"
                              discoideum
Nucleic Acids Res. 32 (5), 1647-1653 (2004)
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                                                                                                                                                                                                                                                                                          Email: hideko@biol.tsukuba.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:44689"
/clone="VSH836"
                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF297930.1 GI:33669691
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DB 1; Length 31;

DEFINITION

AZ451251/c

RESULT 805

ò g ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL COMMENT

TITLE

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Best Local Similarity 90.33
Matches 28; Conservative
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Matches 26; Conserv
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bummanla, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Musinae, Mus.

1 (bases 1 to 32)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Rally, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UTGCIM library" | hote="Vector: PWD42nv; Purified genomic DNA from M.musculus G78L/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                              Gaps
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                                                              Indels
5.7e+02;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0250 row: I column: 05
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
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                               90.3%; Pred. No. 5.7e
:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 32.
Location/Qualifiers
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AZ451251.1 GI:10606869
GSS.
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                           Best Local Similarity 90.3
Matches 28; Conservative
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source

FEATURES

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Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing, Bases called and trimmed with phred
vo.020425.c. Vector identified by cross match with the -minscore 20
and -minmactch 12 options. Vector:pBlueScriptII(SK+) R. Sitel: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pooled early embryos, from 8 - cell stage to blastocysts.
Clones available from UK Centre for Functional Genomics in Farm
Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,
www.arkgenomics.org.
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                                                                                                                                                                                                                                                                          AJ659204 KN277 Sus scrofa cDNA clone C0005215_E14, mRNA sequence.
AJ659204
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Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of CDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db xref="taxon:9823"
/clone="C0005215_E14"
/tissue type="mbryo"
/note="Vector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled early embryos, from 8-cell stage
to blastocysts."
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                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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100.0%; Pred. No. 5.4e+02;
     Pred. No. 5.8e+02;
                                                                                        90.3%; Pred. ....
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tive 0; Mismatches
                                                                                                                                         32 AAAAACAAAACAAAACAAAAAAAAA 2
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    .26
    organism="Sus scrofa"

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Genomics and Bioinformatics
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Schistosoma mansoni
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AM046959
AM046959.1 GI:72292765
                                                              Schistosoma mansoni
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Matches 26; Conservative
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Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C. Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni Unpublished (2005)
Contact: Ivens AC
Pathogen Microarrays Group
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
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Strigeidida; Schistosomatoidea; Schistosoma.

1 (bases I to 26)

Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S.

Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C.

Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni
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Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
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Bukaryota, Metazoa, Platyhelminthes; Trematoda; Digenea; Strigeidida, Schistosomatoidea; Schistosomatoidea; Schistosomatoidea; Schistosomatoidea; Schistosomatoidea; Schistosomatoidea; Ito 20.

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Inlon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S. Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C. Mikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C. the lung schistosomulum of Schistosoma mansoni Unpublished (2005)
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Matches 26; Conservative 0; Mismatches 0;
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Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
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Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
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DEFINITION

CF278359/c

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LOCUS

ACCESSION VERSION KEYWORDS

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

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Fax: 82 31 321 6355
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 655
Email: bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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rative 0; Mismatches 0;
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Location/Qualifiers
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Unpublished (2003)
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SM Oryza sativa (japonica cultivar-group)

Coryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

El (Masea I to 26)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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YongJin, KyeongGi, Korea

Tel: 82 31 321 6355

Email: bhanhm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                 CF278359
14ETL--04-D22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Vyga setiva (japonica cultivar-group) cDNA clone 14ETL--04-D22,
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 26)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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14ETL--09-P01.gl Rice etiolated leaf plasmid cDNa library (14ETL)
0yza sativa (japonica cultivar-group) cDNA clone 14ETL--09-P01,
mRNA sequence.
CF282426
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/clone="14ETL-04-D22"
/tissue_trype="ladf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/lab_host="E.coli DH108"
/lab_host="E.coli DH108"
/lab_host="E.coli DH108"
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/mol type="mRNA"
/cultivar="Nackdong"
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  CF278359.1 GI:33655745
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clade; Ehrhartoideae; Oryzeae; Oryza.
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Bukaryota, Viridiplantea cultivar-group)
Bukaryota, Viridiplantea cultivar-group)
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Bukaryota, Viridiplantea cultivar-group)
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade, Ehrhattoideae, Oryzeae, Oryza.

1 (bases 1 to 26)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
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7LEAF--08-M19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--08-M19, mRNA
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
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100.0%; Pred. No. 5.4e+02;
ative 0; Mismatches 0;
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CF299701.1 GI:33671462
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    Query Match 0.9
Best Local Similarity 100.
Matches 26; Conservative
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Enbryophyta; Tracheophyta;
Spermatophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 26)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/lab_host="R.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonuclectides and then used as templates for RT-PCR."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division Genomics and Genetics Institute, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/mol_type="mRNA"
/cultivar="Nackdong"
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/lab_host="E.coli DH10B"
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100.0%; Pred. No. 5.4e+02;
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/clone="ABF--06-J01"
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/cultivar="Nackdong"
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Majolaiophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

El (Basea I to 26)

El (Basea I to 26)

Song, S. I., Kim, J. K., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B. H.

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Yonglin, KyeongGi, Korea

Tel: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
cultivar="Nackdong"
/db xref="taxon 39947"
/clone="NACL-07-J02"
/clssue Vype="callus"
/dev stagg="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH108"
/clone lib="ABF3-overexpressing transgenic rice plasmid cDNA lIbrary (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="Rice callus plasmid cDNA library (NACL)" / Inde="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                               CF331439

NACL--07-J02.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--07-J02, mRNA
                                                                                                                                                                                                                                  Gaps
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Best Local Similarity
Matches 26; Conserv
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COMMENT
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AW327613 26-JAN-2000 dQ0lb09.yl NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846536 3', mRNA sequence.

DEFINITION RESULT 818 AW327613/c

LOCUS

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ACCESSION

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ISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

CE 1 (bases 1 to 26)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Straubberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Edge BioSystems

Contact: Robert Strauberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Edge BioSystems

Contact: Arcz Arczyed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: NIH Intramural Sequencing Center (NISC)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbr/image/limage.html

Plate: LLCM0028 row: C column: 17

Seq primer: M13RP1 reverse primer (ABI).
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Vitis vinifera
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
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1 (bases 1 to 26)

Abbal, P., Agasse, A., Agacages, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Handi S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="T cell leukemia"
/cell line="MGC2"
/clone lib="NH MGC_2"
/nore="Organ: Blood; Vector: pOTB7a; Library prepared
Edge BioSystems."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Universite de Bordeaux I, Institut National de la Recherche
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0.9%; Score 26; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0;
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Fax: 00-33-(0)5-57-12-25-48
Email: 9.hamdl@bordeaux.inra.fr
Seg primer: T7.
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AW327613.1 GI:6798108
EST.
                                                                  Homo sapiens (human)
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CN545888/c
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                                                                                              /db_xref="taxon:29760"
/clone="B3CS00GL004B11"
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/clone lib="Green Grape Skin Triplex2 Library"
/note="Organ: Fruit skin, Vector: Lambda TriplEx2, Site_1: SfilR; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS45225 26 bp mRNA linear EST 30-APR-2004 EST 17169 Green Grape Skin Triplex2 Library Vitis vinifera CDNA clone B3CS00GL004F11 3', mRNA sequence.
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/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Vitis vinifera

Vitis vinifera

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,

rosids, Vitaceae, Vitis.

1 (bases I to 26)

Abbal, P., Agases, A., Ageorges, A., Atanassova, R., Barrieu, F.,

Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,

Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (akin, pulp

or seeds) at Various Developmental Stages
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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100.0%; Pred. No. 5.4e+02;
cive 0; Mismatches 0; Indels
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100.0%; Pred. No. 5.4e+02;
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                                    /organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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CN545225.1 GI:46909680
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Matches 26; Conservative
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Matches 26; Conserv
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RESULT 821

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Eukaryota; Viridiplantae; Streptophyta; Eukaryota; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosida; Vitecaeae; Vitis.

1 (Dases 1 to 26)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F., Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N. Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

AL Onpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
CNS45546 26 Dp mRNA linear EST 30-APR-2004 EST 17490 Ripe Grape Skin Triplex2 Library Vitis vinifera CDNA clone B3CS00RL003D01 3', mRNA sequence.
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| Clone lib="Ripe Grape Skin Triplex2 Library"
| Ance="Organ: Eruit skin; Vector: Lambda TriplEx2; Site_1:
| Sfilk; Site_2: SfilB; Oriented library"
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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                                                                                                                                                                                                           Vitis vinifers

Nutris vinifers

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaccae; Vitis.

1 (bases 1 to 26)
Abbal,P., Agense,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
Or seeds) at Various Developmental Stages
Unpublished (2002)
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Universite de Bordeaux I, Institut National de la Recherche
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100.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol type="mRNA"
/cultivar="Cabernet Sauvignon"

    .26
    /organism="Vitis vinifera"

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/clone="B3CS00RL003D01"
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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UMR 619 - Equipe 1
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Contact: Hamdi S.
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Vitis vinifera

Vitis vinifera

Vitis vinifera

Nitis vinifera

Nitis vinifera

Nitis vinifera

Sukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; cosids; Vitaceae; Vitis.

I (bases 1 to 26)

S Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

L Unpublished (2002)

Contact: Hamdi S.
                                                                                                                                                                                                                             /mol_type="mRNA"
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/db_xref="taxon:29760"
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/dev stage="ripening stage"
/clone lib="Ripe Grape Skin Triplex2 Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNJ966UB EST 18752 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera CDNA clone B3CS58RB008H03 3', mRNA sequence.
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Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Stte_1: SfilA; Site_2: SfilB; Oriented library"
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Universite de Bordeaux I, Institut National de la Recherche
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0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels
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/organism="Vitis vinifera"
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                                                                         Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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26 bp mRNA linear EST 30-APR-2004 EST 18420 Turning Grape Berry Lambda Triplex2 Library Vitis vinifera cDNA clone B3CS37TB007C08 3', mRNA sequence.
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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it64e03.gl Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
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Brenner,E.D. Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N., Brenner,E.D., Twighnespy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W., Benfey,P., Coruzzi,G. and Stevenson,D.
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1 (bases 1 to 26)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Handi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
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/note="Organ: Fruit without seeds; Vector: Lambda

TriplEx2; Site_1: SfilA, Site_2: SfilB, Oriented library"
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Universite de Bordeaux I, Institut National de la Recherche
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0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels
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2709 AAAAAAAAAAAAAAAAAAAAAA 2734
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Fax: 00-33-(0)5-57-12-25-48
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hote="Organ: mature, unfertilized reproductive strobili;
Vector: pBR-CMV; Site 1: XhOI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Gnetophyta, Gnetopsida, Gnetales, Gnetaceae, Gnetum.
1 (bases 1 to 26)
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Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8884
Email: mccombie@cshl.org
Seq primer. -21MlJuhiyRev.
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/note="Organ: mature, unfertilized reproductive strobili;
/note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express CDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"
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Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8884
Email: mccombie@cshl.org
Seq priner: -21M13UnivRev.
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    /organism="Gnetum gnemon"

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/organism="Gnetum gnemon"
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/db_xref="taxon:3382"
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/db_xref="taxon:3382"
/sex="female"
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DN955188.1 GI:63027326
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Best Local Similarity 100.0
Matches 26; Conservative
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/mol_type="mRNA"
/db xref="teaxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: :pBK-CMV; Site_1: XhoI;
Site_2: Eco_RI; Stratagene_ZAP Express_CNNA_Synthesis
The library was size-fractionated to enrich for large
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                                                                                                                                                                                                                                                                                                                  DR073125 26 bp mRNA linear EST 08-JUN-2005
ik86f11.gl Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

1 (bases 1 to 26)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Expressed tag sequences from Ginkgo female leaf (NYBG)
Umpublished (2005)
Contact: W. Richard McCombie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A2359871 26 bp DNA linear GSS 02-OCT-200 1M0102H23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0102H23 R, genomic survey sequence.
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia;
Buncheria; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                                                            Gaps
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      Length 26;
                                                            Indels
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Fax: 516 367 8874
Email: mccombie@cehl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
O.9%; Score 26; DB 1; L. Local Similarity 100.0%; Pred. No. 5.4e+02; es 26; Conservative 0; Mismatches 0;
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/organism="Ginkgo biloba"
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DRÓ73125.1 GI:67050976
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84112, US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNR Resource Cocannow From Cocannow Charles () The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM92 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male"
/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
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                                                                                                                                                                          Rm. 306. Biomedical Polymers Research Bldg., 20 S. 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0102 row: H column: 23
Seq primer: CACACAGGAAACAGCATATGACC
Class: plasmid ends
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Local Similarity 100.0%; Pred. No. 5.4e+02;
nes 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C578L/6J"
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clone="UUGC1M0102H23"
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated for sheared DNA
was blunt end-repaired with T4 DNA polymerses and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transfermed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance." 5 ö GSS 02-OCT-2000 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 28) Dunn, D. Aoyagi A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von AZ389765 10Kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0150D13R Acuse 10Kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0150D13 R, genomic survey sequence. Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Gapa . 0 Length 26; 0; Indels 0.9%; Score 26; DB 1; Le .00.0%; Pred. No. 5.4e+02; Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0130 row: E column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers Query Match
Best Local Similarity 100.0%; Pred. No. 5.4
Matches 26; Conservative 0; Mismatches /organism="Mus musculus" /mol type="genomic DNA" /strain="C57BL/6J" /db xref="taxon:10090" /clone="UUGC1M0130E08" 2709 AAAAAAAAAAAAAAAAAAAAAAAAA 2734 Contact: Robert B. Weiss University of Utah Genome Center University of Utah 1 AAAAAAAAAAAAAAAAAAAAAAA 26 Mus musculus (house mouse) AZ389765.1 GI:10503473 /sex="Male" Unpublished (2000) Tel: 801 585 5606 Fax: 801 585 7177

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
            Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
llaert Length: 10000 Std Error: 0.00
Plaete: 0189 row: M column: 07
                                                        plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Moouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6/ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gil 4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
                                                                                                                                                                             Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: D column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Prec. ...
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                                                                        Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
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/sex="Male"
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AZ414673.1 GI:10538686
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Best Local Similarity 100.0
Matches 26; Conservative
                                                        plasmid inserts
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84112, USA
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb12 (gilfa712114 [gb] [AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clome lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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100.0%; Pred. No. 5.4e+02;
ive 0; Mismatches 0; Indels
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Plate: 0189 row: M column: 07
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
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AZ624441/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/ clone lib="Mouse 10kb plasmid UUGCIM library"
/ clone lib="Mouse 10kb plasmid UUGCIM library"
/ note="Weetor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) as obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
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polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gil 47321H (gb|AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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1M0439E17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0439E17 R, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                        S. 2030 E., SLC,
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Dalam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
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                                                                                                                                                                        Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0404 row: E column: 16
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC1M0404E16"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="Male"
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AZ612722/c
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Laboracy you'be DNA Resources (documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAD42 (gilfa732114 [gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0463G07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0463G07 F, genomic survey sequence.
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Eukaryota; Metazoa; Chordaka; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
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Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42rr; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0439 row: E column: 17
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
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                                                                  plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0439E17"
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Rm. 308, Bio
84112, USA
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1M0474H08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0474H08 F, genomic survey sequence.
AZ627846
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Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
I (basea 1 to 26)
Dunn, D., Aoyagi A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                           Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                              plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Reseau
                                                                                                                                                                                                                                                                                  Insert Length: 10000 Std Error:
Bate: 0463 row: G column: 07
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC1M0463G07"
                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Mus musculus
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gill491/32114 gbl/AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complamentary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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smid UUGCIM library Mus musculus genomic
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                                                                                     Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/67 (male) was obtained from the Jackson
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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clone UUGCIM0525H15 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                             Tel: 801 585 5606

Sex: 801 585 717

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
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age primer: CGTTGAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
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/strain="C57BL/6J"
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/clone="UUGC1M0474H08"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was blute and arragiresources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt ends repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|Ar129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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2M0058023F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0058023 F, genomic survey sequence.
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                                                                                                                                                                                               S. 2030 E., SLC,
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                              Rm. 308, Biomedical Polymers Research Bldg., 20 84112, USA
Tel: 801 885 506
Fax: 801 885 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0525 row: H column: 15
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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100.0%; Pred. No. 5.4
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol type="genomic DNA"
/brain="C57BL/61"
/db xref="taxon:10090"
/clone="UUGCIM0525H15"
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Location/Qualifiers
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Mus musculus
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AZ800453.1 GI:12952583
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Best Local Similarity 100.
Matches 26; Conservative
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                                 TITLE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwMD42 (gilfa732114 [gb] [AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-GOld (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,

Sciurognathi, Muroidaa, Muridae, Murinae, Mus.

1 (bases 1 to 26)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
                                                                                                                                                                                       University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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/clone lib="Mouse lokb plasmid UUGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                             Std Error: 0.00
                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunndgenetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0058 row: O column: 23
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
High quality sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                            Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0058023"
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GSS.
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Stanford University
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| Jab host="E. coli strain XL10-Gold, T1-resistant, F-"
| / Clone | 11b="Wouse 10kb plasmid UUGCSN library"
| / Clone | 12b="Wouse 10kb plasmid UUGCSN library"
| / Inde="Wetcor: PWD42nv; Purified genomic DNA from
| Laboratory Mouse DNA Resource
| Laboratory Mouse DNA Resource
| (http://www.jax.org/resources/documents/dnares/). The DNA
| was hydrodynamically sheared by repeated passage through a
| O.005 inch orifice at constant velocity. The sheared DNA
| was blunt end-repaired with T4 DNA polymerase and T4
| polymucleotide kinase. Adaptor oligonucleotides were
| ligated to the blunt ends in high molar excess. The
| adaptored DNA was purified and size-selected for a 9.5 to
| 10.5 kb range using preparative agarose gel
| electrophoresis. Vector DNA was prepared from a derivative
| of pWD42 (gil 4772114|gb|AR129072.1), a copy-number
| inducible derivative of plasmid R1. The vector was ligated
| with adaptors complementary to the insert adaptors and
| purified. The sheared, adaptored mouse DNA was annealed to
| chemically-competent E. coli Xiii0-Gold (Stratagene) cells
| and selected for ampicillin resistance."
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Drosophila melanogaster
Bukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
I (basea I to 20;
Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,
                                                                                                                                                                Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0233 row: N column: 01
Seq primer: CGTTGTAAAACGACGCCAGT
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                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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Pred. No.
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/clone="UUGC2M0233N01"
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Location/Qualifiers
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CZ490199
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Best Local Similarity 100.C
Matches 26; Conservative
                                                   plasmid inserts
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84112, US.
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/d_nstl= takelizis piggyBac WH insertions"
/d_nstl= takelizis piggyBac WH insertions"
/note="Vector: piggyBac WH (GenBank accession number
AY515140); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the WH element using the
constitutive alpha-1 tubulin:piggyBac transposase source.
We remobilized the WH element from a single ammunition
element on the Binsinscy balancer chromosome in dysgenic
females. We outcrossed dysgenic virgin females in vials to
the isogenic w- strain and selected new hops in the
following generation. All lines were mapped to a
chromosome by standard genetic methods, examined for
homozygous viability, and used for recovery of flanking
genomic sequence by inverse PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The piggyBac insertion position is unspecified in the 26 bases. This insertion position refers to the first base of the 4 base TTAA target recognition sequence. Class: transposon insertion site.

Location/Qualifiers
Ryner, L., Cheung, L.M., Chong, A., Brickson, C., Fisher, W.W., Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C., Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zho, L., Chen, F., Swimmer, C., Kopczynski, C., Duyk, G., Winberg, M.L. and Margolis, J. A. complementary transposon tool kit for Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                                                                                                                                                                                                                                                            Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Pax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
piggyBac element.
The piggyBac insertion position is unspecified in the 26 base
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/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
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0.9%; Score 26; DB 1; Lr
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                             using P and piggyBac
Nat. Genet. 36 (3), 283-287 (2004)
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Walbot, V.
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Tue Nov

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Query Match
Best Local Similarity
Matches 26; Conserv
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DU835360/c
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Brassica, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

E. I. (bases I to 26)
Syang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Saulal (KBrS) BAC clone
Unpublished (2005)
Brassica Genomics Team
National Institute of Agricultural Biotechnology
25 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Bmail: pbeomerae.go.kr
Bmail: pbeomerae.go.kr
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B55 California Ave, Palo Alto, CA 94304, USA
Flat: 650 723 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence
plate: 4012001 row: C column: 02
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KBrS010P08F KBrS, Brassica rapa Sau3AI BAC library Brassics subsp. pekinensis genomic clone KBrS010P08, genomic survey
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1. .26
                                                                                                                                                                                                                                                                                                                                           organism="Zea mays"
                                                                                                                                                                                                                                        Class: transposon-tagged.
Location/Qualifiers
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Matches 26; Conservative
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Seg primer: T7
Class: BAC ends.
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 26)
Yang, T.J., Kwon, S.J., Klm, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suvon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Bmail: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS016105
                                                                                                                                                         /lab host="E. coli DH10B"
/lab host="E. coli DH10B"
/clone lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCGGIBACI; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
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/db_xref="taxon:51351"
/clone="KBrS016105"
/lab host="B. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="vector: pCUGIBACI; Site_1: Sau3AI; Brassica rapa spekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."
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KBrS016105R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS016105, genomic survey
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/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiffu"
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Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0;
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Pred. No. 5.4e+02;
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100.0%; Pred. No. ...
0; Mismatches
                                                                              /sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS010P08"
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/cultivar="Chiifu"
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Class: BAC ends.
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/mol_type="genomic DNA"
/strain="TREU927"
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAAAAAAAAAAAAAAAAAAAAAA 26
                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:5691"
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                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="324d07"
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CN545777/c
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                                                      DAN34224 CSS 10-JAN-2006 KBrB031P17R KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB031P17, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E.coli DH10B"
/clone lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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                                                                                                                                                                                                    Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pbeom@rda.go.kr
i sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                                                                                                                                                                                                                                                              1 (bases 1 to 26)
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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1 (bases 1 to 26)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Direct Submission
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Trypanosoma brucei
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae,
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
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100.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Institute of Agricultural Biotechnology 225 Secdun-Dong, Suwon, 441-707, Korea Fels. +82-31-299-1670 Fax: +82-31-299-1672 Email: pbeom@rda.go.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              species="pekinensis"
|db_xref="taxon:51351"
|clone="KBrB031P17"
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1. .26
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Brassica Genomics Team
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: M13 Reverse
Class: BAC ends.
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TA324D07P
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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 bp mRNA linear EST 30-APR-2004 EST 17721 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA CLORe B3CS00RL005G11 3', mRNA sequence.
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/mol_type="mRNA"
/mol_type="mRNA"
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/db xref="texon:29760"
/clone="B3CS00RL005G11"
/dev_grage="ripening stage"
/clone lib="Ripe Grape Shin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
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1 (bases 1 to 27)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp Oupublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Trypanosoma brucei"
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100.0%; Pred. No. ...
0; Mismatches
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CNS45880/c

DEFINITION

ACCESSION

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

RESULT 846

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/clone liber 4021 - RescueMu Grid V"
/clone liber 4021 - RescueMu Grid V"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi, Site 2: BgJII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units: For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/' Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHi
and BgIII, and ligated to form circular plasmids DH10B
cells were transformed and then screened on LB plates with
ampicillin."
                                                                                                    Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
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Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, B-mail: barrell@sanger.ac.uk and
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                  Email: walbotderanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4021014 row: C column: 04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
/mol type="genomic DNA"
/mol type="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue type="adult"
/lab_nost="DH108"
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                                                                                                                                                                                                                          855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
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100.0%; Pred. No. 5.5e+02;
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                                                                                                                                                                              Department of Biological Sciences
Stanford University
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Best Local Similarity 100.
-108 26; Conservative
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                                                                                                                                                            Contact: Walbot
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COMMENT
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                                                                                                                                                                                                                                                                                                                              CNE45880 27 bp mRNA linear EST 10-APR-2004 EST 17824 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00RL002H10 3', mRNA sequence.
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/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
SfilA; Site_2: SfilB; Oriented library"
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Vitis vinifera
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 27)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Zea mays
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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                                                           0.9%; Score 26; DB 1; Length 27;
100.0%; Pred. No. 5.5e+02;
tive 0; Mismatches 0; Indels
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llarity 100.0%; Pred. No. 5.5e+02;
Conservative 0; Mismatches 0;
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/mol_type="mRNA"
/culfivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CSOORLOO2H10"
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Fax: 00-33-(0)5-57-12-25-48
Email: 8.hamdi@bordeaux.inra.fr
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CN545880.1 GI:46910505
                                                                                                              Conservative
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Matches 26
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GSS 13-DEC-2000

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RESULT 847

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CZ919667

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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AZ819924
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Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
VO.020445.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI
R. Site2: NOLI 5' Seq Primer MIJF Normalised library constructed
from pooled early embryos, from 8 - cell stage to blastcoysts.
Clones avallable from UK Centre for Functional Genomics in Farm
Animals, Roslin Institite, Roslin, Midlothian, UK, EH25 9PS,
www.arkgenomics.org.
Location/Qualifiers
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to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tighr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
evelopment of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
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// Corganisme="Sus scrofa"
// Anol_type="mRMa"
// Ab_xref="taxon:9823"
// Clone="C0005212 K01"
// Clone="Type="embryo"
// Clone_Tib="Wal77"
// Note="Wector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2: NotI; Single pass sequencing. Normalised library
constructed from pooled early embryos, from 8-cell stage to blastocysts."
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Pred. No. 5.5e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                 /organism="Trypanosoma brucei"
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="257b07"
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Genomics and Bioinformatics
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Best Local Similarity 96.3%
Matches 26, Conservative
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Best Local Similarity 100.0
Matches 26; Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gql 4732114 [gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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That are the control of the con
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                                                                                                                                                                                                                                                                                                                                                            AZ819924 10SS 20-FEB-200 2M0091A19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0091A19 R, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sclurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0091 row: A column: 19
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/60"
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
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/clone="UUGC2M0091A19"
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Fax: 801 585 7177
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84112, USA
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RESULT 851 CN545889/c

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DEFINITION

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REFERENCE AUTHORS JOURNAL

COMMENT

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E., SLC,

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Laboratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Schistosoma mansoni
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosoma.
1 (bases 1 to 31)
Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S.,
Nikolaidou-Katsaridou, N., Quall, M.A., Wilson, R.A. and Ivens, A.C.
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Female"
/lab host="E. coli strain XL10-Gold, Tl-resistant, F-"
/lab host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse lobb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Mouse whole genome scaffolding with paired end reads from 10kb
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                            plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
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Pred. No. 5.8e+02;
                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0230 row: I column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0230124"
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                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                        CNS45889 30 bp mRNA linear EST 30-APR-2004 EST 17833 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA COUR B3CS00RL006A08 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organisme"vitis vinifera"
/mol type="mRNA"
/mol type="mRNA"
/mol type="mRNA"
/doulivar="cabernet Sauvignon"
/db xref="taxon:29760"
/clone="B3CS00RL006A08"
/clone="stage="ripening stage"
/clone="lb"="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
SfilA; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A2962183
2M0230I24R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0230I24 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wiridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

1. (bases 1 to 30)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
1 (bases 1 to 30)
Dunn, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
                               1 AAAAAAAAAAAAAAAAAAAAA 26
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Tel: 00-33-(0)5-57-12-25-50
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CNS45889.1 GI:46910514
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FEATURES

EST 20-SEP-2005

SOURCE ORGANISM

REFERENCE AUTHORS

RESULT 852

ò 셤 AZ962183

DEFINITION

ACCESSION

VERSION KEYWORDS

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Gaps

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; caryophylalaes, Amaranthaceae; Beta.

(aryophylalaes, Amaranthaceae; Beta.

(bases 1 to 29)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,Ju.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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Vitis vinifera
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitacae; Vitis.
1 (bases 1 to 29)
             S013297-024-004-B01-T7 MPIZ-ADIS-024-inflorescence Beta vulgaris CDNA clone 024-004-B01 3-PRIME, mRNA sequence. BQS83967. GI:26113544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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                                                                                                                                                                                                                                                                                                                                                               Plant C. 12472698
Contact: Weisshaar B ADIS DNA core facility at MDIZ ADIS DNA core facility at MDIZ Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Meg 10, 50829 Koeln, Germany Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 29 Std Error: 0.00
Plate: 4 row: B column: 01
Plate: 4 row: B column: 01
Seq primer: T7; GTAAAACGACTCATATAGGGC.
Location/Qualifiers
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Best Local Similarity 93.13
Matches 27; Conservative
                                                                                                                         Beta vulgaris
Beta vulgaris
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CN545957/c
                                                                                                                                           ORGANISM
                  DEFINITION
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Collins/Besansky Lab
Center for Tropical Disease Research and Training, University of
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Location/Qualifiers
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Anopheles funestus
Anopheles funestus
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
1 (bases 1 to 32)
Besansky, N.J., Serazin, A.C. and Dana, A.
Towards the transcriptome of Anopheles funestus: a molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Organism="Anopheles funestus"
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/mol_type="mRNA"
/strain="West African"
/db_xref="Leaxon:62324".
/sex="male and female"
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/clone_lib="ESTS from wild-caught Anopheles funestus
/populations"
/note="Vector: LambdaTriplEx2"
                                                                                                                                                                                                    /clone="SmlC21b09.glk"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"
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                                                                                                                                                                                                                                                                                                                Score 26; DB 1; Le
Pred. No. 5.9e+02;
                                                                                                                  / 31
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
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Contact: Ivens At
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
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CD577496.1 GI:48718511
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Tel: 5746319321
Email: nbesansk@nd.edu
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Best Local Similarity 96.3
Matches 26; Conservative
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R59306 32 bp mRNA linear EST 24-MAY-1995 yh16c10.sl Soares infant brain lNIB Homo sapiens cDNA clone IMAGE:37903 3' similar to gb:M29064 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1 (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="ripening stage"
/clone lib="Ripe Grape Skin Triplex2 Library"
/noce="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
SfilR; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                    Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Handi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Trag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UNR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.

1 (bases 1 to 32)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hillier,L., Hullman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.9%; Score 25.8; DB 1; Length 29; Best Local Similarity 93.1%; Pred. No. 5.8e+02; Matches 27; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; UD
5.8e+02;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/culfivar="cabernet Sauvignon"
/culfivar="cason:29760"
/clone="B3CS00RL006G11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Vitis vinifera"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 AAAAAAAAAAAGAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                     Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: 8.hamdi@bordeaux.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
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                                                                                                                                                                                                                                                                                                                                                              Seq primer: T7.
Location/Qualifiers
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The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
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EST.
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R59306/c
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         AUTHORS
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KEYWORDS
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                                                                           TITLE
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SM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Murcidea; Murcidea; Musinae; Mus.

1 (bases 1 to 32)
S Dunn, D., Aoyagi, A., Barber, M., Beaconn, T., Duval, B., Hamil, C.,
Islam, H., Longack, S., Mahmoud, M., Menen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Conteat: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1M0048A19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.9%; Score 25.6; DB 1; Length 32; Best Local Similarity 87.5%; Pred. No. 6.3e+02; Matches 28; Conservative 0; Mismatches 4; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 5td Error: 0.6
Plate: 0048 row: A column: 19
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                              'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC1M0048A19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 32.
Location/Qualifiers
                                                                      /mol_type="mRNA"
/db_xref="GDB:410444"
/db_xref="taxon:9606"
/clone="IMAGE:37903"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
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                                                                                                                                                                           /sex="female"
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COMMENT
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                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalvel (gill 4732114 [gb] API29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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/wolltype="genomic DNA"
/wolltype="genomic DNA"
/wolltype="genomic DNA"
/wolltype="leavon:4577"
/tissue type="leavon:4577"
/tissue type="leavon:4577"
/tissue type="leavon:4577"
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/dev stage="adult"
/lab.host="bH108"
/lone lib="4013 - RescueMu Grid O"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site I: BamHI; Site 2: BglII; RescueMu is a 4-9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
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4013010802.2EL_x1 4013 - RescueMu Grid O Zea mays genomic, genomic
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence. Plate: 4013010 row: B column: 02 Class: transposon-tagged.
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0
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
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                                                                                               Laboratory Mouse DNA Resource
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/organism="Zea mays"
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C2915120
C2915120.1 GI:71932199
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Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Walbot, V.
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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COMMENT
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/organism="Zea mays"
//organism="Zea mays"
//organism="Zea mays"
//oultivar="mixed background W23/A188/B73/K55"
//tissue_type="leaf"
//tissue_type="leaf"
//dev_stage="adult"
//dev_stage="adult"
//deb_bost="DH10B"
//clone_lib="4021 - RescueMu Grid V"
//note="Gorgan: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
//RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/. Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CZ918635 32 bp DNA linear GSS 08-AUG-2005 4021010C04.2EL yl 4021 - RescueMu Grid V Zea mays genomic, genomic cz918635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                   site 'http://www.mutransposon.org/project/RescueMu/'. Gr
O was grown at Stanford in 2001. DNA was extracted from
leaf strips, double digested using BamHI and BglII, and
ligated to form circular plasmids. DH10B cells were
transformed and then screened on LB plates with
ampicillin."
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Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021010 row: C column: 04
units. For more information on RescueMu, go to the web
                                                                                                                                                                                                                                                               Gaps
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Pax: 650 723 2227
                                                                                                                                                                                                           Score 25.6; DB 1;
Pred. No. 6.3e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.9%; Score 25.6; DB 1; Best Local Similarity 87.5%; Pred. No. 6.3e+02; Matches 28; Conservative 0; Mismatches 4;
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Location/Qualifiers
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1 Similarity 87.5%;
28; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 32)
                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays
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TITLE
JOURNAL
                                                                                                                                                                                                                                                               Matches
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KEYWORDS
SOURCE
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2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

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Query Match
Best Local Similarity 96.3%;
Matches 26; Conservative
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                                                                                                                     RESULT 862
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AUTHORS
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COMMENT
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KEYWORDS
SOURCE
                                                                                                                                               AZ458228
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/clone_lib="mouse lokb plasmid UUGCIM library"
/clone_lib="mouse lokb plasmid UUGCIM library"
/clone_lib="mouse lokb plasmid UUGCIM library"
/note="weetor: pwD42nv; Purified genomic DNA from M.
musculus (C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
/http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarces gal
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Mus.

E 1 (bases 1 to 27)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah
University of Utah
University of Utah
                                                                                                                                                              AZ434285
1M0220B08R Mouse 10kb plasmid UUGCIM library Mus musculus genomic UUGCIMUUGCIM0220B08 R, genomic survey sequence.
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0220 row: B column: 08
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
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/clone="UUGC1M0220B08"
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                                                                                                                  RESULT 861
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AUTHORS
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KEYWORDS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwAp42 (gql #732114 [gb] AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                          AZ458228
1M0262C12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic close UUGC1M0262C12 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Voctor: PWD47ny; Purlited genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                               1 AAAAAAAAAAAAAAAAAAAA 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 27.
Location/Qualifiers
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/clone="UUGC1M0262C12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                           AZ458228.1 GI:10616353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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Gaps ; 0

Length 27; 1; Indels

0.9%; Score 25.4; DB 1; 96.3%; Pred. No. 5.9e+02; tive 0; Mismatches 1;

Query Match Best Local Similarity 96.3[†] Matches 26; Conservative

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Gaps

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0.9%; Score 25.4; DB 1; Length 27; 96.3%; Pred. No. 5.9e+02; lve 0; Mismatches 1; Indels

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/lab host-#E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42Dry; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated motar excess. The
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4732114 gb| AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                               AZ941721 27 bp DNA linear GSS 26-APR-2001 2M0201004R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0201004 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
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Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
1 AAAAAAAAAAAATAAAAAAAAA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
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Best Local Similarity 96.3°
Matches 26; Conservative
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Fax: 801 585 7177
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84112, US
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                                                                                                          RESULT 863
AZ941721/c
                                                                                                                                                                                     DEFINITION
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AZ970621
2M0243N14R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0243N14 R, genomic survey sequence.
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84112, USA
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                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                 1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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0.9%; Score 25.4; DB 1;
Best Local Similarity 96.3%; Pred. No. 5.9e+02;
Matches 26; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0243 row: N column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plate: 0243 row: N column: 14
Seg primer: CACACAGGAAACAGCTATGACC
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0243N14"
/sex="Female"
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Location/Qualifiers
                                                                                                                                      Mus musculus (house mouse)
Mus musculus
                                                                                          AZ970621.1 GI:13841848
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Fax: 801 585 7177
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0; Mismatches

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Gaps ö

Indels

27

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LOCUS

ACCESSION VERSION KEYWORDS ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

RESULT 865 DX070376/c

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Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
H444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yb34c09.sl Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:73072 3' similar to similar to gb:S41458 ROD CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT (HUMAN), mRNA sequence.
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I (bases 1 to 28)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,

Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M.,

Hawkins, M., Holtman, M., Morris, M., Parsons, J., Prange, C., Rifkin, L.,

Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J.,

Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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/mol_type="mRNA"
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/db xref="taxon:9666"
/clone="IMAGE:25521"
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                                                                                                                                                                                             The WashU-Merck EST Project Unpublished (1995)
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Best Local Similarity 92.9
Matches 26; Conservative
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/ db_xref="taxon:51351"
/clone="KBrB079M05"
/lab_host="E.coli DH108"
/clone lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pcu(GIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 bp mRNA linear EST 04-MAY-1995 yf50c03.sl Soares infant brain INIB Homo sapiens cDNA clone IMAGE:25521 3' similar to gb:J03040 SPARC PRECURSOR (HUMAN);, mRNA
                                                                                                                                                                                                                                   DX070376 CSS 10-JAN-2006 KBEB079M05F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB079M05, genomic survey
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Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Beom-Seok Park
Brassica Genomics Team
Artional Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Email: pbeom@ada.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
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/mol_type="genomic DNA"
/cultivar="Chiifu"
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           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   DX070376
DX070376.1 GI:84764672
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1 (bases 1 to 28)
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Class: BAC ends.
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EST 06-FEB-1995

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RESULT 866 R37697/c DEFINITION

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/organism="Oryza sativa (japonica cultivar-group)"
Insert Length: 10000
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Musinae; Mus.

E 1 (bases 1 to 28)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ836072 28 bp DNA linear GSS 20-FEB-2001 2M0130K08R Mouse 10kb plasmid UUGCIM library Mus musculus genomic close UUGCZM0130K08 R, genomic survey sequence.
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             Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                         High qality sequence starts: 1
High qality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
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                                                                                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.9%; Score 25.4; DB 1; Length 28; 92.9%; Pred. No. 6e+02;
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/organism="Homo sapiens"
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High quality sequence stop: 1.
Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ836072.1 GI:13005980
                                                                Contact: Wilson RK
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Best Local Similarity
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84112, USA
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymcleoride kinase. Adaptor oligonucleorides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pware (173114|gbl=R129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Durza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Strebup)

Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae, BEP

Lolade; Ehrhartoideae; Oryzae;

Oryzae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Large-scale Sequencing Analysis of Rice ESTs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
                         Plate: 0130 row: K column: 08
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 AAAAAAAAAAAAAAGAAAAAAAAA 2
                                                                                                                             High quality sequence stop: 28.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                         /clone="UUGC2M0130K08"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com,
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Similarity
27; Conserv
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VERSION
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JOURNAL
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SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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//deb_host="adult"
//lab_host="DH10B"
//clone lib="4001 - RescueMu Grid V"
//clone lib="4001 - RescueMu Grid V"
//note="Organ: leaf; Vector: RescueMu (engineered from
//note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/. Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="t-taxon:39947"

/db_xref="t-taxon:39947"

/clone="7LEAF--03-N11"

/tissue_type="leaf"
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/db host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for RT-PCR."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C2919253 30 bp DNA linear GSS 08-AUG-2009
4021012D11.2EL x1 4021 - RescueMu Grid V Zea mays genomic, genomic
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: walbotostanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4011012 row: D column: 11

Class: transposon-tagged.

Location/Qualifiers
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/cnltivar="mixed background W23/A188/B73/K55"
/tissue_type="leaf"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                        Length 30;
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Tel: 650 723 2227
Fax: 650 725 8221
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                                                                                                                                                                                                                                                                                                                                                                                       30 AAAAGAACAAAAAAAAAAAAAAAAAA 1
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/organism="Zea mays"
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CZ919253
CZ919253.1 GI:71939587
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Best Local Similarity
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Zea mays
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CZ919253
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ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
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0.9%; Score 25.2; DB 1; Length 30;

Query Match

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DX082113 30 bp DNA linear GSS 10-JAN-2006 KBrB095E11R KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB095E11, genomic survey sequence.

DX082113
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/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/clone_losetor: pCUGIBAC1; Site_l: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica, rapa subsp. pekinensis
Brassica, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 30)
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Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
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/mol_type="genomic DNA"
/cultivar="Chiffu"
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                          Indels
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Best Local Similarity 90.0%; Pred. No. 6.4e+02; Matches 27; Conservative 0; Mismatches 3;
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Pred. No. 6.4e+02;
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Tel: +82-31-299-1670
Fax: +82-31-299-1672
                                                                            2709 AAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
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/db_xref="taxon:51351"
/clone="KBrB095E11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Brassica Genomics Team
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: M13 Reverse
Class: BAC ends.
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90.08;
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CF291646/c
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/mol trype="genomic DNA"
/culfivar="mixed background W23/A188/B73/K55"
/tiseue_trype="leaf"
/tiseue_trype="leaf"
/tiseue_trype="leaf"
/tiseue_trype="leaf"
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/dow stage="adult"
/lab_host="DH10B"
/dlone_lbb="4021 - RescueMu Grid V"
/lab_host="DH10B"
/dlone_lbb="4021 - RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/. Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Itali, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
LD Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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                                                                                                      Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 31)
                                                                                                                                                                                                                          855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stranford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021010 row: E column: 09
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Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                          Class: transposon-tagged.
Location/Qualifiers
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Tel: 82 31 330 6193
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Matches 27; Conserv
                                                                      Walbot, V
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(14ROOT) Oryza
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                          /dev stage="14 days after germination"
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/clone lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/clone lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Squencing Analysis of Rice ESTs
Unpublished (2003)
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                                                                                                             /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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                                                                                                                                                                                             /db xref="taxon:39947"
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/clone="14ROOT--02-C14"
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S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
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with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                    CF299288 15-AUG-2003 25 bp mRNA linear BST 15-AUG-2003 7LEAF--03-E01.gl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-E01, mRNA
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza,
I (basea I to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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25 AAAAAAAAAAAAAAAAAAAA 1
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CF300333/c
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/cultivar="mkNA"
/cultivar="mkNA"
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/lab_nost="E.coli DH10B"
/clone lib="colabAcl-overexpressing transgenic rice plasmid cDNA library (HD)"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhatcideae; Oryzeae; Oryza;
1 (bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTE
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pcR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for Ihr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
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Pred. No. 66+02;
0; Indel8
                                                                                                                                            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
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100.0%; Pred. No. oc.
0, Mismatches
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/clone="HD--05-J05"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhuahm@ggbio.com, bhua
Location/Qualifiers
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/cultivar="Nackdong"
                                                                                                                                                                       Location/Qualifiers
                                                           Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/mol_type="mRNA"
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Matches 25; Conserv
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CF330786/c
                                                                 REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:19947"
/clone="HD--07-103"
/tissue_type=="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/dev_stage="proliferated"
/dab_host="E_coli DH108"
/clone_lib="09HDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatrophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza.

(bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Uppublished 1.0.0.,
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yopgin, Kyeonggi, Korea
Tel: 82 31 313 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                HD--07-I03.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--07-103, mRNA sequence.
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                                                   Gaps
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/mol_type="mRNA"
/cultivar="Nackdong"
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100.0%; Pred. No. 6e+02;
iive 0; Mismatches 0; Indels
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Oryza sativa (japonica cultivar-group)
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            Query Match
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Oryza sativa (japonica cultivar-group)

SM Oryza sativa (japonica cultivar-group)

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzea. Oryza.

El (bases 1 to 25)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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/dev stage="proliferated callus on 2N6 media for 2 weeks"
/dev stage="proliferated"
/lab_nost="E.coli DH10B"
/clone lib="colabAc1-overexpressing transgenic rice plasmid cDNA lIbrary (HD)"
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Oryza sativa (japonica cultivar-group)

Wakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Poaceae; BEP clade; Ehrhartoideae; Oryzae, Oryza.

I (bases 1 to 25)

Kim, J. S., Jun, K.M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H.

Large-scale Sequencing Analysis of Rice ESTs

Contact: Nahm B. H.
                                                                                                                                                                                                                                                                                                                               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
1330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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100.0%; Pred. No. 6e+02;
live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--09-H05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Tue Nov

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/dev_stage="ripening stage"
Colone llb="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin' Vector: Lambda TriplEx2; Site_1:
SfilA; Site_2: SfilB; Oriented library"
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CN546041 25 bp mRNA linear EST 30-APR-2004 EST 17993 Ripe Grape Skin Triplex2 Library Vitis vinifera CDNA clone B3CS00RL007G10 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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1 (basea 1 to 25)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romleu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                Vitis vinifera
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
                                                                                                                                                                                                                                                                                                                  rosids; Vitaceae; Vitis.

1 (bases 1 to 25)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,

Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,

Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25; DB 1; Lengtn 40;
Pred. No. 6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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/organism="Vitis vinifera"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 AAAAAAAAAAAAAAAAAAAAA 1
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/mol Lype="mana"
/mol Lype="mana"
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/mol Expe="green stage"
/dov stage="green stage"
/dov stage="green stage"
/mol Experient Stage Skin Triplex2 Library"
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Sfilh; Site_2: SfilB; Oriented library"
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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/tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/dev stage="proliferated callus on 2N6 media for 30 days"
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/lab_host="E.coli DH10B"
/clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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REFERENCE AUTHORS

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CNS46477 2004 EST 18621 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera cDNA clone B3CS57RB007D09 3', mRNA sequence.
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       BP 81, 33883 Villenave D'Ornon Cedex,
                                                                                                                                                                           1. .25
// Organism="Vitis vinifera"
// mol_type="mRNA"
// mol_type="mRNA"
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// cultivar="Cabernet Sauvignon"
// clone="B3CS1XGB016E10"
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// clone lib="Green Grape Berry Lambda Triplex2 Library"
// note="Organ: Fruit without seeds; Vector: Lambda
// TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Vitis viniters

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Viteaceae; Vitis.

(Dases 1 to 25)

Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,

Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,

Hamdi,S., Romieu,C. and Terrier,N.

or seeds) at Various Developmental Stages

On seeds) at Various Developmental Stages
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/ organism="Vitis vinifera"
/ organism="Vitis vinifera"
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/ cultivar="cabernet Sauvignon"
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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                                              Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: 77
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7
71, Avenue Edouard Bourleaux,
France
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CNS46477.1 GI:46911102
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25 bp mRNA linear EST 30-APR-2004 EST 18499 Turning Grape Berry Lambda Triplex2 Library Vitis vinifera cDNA clone B3CS38TB008B03 3', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                     Viris viniters

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

Loases 1 to 25)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
Or seeds) at Various Developmental Stages
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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Ballia, V.S., Nascimento, L.U. and McCombie, W.R.
ESTs from Canis familiaris right cardiac ventricle (dog)
Unpublished (2004)
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/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
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/clone="B3CS38TB008B03"
2709 AAAAAAAAAAAAAAAAAAAA 2733
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Vitis vinifera
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Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

Spermatophyta; Ginkgophyta; Ginkgoaceae; Ginkgo.

Spermatophyta; Ginkgophyta; Ginkgoaceae; Ginkgo.

Spermatophyta; Ginkgophyta; Ginkgo.

O'Shaughnessy, A.L., Balija, V., Martianssen, R.A., McCombie, R.W., Banfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie

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Tel: 516 367 8884

Fax: 516 367 8874

Email: mccombie@cshl.org

Seq primer: -21M13UnivRev.
                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="Cardiac muscle"
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/lab_host="XLIO Gold"
/lab_host="XLIO Gold"
/clone lib="XLIO Gold"
/clone lib="XLIO Gold"
/clone lib="XIO Intervent on Intervet on Intervet of Normal Intervet on Int
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hote="Organ: leaf, Vector: :pBK-CMV; Site_1: Xhol;
Site_2: Eco RI; Stratagene ZAP Express CDNA Synthesis
The library was size-fractionated to enrich for large
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                                Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Fax: 516 367 8884
                                                                                                                                                                                                       Email: mccombie@cshl.org.
    Location/Qualifiers
    1. 25
    /organism="Canis familiaris"
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/mol_type="mRNA"
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/sex="female"
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                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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       Contact: W. Richard McCombie
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ò a DB 1; Length 25;

0.9%; Score 25;

Query Match

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Ginkgo biloba

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

CE 1 (bases 1 to 25)

Brenner, E. D., Twigg, R. W., Runko, S. J., Katari, M. S., Dedhia, N. N., O'Shaughnessy, A. L., Balija, V., Martienssen, R. A., McCombie, R. W., Benfey, P., Coruzzi, G. and Stevenson, D. Expressed tag sequences from Ginkgo female leaf (NYBG)

AL Unpublished (2005)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA
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ik86c01.gl Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
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ik86c07.gl Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
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1 (bases 1 to 25)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo female leaf (NYBG)
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Site_2: ECO RI; Stratagene ZAP Express CDNA Synthesis
The library was size-fractionated to enrich for large
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100.0%; Pred. No. 6e+02;
vative 0; Mismatches 0; Indels
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Pred. No. 6e+02;
; Mismatches 0;

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    /organism="Ginkgo biloba"

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/db_xref="taxon:3311"
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Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.
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Hominidae, Homo.

Hominidae, Homo.

Massa 1 to 25)

Lee,C.C., Yazdani,A., Wehnert,M., Bailey,J., Couch,L., Xiong,M.,
Coolbaugh,M.I., Chinault,C.A., Baldini,A., Lindsay,E.A., Zhao,Z.-Y.
and Caskey,C.T.H.
Isolation of chromosome-specific genes by reciprocal probing of
arrayed cDNAs and cosmid libraries

Hum. Mol. Genet. 4, 1373-1380 (1995)
7581376

Contact: Caskey,C.T.H.
Location/Qualifiers
                                                                                                                           L32039 25-AUG-1995
HUMXP278B Human placenta Homo sapiens cDNA clone XP278B, mRNA
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                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weises, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA" crr.
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/note="Arrayed cDNAs and cosmid libraries from human
placental fissue"
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Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
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100.0%; Pred. No. 6e+02;
iive 0; Mismatches 0; Indels

    .25
    /organism="Homo sapiens"

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Homo sapiens
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Best Local Similarity 100.
Matches 25; Conservative
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Fax: 801 585 7177
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Ginkgo biloba

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgoales; Ginkgoacea; Ginkgo.

I (bases 1 to 25)

S Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martiensen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie

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PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 884

Fax: 516 367 884

Email: mccombie@cshl.org

Seq primer: -21M13UnyRev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DR073133 25 bp mRNA linear EST 08-JUN-2005 ik86h08.gl Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                     /clone_lib="Ginkgo female leaf (NYBG)"
hote="Organ: leaf; Vector: :pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
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/note="Organ: leaf; Vector: :pBK-CMV; Site_1: XhoI;
Site_2: Eco RI; Stratagene ZAP Express cDNA Synthesis:
The library was size-fractionated to enrich for large
inserts."
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100.0%; Pred. No. 6e+02;
ive 0; Mismatches 0; Indels
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Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21Mi3UnivRev.
Location/Qualifiers
                                                                                                                                                                                                                             /organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
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Tel: 801 585 5606
Fax: 801 585 7177
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Sciurognathi; Murcidea; Muridae; Mus.

1 (bases 1 to 25)

1 (bases 1 to 25)

Salam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

Contact: Robert B. Weiss
University of Utah

Rm. 308, Blamedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1M0088A04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0088A04 R, genomic survey sequence.
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   ddunn@genetics.utah.edu
Length: 10000 Std Error: 0.00
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                            Plate: 0078 row: I column: 24
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C578L/63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.9%; Score 25;
00.0%; Pred. No.
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                                                                                                                                                            db_xref="taxon:10090"
clone="UUGC1M0078124"
                                                                       High quality sequence stop: 25.
Location/Qualifiers
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Mus musculus
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Best Local Similarity 100.0
Matches 25; Conservative
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Fax: 801 585 7177
Email:
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/gex="Male"
//Jab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
//Jab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
//Clone lib="Wouse 10kb plasmid UUGCIM library"
//note="Wetcror: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil #472114|gb]AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (stratagene) cells
and selected for ampicillin resistance."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Balam, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Niederhausern, A. and Wright, D., Weiss, R.,
Duouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.0
Plate: 0088 row: A column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
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Best Local Similarity 100.
Matches 25; Conservative
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Tel: 801 585 5606
Fax: 801 585 7177
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1 (bases 1 to 25)

2 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Roses, R., Tingey, A., von Niederhausern, A. and Wright, D. Waiss, R. Tingey, A., von Disamid inserts

Disamid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gil 4732114 [gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0433H19R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                         /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"/Clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42rv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: B column: 06
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                       /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                            /sex="Male"
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Best Local Similarity 100.0
Matches 25; Conservative
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of puble (1912114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota, Metacoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Musines; Mus.

Loases 1 to 25)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Menen, B., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Miderhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse_l0kb plasmid UUGCIM library"
/note=""Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Contact: Robert B. Weiss
University of Utah Genome Center
University.of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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Pred. No. 6e+02;
0; Mismatches 0; Indels
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0433 row: H column: 19
Seq primer: CACACAGGAAACAGCTATGACC
Class: plaamid ends
High quality sequence stop: 25.
Location/Qualifiers
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100.0%; Pred. No. c...
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0433H19"
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Tel: 801 585 5606
Fax: 801 585 7177
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Tel: 801 58
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University of Utah Genome Center
University of Utah
Genome Center
Winersity of Utah
Han. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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2M0035L19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0035L19 R, genomic survey sequence.
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1 (bases 1 to 25)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Solurognate, Tingey, A., Von Niederhausern, A. and Wright, D., Waiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                       /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library" /note=""Vector: PWD42rv; Putified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                Plate: 0460 row: L column: 02
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism≃"Mus musculus"
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                                                                                                                                                                                                                                      /mol_type="genomic DNA"
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Mus musculus
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AZ788646.1 GI:12928656
                                                                                                                                                                                                                                                                                                                                             sex="Male
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Matches 25; Conservative
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Unpublished (2000)
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Fax: 801 585 7177
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/BEXE"MAIE"
/ Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/ Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/ Clone lib="Wouse lokb plasmid UUGCIM library"
/ note="Vector: PWD42tv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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and selected for ampicillin resistance."
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1 (bases 1 to 25)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rally, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Duval, B., Duone whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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100.0%; Pred. No. 6e+02;
tive 0; Mismatches 0; Indels
                                     Std Error: 0.00
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0035 row: L column: 19
gp primer: CACACAGGAACAGGTATGACC
Class: plasmid ends
High quality sequence stop: 25.
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University of Utah Genome Center
University of Utah
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Matches 25; Conservative
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Class: transposon-tagged.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwdet (gil 4732114 [gb]AF129772.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xilio-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (Dases 1 to 25)

5 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Tingey, A., von Dlasmid inserts

1 Unpublished (200)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Banedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ980407 2001 25 bp DNA linear GSS 27-APR-2001 2M0257M19F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0257M19 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. col; strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: O column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
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0.9%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 6e+
Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0212008"
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AZ980407.1 GI:13851634
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Fax: 801 585 7177
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AZ980407/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0:005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gql 4732114 [gb] AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
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Unpublished (2001)
Contact: Walbot V
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Flat: 650 722 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence
plate: 4013055 row: D column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
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                                      0.00
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0257 row: M column: 19
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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Stanford University
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/clone="UUGC2M0257M19"
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CZ914066.1 GI:71930467
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Best Local Similarity
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Gaps

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GSS 22-DEC-2005

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designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and Bglid, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
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/clome_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="vector: pCtGIBAC1; Site_l: Sau3AI, Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DUB19648 1inear GSS 22-DEC-20 KENS005E24F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS005E24, genomic survey sequence.
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Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          End sequence of Brassica rapa Sau3AI (KBrS) BAC clone Unpublished (2005)
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/organism="Brassica rapa subsp. pekinensis"
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100.0%; Pred. No. 6e+02;
tive 0; Mismatches 0; Indels
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Fax: +82-31-299-1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. No.
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/db_xref="taxon:51351"
/clone="KBrS005E24"
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Brassica Genomics Team
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Class: BAC ends.
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CZ918479.1 GI:71938052
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Contact: Walbot V.
Department of Biological Sciences
Stanford University
Tel: 650 723 2227
Fex: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida; Poales, Poaceae, PACCAD clade, Panicoideee, Andropogoneae, Zea. 1 (2008) to 25) Maropogoneae, Zea. Walbot, V.
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Posaible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021009 row: F column: 02
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/notce="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
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                                                                                                 /molltype="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
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/culTivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
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100.0%; Pred. No. 6e+02;
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                                                                              organism="Zea mays"
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/lab_host="DH10B"
                                                                                                                                                                                                                                    /dev_stage="adult"
/lab_host="DH10B"
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Zea mays
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Unpublished (2005)
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Matches 25; Conservat
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DU834424/c
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S Yangues 1.0 23,

Bark, J.Y. Lim, M.H., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,

Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,

Rahn, J. H. and Park, B.S.

End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)

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BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
                                         DU832111 25 bp DNA linear GSS 22-DEC-2005 KBX509K01R KBxS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS009K01, genomic survey sequence.
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Brassica rapa subsp. pekinensis
Brassica, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 25)
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clome_lib="KBrS, Brassica rapa Sau3AI BAC library"
//note="vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
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25 bp DNA linear GSS 22-DEC-20
KBrS014D09F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS014D09, genomic survey
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sub species="pekinensis"
/db xref="taxon:51351"
/clone="KBrS009K01"
/lab host="E. coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/cultivar="Chiifu"
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DU834405.1 GI:83871001
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RESULT 903
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Contact: Beom-Seok Park
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Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC Email: pbeom@rda.go.kr
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Brassica rapa subsp. pekinensis
Brassica, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rossids; eurosids II; Brassicales; Brassicaceae; Brassica.
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d sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
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/clome_lib="KBr5, Brassica rapa Sau3Al BAC library"
/note="Vector: pCUGIBAC1; Site_l: Sau3Al; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
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End sequence of Brassica rapa Sau3AI (KBrS) BAC clone Unpublished (2005)
Contact: Beom-Seok Park
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225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
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                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. 25
/organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/cullivar="Chiffu"
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/mol type="genomic DNA"
/culfivar="Chiffu"
/sub species="pekinensis"
/db_xref="taxon:51351"
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/clone="KBrS014D09"
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DU834424.1 GI:83871020
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Class: BAC ends.
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                                                                                                                                                                                                                                                      Seq primer: T7
Class: BAC ends.
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/lab host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
/pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                               Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
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Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, B-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
KBrB087B17F KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB087B17, genomic survey
sequence.
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T. brucei sheared genomic DNA clone 324e10, forward sequence,
genomic survey sequence.
AL493396
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Constructed at the Institute for Genomic Research (TIGR),
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/organism="Brassica rapa subsp. pekinensis"
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No. 6e+02;
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.9%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 6e+ Matches 25; Conservative 0; Mismatches
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/clone="KBrB087B17"
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/cultivar="Chiifu"
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantas, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (Dases I to 25)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
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Mational Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Exar: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3Al BAC clone
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svallable at NIAB."
             /clone="KBrS014E03"
/lab_host="E. coli DH10B"
/clone lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
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mol type="genomic DNA"
/oultivar="Chiifu"
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DKFZp566J0546 r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
AL036686
Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (

described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Barrell, oxford University Press, 1999).

Details nel f. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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/strain="TREU927"
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/organism="Homo sapiens"
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EST (Ottenwaelder, et al.)
Unpublished (1999)
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Homo sapiens
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Eukaryota; Metazoz, Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosoma.

Strigeidida; Schistosomatoidea; Schistosoma.

Strigeidida; Schistosomatoidea; Schistosoma.

Eu (Dases 1 to 26)

Es Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S., Nikolaidou-Katearidou, N., Quall, M.A., Wilson, R.A. and Ivens, A.C. Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni

Unpublished (2005)

Contact: Ivens AC

Pathogen Microarrays Group

Wellcome Trust Sanger Institute

Hinxton, CB10 1SA, UNITED KINGDOM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="Brain"
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/lab_host="DHIOB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 20-SEP-2005
                                                                                                                                                                                                                                                                                                    Murray. F.

By Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Fal: +44 (0)131 527 4200
Fax: +44 (0)131 527 0430
Email: frazer: murray@bbsrc.ac.uk
                                                                                                                                                                                               Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AM048107 20-SE AM048107 Schistosoma mansoni lung schistosomu Schistosoma mansoni lung schistosomulum Schistosoma AM048107 SCHISTOSOMA Clone SmlC22b02.q1k, mRNA sequence.
AL587774 BP Chicken Brain Library Gallus gallus cDNA clone
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o. 6.2e+02; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 26
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/clone="ROSO63A11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2709 AAAAAAAAAAAAAAAAAAAA 2733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                               ROS063A11, mRNA sequence.
                                                                                    AL587774.1 GI:13192808
                                                                                                                                        Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AM048107.1 GI:75967881
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                                                                                                                                                                                                                                                                                1 (bases 1 to 26)
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                                                          AL587774
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RESULT 912 CF296851/c LOCUS DEFINITION

ઠે 셤 SOURCE ORGANISM

ACCESSION VERSION KEYWORDS REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

FEATURES

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/dev_stage="ripening stage"
/clone lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin, Vector: Lambda TriplEx2; Site_1:
Sfilk, Site_2: FfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 bp mRNA linear EST 08-DEC-2004 018 2 03 c14, mRNA sequence.
                                                                      Vitis vinifera

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Tosids; Vitaceae; Vitis;
1 (baes 1 to 26)
Abbal, P., Agasse, A., Atanassova, R., Barrieu, F.,
Hamdi, P., Dedidechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
Unpublished (2002)
Contact: Hamdi S.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antirrhinum majus (snapdragon)
Antirrhinum majus
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Lamiales; Plantaginaceae; Antirrhineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 27)
Bey, M., Stueber, K., Fellenberg, K., Schwarz-Sommer, Z., Sommer, H., Sadler, H. and Zachgo, S.
Characterization of Antirrhinum Petal Development and Identification of Target Genes of the Class B MADS Box Gene
                                                                                                                                                                                                                                                                                                                                                                               UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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ilarity 100.0%; Pred. No. 6.2e+02;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molekulare Pflanzengenetik
MPI fuer Zuechtungsforsehung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
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15539471
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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EST.
CN545723.1 GI:46910348
                                                 Vitis vinifera
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Best Local Similarity
Matches 25; Conserv
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/clone lib="Rice leaf plasmid cDNA library I (300GS)"
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with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CN545723 26.bp mRNA linear EST 30-APR-2004
EST 17667 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CSOORLOOSCO3 3', mRNA sequence.
CN545723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CF296851 26 bp mRNA linear EST 14-AUG-2003 30DGS--07-G13.bl Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--07-G13, mRNA
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 26)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESrs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Trongln, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                          /mol_type="mRNA"
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                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                       DB 1; Length 26;
6.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
                                                                                                                                                                                                                                                         0; Indels
     'organism="Schistosoma mansoni"
                                                                                                                                                                                                       0.9%; Score 25; DB
100.0%; Pred. No. 6.2
:ive 0; Mismatches
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Best Local Similarity 100.0
---Ahas 25; Conservative
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Best Local Similarity
Matches 25; Conserv
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CN545723/c LOCUS DEFINITION

ACCESSION

RESULT 913

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Gaps

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Length 26 0; Indels

TA244G08P/c

RESULT 915

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ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

FEATURES

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Urosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota, Badopterygota, Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 28)
Thibault, S. T., Singer, M. A., Miyazaki, W. Y., Milash, B., Dompe, N. A., Singh, C. M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L., Ryner, L., Cheung, L. M., Chong, A., Erickson, C., Fisher, W. W., Greer, K., Hartouni, S. R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Laufer, A., Mazzotta, J., Smith, R. D., Stevens, L. M., Stuber, C., Swimmer, C., Kopczynski, C., Duyk, G., Winberg, M. L. and Margolis, J. A. complementary transposon tool kit for Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/mol type="genomic DNA"
/mol type="genomic DNA"
/strain="stoopenic w- strain"
/db xref="taxon:722"
/clone_lib="Exelixis piggyBac PB insertions"
/note="vector: piggyBac PB Censenic was mutagenized by remobilization of transposable elements. We remobilizated the PB element using the remobilization of transposable elements. We remobilizated by selement using HBP70:piggyBac transposase from a single ammunition element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 37oC water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 310 490 8790
Email: RHOskins@1bl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of piggyBac element.
The piggyBac insertion position is unspecified in the 28 base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AM042970 Schistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA clone SmlC25d11.q1k, mRNA sequence.
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         CZ469056.1 GI:62963069
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      VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TA244G08P 31 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 244g08, forward sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAt 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
innert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus,
Cambridge CBlO 1SA, E-mail: barrell@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: nelsayederigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/
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                                                                                                                                                                                                                                                                              Gaps
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Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
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                                                                                  /clone="018 2 03 c14"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
                                                                                                                                                                                                                 Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 31;
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                                                                                                                                                                                                           Query Match
0.9%; Score 25; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 25; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 6.7e+02;
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/organism="Trypanosoma brucei"
/organism="Antirrhinum majus"
/mol_type="mRNA"
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/db_xref="taxon:5691"
/clone="244908"
                                                                                                                                                                                                                                                                                                                                    2709 AAAAAAAAAAAAAAAAAAAAAA 2733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence.
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Warches 25; Conservative
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EST 20-SEP-2005

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                                                        Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

En (Dasses 1 to 26)
Es 1 (Dasses 1 to 26)

Es 1 (Dasses 1 to 26)

Is Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S.,
Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C.

Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
Contact: Ivens AC
Pathogen Microarray Group
Wellcome Trust Sanger Institute
Hinxton, CB10 18A, UNITED KINGDOM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ingoletaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemannadkfz-heidelberg.de; sequenced by EMBL (European
Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZp459P0513) is available at the RZPD in Berlin. Please contact
the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/projects/cdna/.
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1 (bases, Pongo.
Ansorge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pongo pygmaeus mRNA (Ansorge, W., Krieger, S., Regiert, T., et al.)
Unpublished (2004)
Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 bp mRNA linear EST 07-JUL-;
DKFZp459P0513_r1 459 (synonym: pcorl) Pongo pygmaeus cDNA clone
CR5464444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="SmlC25d11.q1k"
/dev stagg="lung schistosomulum"
/clone lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.9%; Score 24.4; DB 1; Length 26; larity 96.2%; Pred. No. 6.7e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Schistosoma mansoni"
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/db_xref="taxon:9600"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAAAAAAAAAAAAAAAAAAAAAA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:6183"
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Pongo pygmaeus
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CR546444.1 GI:49898669
                      Schistosoma mansoni
Schistosoma mansoni
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COMMENT
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pubply (gilly | A712114 | gb| | AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
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                                                           /clone_lib="459 (synonym: pcor1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ355083 166 DNA linear GSS 02-OCT-200 IMO094D14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0094D14 R, genomic survey sequence.
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Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Winversity of Utah
Rm. Selomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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/clone_lib="Mouse_l0kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 26)
Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Waiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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                                                                                                                                                    Score 24.4; DB 1; Length 26;
Pred. No. 6.7e+02;
0; Mismatches 1; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: D column: 14
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0094D14"
                                                                                                                                                                                                                                                                                                                                                1 AAAGAAAAAAAAAAAAAAAAAA 26
/dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                             25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                              Query Match
Best Local Similarity
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi |4712114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0460L01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0460L01 R, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroldea, Muridae, Murinae, Mus
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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                                                                                                                                             0.9%; Score 24.4; DB 1; Length 26; 96.2%; Pred. No. 6.7e+02;
                                                                                                                                                                                                 1; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: L column: 01
Seg primer: CACACAGGAAACAGCTATGACC
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/mol type="genomic DNA"
/strain="C57BL/60"
/db xref="taxon:10090"
/clone="UUGCIM0460L01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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                                                                                                                                                                                                    Conservative
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Fax: 801 585 7177
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                                                                                                                                          Query Match
Best Local Similarity
Matches 25; Conserv
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84112, US
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COMMENT

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi |4732114 | gb |AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ635695 26 bp DNA linear GSS 13-DEC-2000 1M0493G18F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0493G18 F, genomic survey sequence.
purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.

1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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University of Utah Genome Center
University of Utah
Nm. 108. Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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/lab.host="E. Coli strain Xillo-Gold, Tl_resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jacksoi Laboratory Mouse DNA Resource
                                                                                                                                                                                                         ö
                                                                                                                                              Length 26;
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Pred. No. 6.7e+02;
0; Mismatches 1;
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/strain="C57BL/6J"
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/clone="UUGC1M0493G18"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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AZ635695.1 GI:11757885
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1 Similarity 96.2%;
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CZ919575.1 GI:71940233
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/do_trafe="acon:"dixed background w23/A188/B73/K55"
/db_trafe="acon:4577"
/tissue_type="last"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="DH108"
/clone_lib="4021 - RescueMu Grid V"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BgIII;
/clone_lib="adult"
/clone_lib="adult"
/clone_lib="adult"
/clone_lib="adult"
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purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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4021006D12.2EL x1 4021 - RescueMu Grid V Zea mays genomic, genomic
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Unpublished (2001)
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Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4001006 row: D column: 12
Class: transposon-tagged.
Location/Qualifiers
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                                                                                                                                              Length 26;
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96.2%; Pred. No. 6.7e+02;
tive 0; Mismatches 1;
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Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
Fax: 650 725 8221
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/organism="Zea mays"
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Best Local Similarity 96.2
Matches 25, Conservative
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PBlueScript backbone), Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site. http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglIII, and ligated to form circular plasmids. DH108 cells were transformed and then screened on LB plates with ampicillin."
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26 bp DNA linear GSS 08-AUG-2005 - RescueMu Grid V Zea mays genomic, genomic
                                                                                                                                                                                                                                                                                                                                                                                                Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot \nu
                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta, Liliopsida; Poales, Poaceae; PACCAD
Clade, Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 26)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: walbotdetanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021013 row: G column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="lat."
/clone_lb="4021 - RescueMu Grid V"
/note="Organ: leaf; Vector: RescueMu (engineered from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pan troglodytes DNA, clone: RP43-084C22.T7, genomic survey
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.9%; Score 24.4; DB 1;
96.2%; Pred. No. 6.7e+02;
ative 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Biological Sciences
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Location/Qualifiers
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7 10:41:28 2006
Tue Nov
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Query Match
Best Local Similarity
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                                                                                                 source
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JOURNAL
COMMENT
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                                                                                                                      Loses I to 26).

Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, Y., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submission
Submitted (Or-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bloscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstoneomail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409 BAC library RP-43 This BAC
clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Populus trichocarpa

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicotyledons;
rosids; eurosids I; Malpightales; Salicaceae; Saliceae; Populus.

1 (bases 1 to 27)
Ralph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y.,
Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G.,
Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A.,
Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A.,
Bohlmann, J.
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Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                  Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. BAC end sequences of Library RP-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WS01212.BR NOS FT-GT-FL-A-3 Populus trichocarpa cDNA clone WS01212 NOS 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.9%; Score 24.4; DB 1; Length 26; 96.2%; Pred. No. 6.7e+02; Live 0; Mismatches 1; Indels

    .26
    /organism="Pan troglodytes"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/clone="RP43-084C22.T7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
                                                                                                                                                                                                                                                                                                                                                                 clone tracking errors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Joerg Bohlmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DT471186.1 GI:73868448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing: T7
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                                                                                                               (bases 1 to 26)
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Best Local Similarity
Matches 25; Conserv
                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                         PRIMERS
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REFERENCE
AUTHORS
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JOURNAL
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/exes="Females"
/lab_host="E. coli DH10B T1 phage resistant cells"
/lab_host="E. coli DH10B T1 phage resistant cells"
/lab_host="E. coli DH10B T1 phage resistant cells"
/lone_lib="Pr-GT-FL-A-3"
/note="Vector: pBluescript I1 SK (+) XR; Site_1: SstI (5')
end of cDNA); Site_2: XhoI (3' end of cDNA); Foung and
mature leaves, along with green steems, from 8 year old
trees harvestee outhin the Boise Cascade region of
Washington state on May 15th, 2001. mRNA was isolated from
each tissue source independently and equal quantities of
mRNA from each tissue were then pooled. cDNA was prepared
from 20 micrograms of mRNA according to the full-length
cDNA library construction method described by Carninci P.
et al. (2000), Genome Research 10(10):1617-1630 and
directionally ligated into the pBluescript II SK (+) XR
vector digested with SstI (5' end) and XhoI (3'). Plasmid
DNA was then transformed by electroporation into DH10B
cells (Invitrogen) for propagation."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace consertium (orerall poor quality
Seq primer: mil -40 forward
High quality sequence stop: 1.
Location/Qualiflers
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.9%; Score 24.4; DB 1; Length 27; 92.6%; Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="383-2499 (Nisqually-1)"
/db_xref="taxon:3694"
/clone="W501212_N05"
                                                                                                                                                                                                            organism="Populus trichocarpa"
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                                       05
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Email: bohlmann@msl.ubc.ca
Plate: WS01212 row: N column:
High quality sequence stop: 126
POLYR=Yes.
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                                                                                                                                           Location/Qualifiers
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Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N52529
N52529.1 GI:1193695
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Homo sapiens
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0.9%;
                                                                                                                                                                                                                                                                                                                               25; Conservative
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Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
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Best Local S
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                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ramanlia; Eutheria; Earchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

E 1 (Dases 1 to 27)

S Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Relly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Inpublished (2000)

L Contact: Robert B. Weiss

University of Utah

University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS 21-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ862643 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0170J19F F. genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                 Length 27;
                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                 Score 24.4; DB 1;
Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84112, usr
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                              2705 TACTAAAAAAAAAAAAAAAAAAAAA 2731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: 0170 row: J column: 19
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'organism="Mus musculus"
organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0170J19"
                                                                                                                                                                                                                                                                                                                                                                                27 TTCNAAAAAAAAAAAAAAAAAAA 1
           /mol_type="mRNA"
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                                             'db_xref="taxon:9606"
                                                            'clone="IMAGE:244702"
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Plate: 0170 row: J c
                                                                                                                                                                                                                                                                                                   0.9%;
                                                                            sex="male"
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Best Local Similarity 92.6
Matches 25; Conservative
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(http://www.har.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gilfa732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF299294
7LEAF--03-E04.gl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-E04, mRNA
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 28)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyoengqi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhrahm@qgbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue type="leaf"
/dev_steage="7 days after germination"
/lab host="R-ooli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Pred. No. 6.8e+02;
0; Mismatches 1; Indels
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/clone="7LEAF--03-E04"
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/cultivar="Nackdong"
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2709 AAAAAAAAAAAAAAAAAAAAAAA 2734

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estGwatson.wustl.edu
Insert Size: 51
High qality sequence starts: 1 High qality sequence stops: 1
High qality sequence starts: 1 High qality sequence stops: 1
High qality sequence the IMAGE Consortium (info@image.lln.gov)
for further information. Trace considered overall poor quality
Insert Length: 51 Std Error: 0.00
Seq primms: -21ml3
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                          T52836 and the stratagene ovary (#937217) Home aspiens cDNA clone IMAGE:68057 3' similar to similar to gb:x53463 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (HUMAN), mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                       Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Moore, B., Morris, M., Passons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Travaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2709 AAAAAAAAAAAAAAAAAAAAAA 2734
             AAAAACAAAAAAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                           Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                         T52836.1 GI:654696
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Matches 25, Conserv
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KEYWORDS
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                                                                                      RESULT 929
T52836/c
                                                                                                                                            DEFINITION
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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The
Olivery Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                   Sciurognath; Murcidea; Muridae; Musines; Margai, A., Barber, M., Beacen, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

In upublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Research Bldg., 20 S. 2030 E., SLC, UT
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28 bp DNA linear GSS 04-OCT-200
1M0303L24F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0303L24 F, genomic survey sequence.
AZ481286
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
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Pred. No. 6.9e+02;
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Fax: 801 585 7177
Email: ddunnogenetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0303 row: L column: 24
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/65"
/db_xref="taxon:10090"
/clone="UUGC1M0303L24"
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Location/Qualifiers
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                                                                                                                                                                                                               Mus musculus (house mouse)
Mus musculus
                                                                                                                                                       AZ481286.1 GI:10642351
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Best Local Similarity
Matches 25; Conserv
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84112, USA
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RESULT 931 CF299155/c

RESULT 930 AZ481286/c

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CL693162
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota, viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Majonica cultivar-group)

Clade; Ehrhartoideae; Oryzaa.

E 1 (bases 1 to 29)

S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)

Contact: Nahm B.H.

Genemics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongil University

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Fax: 82 31 321 6355

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM Ginkgo biloba

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Ginkgophyta; Ginkgoaceae; Ginkgo.

1 (bases 1 to 29)

S Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,

O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McComble, R.W.,

Engressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

Londact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8884

Email: mcCombie@cshl.org
CF299155
TLEAF--03-B02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-B02, mRNA
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/clone="7LBAF--03-B02"
/tishue_type="lasf"
/des stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice_leaf_plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                          /clone lib="Ginkgo female leaf (NYBG)" /note="Organ: leaf; Vector: :pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis The library was size-fractionated to enrich for large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

1 (bases 1 to 29)
Srinivasan, J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J. AppabB: an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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Max-Planck-Institute for Developmental Biology
Max-Planck-Institute for Developmental Biology
Speannatr. 37-39, Tuebingen D-72076, Germany
Tal: 00497071601498
Email: ralf:sommer@tuebingen.mpg.de
Fmail: ralf:sommer@tuebingen.mpg.de
Fins library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: foomid ends.
Location/Qualifiers
Original 3 prime EST has been reverse completed to be in 5
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Pred. No. 7.2e+02;
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    .29
    Coganism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"

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/organism="Ginkgo biloba"
                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
                                                         Seq primer: -21M13UnivRev.
Location/Qualifiers
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Pristionchus pacificus
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The genome of the host-cell transforming parasite Theileria annulata and a comparison with T. parva Unpublished (2005) Contact: Pain A. Contact: Pain A.
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                                             TA378G07P 29 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 378g07, forward sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Animographic actual constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Gases 1 to 24)

Pain, A., Renauld, H., Berriman, M., Murphy, L., Yeats, C.A., Weir, W., Kerhornou, A., Aslett, M., Elshop, R., Bouchier, C., Cochet, M., Coulson, R.M. R., Cronin, A., de Villiers, E., Fraser, A., Fosker, N., Gardner, M., Goble, A., Maser, P., McKellar, S., Harris, D.E., Katzer, F., Larke, N., Lord, A., Maser, P., McKellar, S., Harris, D.E., Katzer, F., Nene, V., O'Neil, S., Price, C., Quail, M.A., Rabbinowitsch, E., Rawlings, N.D., Rutter, S., Saunders, D., Seeger, K., Shah, T., Squares, S., Tilvey, A., Walker, A.R., Woodward, J., Bobbelaere, D.A.E., Langsley, G., Rajandream, M.-A., McKeever, D., Shiels, B., Tait, A., Barrell, B. and Hall, N.
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                                                                                                                                                                                                                                                                                        Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                            Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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39.7%; Pred. No. 7.2e+02;
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/strain="TREU927"
/db_xref="t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic survey sequence.
                                                                                                                                  AL497621.1 GI:11873343
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1 (bases 1 to 29)
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The Pathogen Sequencing Unit
The Wellcome Trust Sanger Institute
The Wellcome Trust Sanger Institute
Genome Campus, CB10 1SA, UNITED KINGDOM
Piroplasm cDNA library: Frank Katzer and Brian Shiels, Division of
Veterinary Infection and Immunity, ICM, University of Glasgow, UK.
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/clone lib="Schistosoma mansoni lung schistosomulum"
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/clone="TAC20g08_plka"
/dev stage="piroplasm"
/lab host="Bos taurus (cow)"
/clone_lib="Theileria annulata piroplasm"
/note="country: Turkey:Ankara"
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100.0%; Pred. No. 6.8e+02;
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/mol_type="mRNA"
/isolate="Ankara (clone D7)"
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Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 18A, UNITED KINGDOM.
Location/Qualifiers
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Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

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Eullon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S., Nikolaidou-Kataaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C. Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni

Unpublished (2005)

Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Wellcome Trust Sanger Institute
Hinxton, CB10 158, UNITED KINGDOM.
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Strigeidida; Schistosomatoidea; Schistosoma.

Strigeidida; Schistosomatoidea; Schistosoma.

E 1 (bases 1 to 24)

S Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S., Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C. Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni

U Unpublished (2005)

Contact: Ivens AC

Pathogen Microarrays Group

Wellcome Trust Sanger Institute

Hinxton, CB10 1SA, UNITED KINGDOM.
AM045511 Schistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA clone SmlC18g01.q1k, mRNA sequence.
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| dev stage="lung schistosomulum"
|clone_lib="Schistosoma mansoni lung schistosomulum"
| hote="country: Puerto Rico"
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/mol_type="mRNA"
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Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

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Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S., Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C. Mikroarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni
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Laboratory of Sensory System
Destitute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
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/mol_type="mRNA"
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Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
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Email: xu.zlang@ion.ac.cn
This clone is also available at Chinese National Human Genome
This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
Pudong New Area, P.R.China. Please contact with Zhang Xu
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
PCR PRImers
PORWARD: T3
BACKWARD: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BX554611 Blossina morsitans morsitans adult infected gut Glossina morsitans clone Tsel6d06_plc, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Nopptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.

1 (bases 1 to 24)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetee fly Glossina morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 All clones with suffix glc are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 ISA, UK
Request for clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 24;
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/mol_type="mRNA"
sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tsel6d06_plc"
                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_lib="Rat DRG Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.9%; Score 24; DB 1; Le
100.0%; Pred. No. 6.8e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                           1. .24

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="DRNBAR06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2709 AAAAAAAAAAAAAAAAAAAAAAA 2732
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School of Biological Sciences,
University of Wales,
Bangor LLS7 2UW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAAAAAAAAAAAAAAAAAAA 24
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                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.99
Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                Seg primer: T3
POLYA=No.
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AUTHORS
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E 1 (bases 1 to 24)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongjin, Kyeonggj, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                           /note="country: Zimbabwe; EST from adult gut infected with T.brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF276855 24 bp mRNA linear EST 14-AUG-2003 14ETL--02-C19.gl Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--02-C19,
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
                                                                                                                                                                                                                                    Gaps
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/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                     0.9%; Score 24; DB 1; Length 24;
100.0%; Pred. No. 6.8e+02;
tive 0; Mismatches 0; Indels
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/clone="148TL--02-C19"
/tissue_type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.9%; Score 24; DB 1; Le
100.0%; Pred. No. 6.8e+02;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 24; Conservative
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Seq primer: T7.
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CN545249/c
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzeae; Oryza.

(bases 1 to 24)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                  Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida; Poales, Poaceae; BEP
clade, Ehrhartoideae; Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxxon:39947"
/clone="7LBAF--06-H15"
/tismuc_type="leaf"
/dev_stage="Toafa after germination"
/lab_nost="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                          Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                      Lee, T.H., Shin, Y.C.,
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa (japonica cultivar-group)"
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                                                                                                                                                                                                                                                                                                                                                       Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
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Location/Qualifiers
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                                                                                                                           1 (bases 1 to 24)
Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="Nackdong"
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CF301561.1 GI:33673322
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Best Local Similarity
Matches 24; Conserva
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CF320862/c
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/tissue type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab host="E.coli DH10B"
/clone lib="0sHDACl-overexpressing transgenic rice plasmid
/clone lib="0sHDACl-overexpressing transgenic rice plasmid
/note="vector: pCR4-TOPO; Site_1: EcoR1; Callus was
treated with ABA(20um) for lhr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis;
1 (bases 1 to 24)
Abaal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
Or seeds) at Various Developmental Stages
Unpublished (2002)
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Universite de Bordeaux I, Institut National de la Recherche
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                                                                                                                                                                                                                                                                                                                                                                                                        ch 0.9%; Score 24; DB 1; Length 24; I Similarity 100.0%; Pred. No. 6.8e+02; 24; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 6.8e+02;
ive 0; Mismatches 0;

    .24
    forganism="Vitis vinifera"
/mol type="mRNA"
/culTivar="Cabernet Sauvignon"

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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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/db_xref="taxon:39947"
/clone="HD--11-012"
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CN545249.1 GI:46909874
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Vitis vinifera
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CN545784/c
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'Vitis vinifera

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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;

Spermatophyta, Magnoliophyta, endicotyledons; core eudicotyledons;

rosids, Vitaceae, Vitis.

I (Bases I to 24)

S Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,

Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,

Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

L Unpublished (2002)

Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne

Universite de Bordeaux I, Institut National de la Recherche
                24 bp mRNA linear EST 30-APR-2004 EST 17251 Green Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00GL006E12 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mana"
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/cultivar="cabernet Sauvignon"
/du cref="tax00GL006E12"
/dev stage="green stage"
/clone_lib="Green Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
SfilA; Site_2: SfilB; Oriented library"
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France
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

1 (bases 1 to 24)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
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Pred. No. 6.8e+02;
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    .24
    /organism="Vitis vinifera"

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Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
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Best Local Similarity
Matches 24; Conserv
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/mol type="mRNA"
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Clone_llb="Ripe Grape Skin Triplex2 Library"
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SfilA, Site_2: SfilB; Oriented library"
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis;

Losaes 1 to 24)
Abaal, P., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
Unpublished (2002)
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/cultivar="Cabernet Sauvignon"
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/clone="B3CS00RL005H06"
                                                                                                                                          Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Best Local Similarity
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JOURNAL
COMMENT
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AUTHORS
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                                                                                                                                                                                                       EST 30-APR-2004
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France
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TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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Vitis viniters

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Vitaceae; Vitis.

(bases 1 to 24)

Abbal.P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,

Couture, C., Dedaldechamp, F., Dolrot, S., Glissant, D., Grimplet, J.,

Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

Unpublished (2002)
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Ginkgophyta, Ginkgoales, Ginkgocaee; Ginkgo.
1 (bases 1 to 24)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
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                          Gaps
                                                                                                                                                                                      24 bp mRNA linear EST 30-A EST 18460 Turning Grape Berry Lambda Triplex2 Library Vitis vinifera cDNA clone B3CS37TB007F12 3', mRNA sequence. CN546689 CN546689.1 GI:46911314
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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Pred. No. 6.8e+02;
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                        Indels
100.0%; Pred. No. 6.8e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Vitis vinifera"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 0.9%; Score 24; DB 1 Similarity 100.0%; Pred. No. 6.8 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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                                                              2709 AAAAAAAAAAAAAAAAAAA 2732
                                                                                         24 AAAAAAAAAAAAAAAAAAAAA 1
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DR073080.1 GI:67050929
                        24; Conservative
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      Best Local Similarity
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DR073080/c
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CN546689/c
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Ginkgo biloba (maidenhair tree)

Ginkgo biloba

Ginkgo biloba

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Ginkgoaceae; Ginkgo.

Spermacophyta; Ginkgoaphyta; Ginkgoales; Ginkgoaceae; Ginkgo.

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1 (bases 1 to 24)

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Brenner, E.D., Twigg, R.W., Martienssen, R.A., McCombie, R.W.,

Graughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,

Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo male leaf (NYBG)

Unpublished (2005)

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: Sil 367 8874

Email: mccombie@cshl.org
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/clone lib="Ginkgo male leaf (NYBG)"
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Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The
Library was size-fractionated to enrich for large
inserts."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="female"
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/clone lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: :pBK-CMV; Site_1: XhoI;
Site_2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
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O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W., Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Impubliahed (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
Po Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
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100.0%; Pred. No. 6.8e+02;
ative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
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/db_xref="taxon:3311"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 Email: mccombie@cshl.org
Seg primer: -21M13UnivRev.
Location/Qualifiers
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Matches

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

RESULT 952

AZ328848

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0; Indels

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0.9%; Score 24; DB 1; Le
100.0%; Pred. No. 6.8e+02;
Query Match
Best Local Similarity
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         24; Conservative
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Fax: 801 585 7177
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         Matches
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SOURCE
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plssmid UUGCIM library"
/note="Twector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6/ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD47 (gil 4/732114 gb] AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                  AZ328848 108b plasmid UUGCIM linear GSS 29-SEP-2000 lM0052M17R Mouse 108b plasmid UUGCIM library Mus musculus genomic close UUGCIM0052M17 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Musinae; Mahmoud, M., Beacorn, T., Padersen, E., Padersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Misher Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0052 row: M column: 17
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rm. 308, Biomedical
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@geneti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Conservative
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24;
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source

FEATURES

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalot (gilfa732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Genome Center
University of Utah
Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                          GSS 02-OCT-2000
                                                                                                            1M0109G10F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0109G10 F, genomic survey sequence.
AZ363562.1 GI:10477262
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buteria; Buteria; Buteria; Buteria; Buteria; Sciurognathi; Muroidea; Muridae; Musinae; Mus.

1 (bases 1 to 24)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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/clone_lib="Mouse 10kb plasmid UUGCIM library."
/note="Wector: PWD42try; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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100.0%; Pred. No. 6.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@grift
Insert Length: 10000 Std Error:
Plate: 0109 row: G column: 10
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .24 /organism="Mus musculus"
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1 AAAAAAAAAAAAAAAAAAAA 24
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Mus musculus
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Best Local Similarity
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Tue Nov

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0; Gaps

Indels

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0; Mismatches

24; Conservative

Matches

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/clone_lib="Mouse 10kb plasmid UUGCIM library"
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Unpublished (1200)

Contact: Robert B. Weiss
University of Utah
University of Utah

Weiss Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                          GSS 02-OCT-2000
                                                                                                                                                                                                                   AZ386491 24 bp DNA linear GSS 02-OCT-200
1M0145D02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0145D02 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: D column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
2709 AAAAAAAAAAAAAAAAAAAAAAA 2732
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/clone="UUGC1M0145D02"
                                           1 AAAAAAAAAAAAAAAAAAAA 24
                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
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Fax: 801 585 7177
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                                                                                                                                                          RESULT 954
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AUTHORS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was bluch orifice at constant velocity. The sheared DNA was blunc end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAP2 (gil 4732114|gb]AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xilio-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0152H07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse lokb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0152 row: H column: 07
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
  0; Mismatches
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University of Utah Genome Center
University of Utah
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                                                     2709 AAAAAAAAAAAAAAAAAAA 2732
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Location/Qualifiers
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  24; Conservative
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AZ390642/c
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Length 24;

0.9%; Score 24; DB 1; L 100.0%; Pred. No. 6.8e+02;

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0; Gaps

0; Indels

0; Mismatches

24; Conservative

Matches

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil 4732114 |gb| AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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1M0264A05F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0264A05 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
NiederAhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
        Gaps
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     0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: A column: 05
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732
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/clone="UUGC1M0264A05"
                                                                                        24 AAAAAAAAAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
  Conservative
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Fax: 801 585 7177
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84112, USA
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Length 24;

0.9%; Score 24; DB 1; Le 100.0%; Pred. No. 6.8e+02;

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose golelectrophoresis. Vector DNA was prepared from a derivative of pMAPA2 (gil-flA732114[gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                               AZB44621 24 bp DNA linear GSS 14-DEC-2000 1M0508F12R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0508F12 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Muse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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musculus C57BL/6J (male) was obtained from the Jackson
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100.0%; Pred. No. 6.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: dunnogenetics.utah.edu
Insert Length: 10000 Std Error: C
Plate: 0508 row: F column: 12
Seg primer: CACACAGGAAACAGCTATGACC
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/strain="C57BL/6J"
2709 AAAAAAAAAAAAAAAAAAA 2732
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High quality sequence stop: 24.
Location/Qualifiers
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/sex="Male"
                              24 AAAAAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus
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Fax: 801 585 7177
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Best Local Similarity
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AZ644621/c
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                                                                                                                                                                                               2M0129405F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0129A05 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Landari, Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Natelly, M., Rose, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wiright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 184112, USA
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
     Gaps
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  Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: A column: 05
Seg primer: CGTTGTAAACGACGCCCAGT
Class: plasmid ends
0; Mismatches
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                   2709 AAAAAAAAAAAAAAAAAAAAA 2732
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Location/Qualifiers
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/clone="UUGC2M0129A05"
                                                                                                 24 AAAAAAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                     AZ834990.1 GI:13004898
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     24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
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AZ834990
                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
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ORGANISM
                                                                                                                                                                                                                                             DEFINITION
     Matches
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0.9%; Score 24; DB 1; Length 24; 100.0%; Pred. No. 6.8e+02;

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gp|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-GGold (Stratagene) cells and selected for ampicillin resistance."
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/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/lone lib="Mouse 10kb plasmid UUGC2M library"
/note="WUGCor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                   A2970038
2M0243J02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
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1. (bases 1 to 24)
Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Gaps
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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
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Mismatches
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Fax: 801 585 7177
Fax: 801 585 7177
Fax: 801 585 7177
Insert Length: 10000 Std Error: 0
Plate: 0243 row: J column: 02
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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ferrain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC2M0243J02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
84112, USA
                                                             2709 AAAAAAAAAAAAAAAAAAAA 2732
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Location/Qualifiers
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0; Gaps

0; Indels

0; Mismatches

24; Conservative

Matches

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/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nr; Purified genomic DNA from M.
musculus C57BL/GJ (female) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dhares). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gil 4732114 gpl AR729072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (bases 1 to 24)

S Dunn, D., Ayagi, A., Barber, W., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Inpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                     AZ984490 24 bp DNA linear GSS 27-APR-2001 2M0266H05F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0266H05 F, genomic survey sequence.
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     Mismatches
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0266 row: H column: 05
Seg primer: CGTYCTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
High quality sequence
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/clone="UUGCZM0266H05"
                                                        2709 AAAAAAAAAAAAAAAAAAA 2732
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Mus musculus
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24; Conservative
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84112, US
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KEYWORDS
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Length 24;

Score 24; DB 1; Le Pred. No. 6.8e+02;

0.9%; S 100.0%;

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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Winversity of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                 AZ993423
2M0278019F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0278019 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Giurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bass 1 to 24)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Meelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Insert Length: 10000 Srd Error: 19
Blate: 0278 row: 0 column: 19
Seg primer: CGTYGTAAAACGACGGCGAGT
Class: plasmid ends
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
2709 AAAAAAAAAAAAAAAAAAA 2732
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Location/Qualifiers
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/clone="UUGC2M0278019"
                              1 AAAAAAAAAAAAAAAAAAAAA 24
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
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AZ993423/c
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Seq primer: T7
Class: BAC ends.
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DX047568/C
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JOURNAL
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JOURNAL
COMMENT
                                     REFERENCE
AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosida, eurosida II; Brassicales, Brassicaceae, Brassica.
1 (bases 1 to 2.), Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Yang T.J., Kwon, S.J., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Beom-Seok Park
Brassica Genomics Team
Mational Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3Al BAC clone
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Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                  DU829467 CBrS, Brassica rapa Sau3Al BAC library Brassica rapa subsp. pekinensis genomic clone KBrS004P08, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. coli DH10B"
/clome_lib="KBrS, Brassica rapa Sau3A! BAC library"
/note="Vector: pCUGIBAC!; Site_l: Sau3A!; Brassica rapa
8sp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
 Gaps
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0
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/cultivar="Chiftu"
/sub_species="pekinensis"
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100.0%; Pred. No. 6.8e+02;
lve 0; Mismatches 0; Indels
Indels
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Conservative 0; Mismatches
0; Mismatches
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                                     2709 AAAAAAAAAAAAAAAAAAAA 2732
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Class: BAC ends.
Location/Qualifiers
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DU830197.1 GI:83866793
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DU829467/c
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L. Casses I to 24)

Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Teal: +82-31-299-1672
Email: pbeom@xida.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantas subsp. pekinensis
Bukaryota; Viridiplantas subsp. pekinensis
Bukaryota; Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

I (bases I to 24)
S Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Bark, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Secolun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1672
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica
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BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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/note="vector: pCUGIBAC1; Site_l: Sau3AI, Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."
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/organism="Brassica rapa subsp. pekinensis"
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0.9%; Score 24; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0;
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DX047568.1 GI:84741865
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Bource

FEATURES

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DXO53980 24 bp DNA linear GSS 10-JAN-2006
KBrB058A21R KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB058A21, genomic survey
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by Yong-Pyo Lim (CNU)."
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases I to 24)
Yang, T.J. Kwon, S.J. Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahnh, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
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Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seedun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
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ilarity 100.0%; Pred. No. 6.8e+02;
Conservative 0; Mismatches 0;
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KBrB058A21
Seq primer: M13 Reverse
Class: BAC ends.
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DX053980/c
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pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantas Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosida II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
Contact: Beom-Seok Park
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0.9%; Score 24; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0;
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Location/Qualifiers
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Class: BAC ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

FEATURES

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AUTHORS REFERENCE

DX049347/c LOCUS DEFINITION RESULT 965

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Gaps

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Page 372

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/mol_type="genomic DNA"
/cultivar="Chiifu"
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Class: BAC ends
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S Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab host="E.coli DH10B"
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pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosids II; Brassicales; Brassicaceae; Brassica.
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Email: pbecm@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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/mol_type="genomic DNA"
/cultivar="Chiifu"
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                                                                                                                                                                                                                                                                                                                                                                                                                              /sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB081P14"
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Class: BAC ends.
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1. .24
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Brassica Genomics Team
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Class: BAC ends.
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Best Local Similarity 100.0
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/clone="KBrB093A19"
/lab_host="E.coli DH10B"
/lab_host="E.coli DH10B"
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pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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by Yong-Pyo Lim (CNU)."
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Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons;
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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                                                                                                                                                                                                                        Length 24;
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
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Similarity 100.0%; Pred. No. 6.8e+02;
14; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 6.8e+02;
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Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
by the tight size distribution (
closeribed in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@rigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
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Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAL 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
innsert libraries for whole genome sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Bmail: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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I (bases 1 to 2).

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Belville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TA354C06P 24 bp DNA linear GSS 13-DB
T. brucei sheared genomic DNA clone 354c06, forward sequence,
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Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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100.0%; Pred. No. 6.8e+02;
iive 0; Mismatches 0;
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Best Local Similarity 100.
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                                          T. brucei sheared genomic DNA linear GSS 13-DEC-2000 genomic survey sequence.
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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M. A. and Barrell, B. G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, B-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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Trypanosoma brucei
Bukaryota, Buglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

Trypanosoma.

I (bases 1 to 24)
Hall, N. Bowan, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Direct Submission
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T. brucei sheared genomic DNA clone 27b08, reverse sequence,
                                                                                                                                                                                                                                                     Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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.00.0%; Pred. No. 6.8e+02;
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/mol_type="genomic DNA"
/strain="TREU927"
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Conservative 0; Mismatches
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/clone="169d12"
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AL453584.1 GI:11850982
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TA169D12P/c
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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma bruce; (TRED'927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayedGitgr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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/dev stage="Unknown"
/dab_nost="Brain"
/dab_nost="Brain"
/clone lib="BP Chicken Brain Library" site_2: Sall; Cloned undirectionally. Primer: Oligo dr. 5' adaptor sequence: 5' TCGACTCGAG3'; 3' adaptor sequence: 5' GCGGCCGCTTTTTTTTTTTTTTTT" 3' Poly A RNA purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALS87648 ALS87648 BP Chicken Brain Library Gallus gallus cDNA clone ROS060C07, mRNA sequence.
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (Dases 1 to 25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: frazer.murray@bbsrc.ac.uk
GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.9%; Score 24; DB 1; Length 24; 100.0%; Pred. No. 6.8e+02;
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/organism="Trypanosoma brucei"
/mol type="genomic DNA"
/strain="TREU927"
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/organism="Gallus gallus"
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Dept. Genomics and Bioinformatics
Roslin Institute
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/clone="95b08"
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/db_xref="taxon:9031"
/clone="ROS060C07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roslin, Midlochian, EH25 9PS,
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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BP Chicken Brain Library
Unpublished (2001)
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Gallus gallus
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                                                      nh1@sanger.ac.uk
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AL587648/c
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Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E.,
Melville, S.E.,
Direct Submission

Lybmitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 ISA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing in genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                        24 bp DNA linear GSS 13-DEC-2000
Terbrucei sheared genomic DNA clone 371f11, forward sequence,
AL495622
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

1 (bases 1 to 24)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
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T. brucel sheared genomic DNA clone 95b08, forward sequence,
AL459003
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Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae,
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0.9%; Score 24; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0;
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/strain="TREU927"
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/clone="371f11"
                                                      1 AAAAAAAAAAAAAAAAAAAAAAAAA 24
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/db_xref="taxon:5270"
/cell type="Mycelia"
/dev_stege="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"
/note="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."
                        Eukaryota; Fungi, Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
Ustilaginomycetidae; Ustilago.
Nugent, K.G., Choffe, K. and Saville, B.J.
Gene expression during Ustilago maydis diploid filamentous growth:
EST library creation and analyses
Fungal Genet. Biol. 41 (3), 349-360 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 bp mRNA linear EST 10-JAN-19: yy66g01.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270480 3' similar to gb:D29805 N-ACETYLLACTOSAMINE SYNTHASE (HTMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                               Saville Lab
University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Email: bsaville@utm.utoronto.ca
Email: bsaville@utm.utoronto.ca
Seq primer: T7 Reverse (5' GAGTAMATACGACTCATATAGGG 3')
High quality sequence stop: 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.

1 (bases 1 to 25)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Helman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forces Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence starts: 1
High quality sequence stores: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Ustilago maydis"
/mol_type="mRNA"
/strain="FBD12"
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Contact: Barry J. Saville
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N33150.1 GI:1153549
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     Ustilago maydis
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Matches 24; Conserv
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     ORGANISM
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TITLE
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                                                                                                                                                                                                                                                                                                                         HD--06-114.gl OsHDACl-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--06-114, mRNA sequence.
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/mol type="mRNA"
/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--06-114"
/tissue_type="callus"
/fev stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="B.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
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D06_G05 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
CF638767
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

(bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yogin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                           Gaps
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                                              Query Match 0.9%; Score 24; DB 1; Length 25; Best Local Similarity 100.0%; Pred. No. 6.9e+02; Matches 24; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 6.9e+02;
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Clonetech (*6854-1)"
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CF317007.1 GI:33688768
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Ustilago maydis
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KEYWORDS SOURCE ORGANISM

ACCESSION VERSION

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

LOCUS DEFINITION CF317007/c

RESULT 976

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Query Match

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RESULT 977 CF638767 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

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                                                                                                                                                                                                                        Wus musculus (house mouse)

Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Matazoa; Chordontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

E 1 (bases 1 to 25)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacze,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausenn,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

University of Utah Genome Center
University of Utah Genome Center
University of Utah
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1M0137N18F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Seq primer: ml3 -40 forward High quality sequence stop: 1. Location/Qualifiers
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Insert Length: 10000 Std Error: 0.00
Plate: 0137 row: N column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                       /organism="Homo sapiens"
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                                                                                                                                        /mol_type="mRNA"
/db_xref="GDB:3880122"
/db_xref="taxon:9606"
/clone="IMAGB:270480"
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Location/Qualifiers
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                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.(
Matches 24; Conservative
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Fax: 801 585 7177
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84112, USA
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AZ381039
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwDAC2 (giffa712114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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D14_A02 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
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Nugent, K.G., Choffe, K. and Saville, B.J.
Nugent, K.G., Choffe, K. and Saville, B.J.
Est library creation and analyses
Fungal Genet. Biol. 41 (3), 349-360 (2004)
                                                                                       /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note=""vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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3359 Mississauga Road North, Mississauga, ON, LSL 1C6, Canada
Tel: 905 629 4702
Fax: 905 828 3792
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Ustilago mydis
Eukaryota, Fungi, Basidiomycota, Ustilaginomycetes,
Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
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Plate: UTM-UM-D126/7-014-UTM row: 02 column: A
Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGGG 3')
High quality sequence stop: 26.
Location/Qualifiers
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/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"
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/mol_type="mRNA"
/strain="FBD12"
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Best Local Similarity 100.0%; Pred. No. 6.9
Matches 24; Conservative 0; Mismatches
/db_xref="taxon:10090"
/clone="UUGC1M0137N18"
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KEYWORDS
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                                                                                                                                                                                                                                                                                                       EST 28-APR-1995
/note="Vector: pSport; mRNA was extracted from diploid mycalia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superseript II cDNA Library Construction Kit."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: esternocolor insert Solze: 367
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLML
This clone is available royalty/free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Trace considered overall poor quality
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 27)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lannon,G., Marra,M.,
Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                 27 bp mRNA linear EST 2 yh72e05.81 Soares placenta NbZHP Homo sapiens cDNA clone IMAGE:135296 3' similar to gb:X53463 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (HUMAN);, mRNA sequence.
                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-Merck EST Project Unpublished (1995)
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                        Score 24; DB 1; Length 26;
Pred. No. 7e+02;
                                                                                                                                  1; Indels
                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert Length: 367 Std Error.
Seq primer: -21m13
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="GDB:541217"
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/clone="IMAGE:135296"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Female"
                                                                                        Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                  R31539.1 GI:787382
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                RESULT 981
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JOURNAL
COMMENT
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AUTHORS
                                                                                                                                                                                                                                                                                 R31539/c
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Laboratory Mouse DNA Resource Library Charactery Mouse DNA Resources (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XI10-GG1d (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)

Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Mus.

E. (Abases I to 28)

E. (Abases I to 28)

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Really,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von

Niederhausern,B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2010 E., SLC, UT

Mall. Sci. USA
                                                                                                                                                                                                                                                                                                                                                                        AZ358038 22-0CT-2000 1M0100F05F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0100F05 F, genomic survey sequence.
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                                                                          Gaps
                                                                          ö
       Length 27;
                                                                      1; Indels
Query Match 0.9%; Score 24; DB 1; I
Best Local Similarity 96.0%; Pred. No. 7.2e+02;
Matches 24; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0100 row: F column: 05
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 28.
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/organism="Mus musculus"
                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0100F05"
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Homo sapiens
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Matches 25;
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                                                                                                                                                                                                                           source
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                                                  TITLE
JOURNAL
COMMENT
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VERSION
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JOURNAL
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   REFERENCE
                   AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Enrhartoideae; Oryza.

E 1 (bases 1 to 27)
S Kim, J.S., Jun, K.M., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF318113 27 bp mRNA linear EST 15-AUG-2003 HD--08-B07.g1 OsHDAC1-overexpressing transgenic rice plasmid CDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--08-B07, mRNA sequence.
CF318113 GI:33689874
                                                                                                                                                                                      CF299084 1inear EST 15-AUG-2003 7LEAF--02-P02.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-P02, mRNA
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; BEP
clade, Ehrhartoideae, Oryzae, Oryza.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps

    .27
/organism="Oryza sativa (japonica cultivar-group)"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.9%; Score 23.8; DB 1; Length 27; 92.6%; Pred. No. 7.4e+02;
   Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                    .
 0.9%; Score 24; DB 1; Ld 100.0%; Pred. No. 7.3e+02; ive 0; Mismatches 0;
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                                                                    2709 AAAAAAAAAAAAAAAAAAAAA 2732
                                                                                                    1 AAAAAAAAAAAAAAAAAAAA 24
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Query Match 0.99
Best Local Similarity 100.9
Matches 24, Conservative
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Best Local Similarity 92.6
Matches 25, Conservative
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                          CF299084/c
                                                                                                                                                                                                        DEFINITION
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                                                                                                                                                          RESULT 983
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JOURNAL
COMMENT
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KEYWORDS
SOURCE
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/tissue_type="callus"
//dev stage="proliferated callus on 2N6 media for 2 weeks"
//dev stage="proliferated"
//lab_host="E.coli DH108"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
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                                                                                                                                                                                         Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongGi, Korea
Yell: 82 31 33 0 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (life@image.llnl.gov) for further information.
Trace considered overall poor quality
1 (bases 1 to 27)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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1 (bases 1 to 27)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hillier,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Holman,M., Hultman,M., Rocaba,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yhl7e07.s1 Soares infant brain INIB Hymo sapiens cDNA clone
IMAGE:37726 3' similar to 9b:M65131 MCTHYLMALONYL-COA MUTASE
PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa (japonica cultivar-group)"
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 23.8; DB 1; Length 27; 92.6%; Pred. No. 7.46+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:39947"
/clone="HD--08-B07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA library (HD)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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                                                                                                                                                                     Contact: Nahm B.H.
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Walbor V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 60 725 8221
Email: Walbou@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013005 row: F column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /most_type="genomics DNA"
/cullivar="mixed background W23/A188/B73/K55"
/db_xref="texon.4577"
/db_xref="texon.4577"
/dev_stage="adult"
/dev_stage="adult"
/lab.host="blost="108"
/clone_lib="4013 - RescueMu Grid O"
/note="Urgan: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
Possible reversed clone: polyT not found
Seg primer: SP6
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 23.8; DB 1;
92.6%; Pred. No. 7.4e+02;
tive 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2707 CTAAAAAAAAAAAAAAAAAAAAAAAAA 2733
                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTGAAAAAAAAAAAAAAAAAAA
                                                                                                          /mol_type="mRNA"
/db_xref="GDB:410267"
/db_xref="taxon:9606"
/clone="IMAGE:37726"
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/organism="Zea mays"
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Location/Qualifiers
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C2914142
C2914142.1 GI:71930586
                                                                                                                                                                                /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.9
Best Local Similarity 92.6
Matches 25; Conservative
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RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DX071727 28 bp DNA linear GSS 10-JAN-2006 KBrB081124F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB081124, genomic survey
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/db_xref="taxon:51351"
/clone="KBrBo31124"
/lab_host="B.coli DH108"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases I to 28)
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: pbeom@rda.go.kr
Acc end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Beom-Seek Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seedun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
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/cultivar="Chiifu"
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DX071727/c
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DU831936 LASS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS013B15, genomic survey sequence.

DU833936.1 GI:83870532

Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 25)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M. H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.

End sequence of Brassica rapa Sau3AI (KBrS) BAC clone Unpublished (2005)

Contact: Beom-Seok Park Brassica Genomics Team

Email: pbeom@rda.go.kr BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone

National Institute of Agricultural Biotechnology 225 Seodun-Dong, Suwon, 441-707, Korea Tel: +82-31-299-1670 Fax: +82-31-299-1672

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Query Match 0.9%; Score 23.4; DB 1; Length 25; Best Local Similarity 96.0%; Pred. No. 7.5e+02; Matches 24; Conservative 0; Mismatches 1; Indels
                   DU833936/c
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was blut cand-repaired by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polyrucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                  AZ404078 11near GSS 03-OCT-2000 IMO172J07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0172J07 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.9%; Score 23.4; DB 1; Length 25; ilarity 96.0%; Pred. No. 7.5e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel:: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0172 row: J column: 07
Seq primer: CGTTGTAAAACGACGGCCAGT

    .25
    /organism="Mus musculus"

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/strain="C57BL/63"
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/clone="UUGC1M0172J07"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 25.
Location/Qualifiers
                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                        AZ404078.1 GI:10528091
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RESULT 988
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KEYWORDS
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases I to 25)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, H.J., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
DUR34323 C2-DEC-2C KENSO13P19F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS013P19, genomic survey sequence.
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2709 AAAAAAAAAAAAAAAAAAAAAAA 2733

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1 AAAAAAAAAAAAAAGAAAAAAAA 25

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Gaps

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/sub species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS013B15"
/lab host="Bc.coli bH10B"
/clone=lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site_1: Sau3AI, Brassica rapa spekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."

/organism="Brassica rapa subsp. pekinensis" /mol type="genomic DNA" /cultivar="Chiifu"

Location/Qualifiers

source

Sed primer: T7 Class: BAC ends.

GSS 22-DEC-2005

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AZ316353
                                                                                                                                                                                                                                                                              RESULT 992
AZ316353
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP
Clade; Enrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 26)
Kim,J.S., Jun.K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                              Brassica Genomics Team
National Institute of Agricultural Biotechnology
Sas Seedun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
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                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_gpecies="pekinensis"
/db_xref="txxon:51351"
/clone="KBrXo13P19"
/lab_host="E. coli DH10B"
/clone="Vector: pCUGIBAC1; Site_1: Sau3A1 BAC library"
/note="Vector: pCUGIBAC1; Site_1: Sau3A1; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
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7LEAF--03-L24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L24, mRNA
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/tisone_type="leaf"
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      End sequence of Brassica rapa Sau3AI (KBrS) BAC clone Unpublished (2005)
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/organism="Brassica_rapa subsp. pekinensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.9%; Score 23.4; DB 1; Length 25; 96.0%; Pred. No. 7.5e+02;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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/cultivar="Nackdong"
                                                                                                                                                                                                                                                                          Location/Qualifiers
                                          Contact: Beom-Seok Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
CF299646
CF299646.1 GI:33671407
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Matches 24; Conservative
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                                                                                                                                                                                                                                 Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                              KBrS013P19
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KEYWORDS
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 29-SEP-2000
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/note="Vector: pCR4-TOPO, Site_1: EcoRI; mRNA was capped with Olgoribonucleotides and Then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ316353 29-SEP-200
1M0034D09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0034D09 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
Bukaryota; Metasoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid inserts
(Contact: Robert B. Weiss
University of Utah Genome Center
Nm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Kose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                                                                                                                                                          Gaps
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                                                                                                                                       Length 26;
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                              1,
                                                                                                                               Query Match 0.9%; Score 23.4; DB 1; Best Local Similarity 96.0%; Pred. No. 7.6e+02; Matches 24; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0034 row: D column: 09
Seq primer: CGTTGTAAACGACGCCAGT
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/strain="C57BL/6J"
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/clone="UUGC1M0034D09"
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Query Match

Matches

VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

DEFINITION AL587582/c

ACCESSION

RESULT 993

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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Enkaryota; Tracheophyta; Spermatophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

El (bases 1 to 29)

El (bases 1 to 29)

Shaughnessy, N. W., Runko, S. J., Katari, M. S., Dedhia, N. N., O'Shaughnessy, A. L., Balija, V., Martienssen, R. A., McCombie, R. W., Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo megasporophyll (NYBG)

Unpublished (2005)

Londact: W. Richard McCombie Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DROG4440 29 bp mRNA linear EST 06-JUN-2005
ip55c01.gl Ginkgo megasporophyll (NYBG) Ginkgo biloba CDNA 3', mRNA
sequence.
                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuvognathi; Muroidea; Muridae; Murinae; Mus. 1 (288 1 to 28) Kato, K. and Matoba, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mccombie@cshl.org
Original 3 prime EST has been reverse completed to be in 5 prime
direction
                                                                                                                                                     Generation of expressed sequence tags from mouse brain Unpublished (2002)
Contact: Kikuya Kato
Contact: Kikuya Kato
Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5589
Eax: 81-743-72-5589
Email: Kato@bs.aist-nara.ac.jp,
URL:http://lovez.aist-nara.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.9%; Score 23.4; DB 1; Length 28; 92.3%; Pred. No. 7.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"
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/mol type="mRNA"
/db_xref="taxon:3311"
/sex="Female"
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/db_xref="taxon:10090"
/clone="BED0010669"
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Ginkgo biloba
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Location/Qualifiers
Mus musculus (house mouse)
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Best Local Similarity 92.3
Matches 24; Conservative
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Gallus gallus

Gallus gallus

Gallus gallus

Gallus gallus

Gallus gallus

Archosauria; Aves; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

E I (bases 1 to 28)

Murray,F. BP Chicken Brain Library

L Unpublished (2001)

Contact: Frazer Murray

Dept. Genomics and Bioinformatics

Roslin Institute

Roslin Midlothian, EH25 9PS, UK

Tel: +44 (0)131 527 4200

Fax: +44 (0)131 527 4200
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    adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                           Score 23.4; DB 1; Length 26;
Pred. No. 7.6e+02;
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Local Similarity 96.0%; Pred. No. 7.6e
Nes 24; Conservative 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059D03"
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AU257468/c LOCUS DEFINITION

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Contact: Libin Jia
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Ginkgo biloba (maldenhalf tree)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 29)
Brenner, E. D., Twigg, R. W., Runko, S. J., Katari, M. S., Dedhia, N. N., O'Shaughnessy, A. L., Balija, V., Martienssen, R. A., McComble, R. W., Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Contact: W. Richard McCombie
Lita Annenberg Hazbor Genome Sequencing Center
Cold Spring Harbor Laboratory
P Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8884
Fax: 516 367 8884
Fax: 516 367 8874
Smail: mccombie@espl.org
Seq primer: -21M13UnivRev.
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                                                                                                                                                                                                                                                      DR072912 29 bp mRNA linear EST 08-JUN-2005
ik79b03.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
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29 bp mRNA linear EST 07-MAR-1995
SySZE07.r3 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:66565 5' similar to gb:X02492 INTERFERON-INDUCED PROTEIN 6-16
PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Ginkgo female leaf (NYBG)"
hote="Organ: leaf, Vector: :pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 29)
                                                                               Gaps
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                                          Length 29;
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larity 96.0%; Pred. No. 8e+02;
Conservative 0; Mismatches 1; Indels
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                                          DB 1;
                                    Score 23.4; DB :
Pred. No. 8e+02;
0; Mismatches
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/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
                                                                                                                 2707 CTAAAAAAAAAAAAAAAAAAAAA 2731
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for large inserts."
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                                    Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative (
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Homo sapiens
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/dev_grage="20 week-post conception fetus"
//dev_grage="D108 (ampicillin resistant)"
/lab host="D1108 (ampicillin resistant)"
/lone="D1208 (ampicillin resistant)"
/note="D208 (ampicillin resistant)"
/note="D208 (ampicillin resistant)"
/note="D208 (ampicillin resistant)
/note="D208 (ampicillin re
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High qulity sequence starts: 1
High qulity sequence stops: 1
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
Seq primer: T7
High quality sequence stop: 1.
Location/Qualifiers
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Jia.L.B., Young,M.F., Touchman,J.W., Bouffard,G.G.,
Beckerrom-Sternberg,S.M., Green,E.D., Powell,J.I., Yang,L.M.,
Robey,P.G., Hotchkiss,R.N. and Francomano,C.A.
SGAP: The Skeletal Genome Anatomy Project
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National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
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                                                                                                                                                                                                                                                                             The Washu-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
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/db_xref="taxon:9606"
/clone="IMAGE:66565"
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Homo sapiens
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FEATURES

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

Sermatophyta; Ginkgophyta; Ginkgoales; Ginkgo.

Sermatophyta; Ginkgophyta; Ginkgoales; Ginkgo.

Spermatophyta; Ginkgophyta; Ginkgo.

O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,

Benfey,P., Coruzzi,G. and Stevenson,D.

Expressed tag sequences from Ginkgo male leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory, NY 11724, USA

Tel: 516 367 8884

Eax: 516 367 8884

Email: mccombie@cshl.org
                                                                                                                                                                                                                                              mRNA linear EST 08-JUN-2005
Ginkgo biloba cDNA 3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Ginkgo male leaf (NYBG)" / clone lib="Ginkgo male leaf; Vector: pBK-CMV; Site_1: XhoI; Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. library was size-fractionated to enrich for large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.8%; Score 23.2; DB 1; Length 29; Best Local Similarity 89.3%; Pred. No. 8.2e+02; Matches 25; Conservative 0; Mismatches 3; Indels
                         Indels
89.3%; Pred. No. 8.2e+02;
iive 0; Mismatches 3
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ik98h02.g1 Ginkgo male leaf (NYBG)
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/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xrefe"taxon:3311"
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Best Local Similarity 89.3
Matches 25; Conservative
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 29)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yoogin, KyeongQi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HD--03-H09 gl OsHDACl-overexpressing transgenic rice plasmid CDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--03-H09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                         EcoRI;
Pamela
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|mol_type="mRNA"
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/lab_host="SURE"
/clone_lib="Normal Human Trabecular Bone Cells"
/note="Organ: Hip; Vector: pBluescript; Site_1:
Library Constructed by Dr. Marian Young and Dr.
Gehron Robey (NIDCR)"
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    Location/Qualifiers
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Pred. No. 8.1e+02;
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                                                                                                                                               /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="NHTBCae16e07"
/sex="Female"
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/clone="HD--03-H09"
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                                                                                                 Location/Qualifiers
Tel: 301-402-4877
Fax: 301-496-7157
Email: libin@helix.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CF314795.1 GI:33686556
                                                                          Seg primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 line."
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

LOCUS

CF314795/c RESULT 999

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Gaps

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Query Match

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FEATURES

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Bos taurus (cattle)
Bos taurus
                                                                            Contact: Mitreva M
                                                    Unpublished (2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Meloidogyne incognita
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.
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                                                                                                                                                                                       SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Mitreva,M., McCarter,J.P., Pape,D., Martin,J., Wylie,T.,
Clifton,S., Budiman,A., Lakey,N., Opperman,C. and Bird,D.McK.
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MIAA-5K22b.b1 Meloidogyne incognita BAC end sequence library (MIAAGSS 001) Meloidogyne incognita genomic, genomic survey
                                                                                                                                                                                     Biomedical Polymers Research Bldg., 20 S. 2030 E.,
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="UUGC2M0103F17"
                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
Email: ddun@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0103 row: F column: 17
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Location/Qualifiers
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                                                                                          Unpublished (2000)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

1 (Dases 1 to 23)
Anderson, S. I., Finlayson, H.A. and Archibald, A.L.
Development of CDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin Institute
Roslin Midlothian, Hazs 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
vo.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(5K+) R. Sitel: EcoRI
R. Site2: Smal 5' Seq Primer T3 Normalised library constructed from
bovine ovary. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:6306"
|/db_wrege="L2"
|/clone llb="Meloidogyne incognita BAC end sequence library (MIAAGSS 001)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII; ABC library constructed by Arief Budiman and Nathan Lakey at Orion Genomics, and David Bird and Charles Opperman at Center for the Biology of Nematode Parasitism at NCSU."
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/db xref="taxon:9913"
/clone="KN261-055_007"
/tisque type="vary"
/clone lib="KN261"
/note="Vector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2:
Survey sequences from the parasitic nematode Meloidogyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                      BAC ends sequenced by Washington University Genome Sequencing
                                                                                                                                                                                              USA
                                                                                                                        Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
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1. 29
7. Corganism="Meloidogyne incognita"
/mol_type="genomic DNA"
/strain="Race 1"
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                                                                                                                                                                                                                                                                                        Email: nematode@watson.wustl.edu
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Location/Qualifiers
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Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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Hopwood, P.A., Zhang, F., Lowden, S., Talbot, R., Burt, D., Archibald, A.
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Schistosoma mansoni
Substosoma mansoni
Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeldida; Schistosomatoidea; Schistosoma.
Strigeldida; Schistosomatoidea; Schistosoma.
I (bases 1 to 23)
Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S.,
Nikolaiddou-Katsaridou, N., Quall, M.A., Wilson, R.A. and Ivens, A.C.
Microarray analysis identifies genes preferentially expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Development of a porcine cDNA microarray
Unpublished (2004)
Contact: Hopwood PA
Dept. of Preclinical Veterinary Sciences
Royal School for Veterinary Studies
Summerhall, Edinburgh, EH9 1QH, UNITED KINGDOM
Sequencing was performed by ARK genomics. This clone is available from ARK- Genomics, Rosin Institute, Roslin, Midlothian EH25 9PS, UK. See www.ark- genomics.org or contact info@arkgenomics.org.
                                                                                                                                                                                                                                                 AJ74297 reverse - unstimulated minus stimulated macrophage Sus AJ747297 ACCOPACE - unstimulated minus stimulated macrophage Sus AJ747297
                                                                                                Gaps
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/cell_type="macrophage"
/clone_lib="reverse - unstimulated minus stimulated
macrophage"
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Smal, Single pass sequencing. Normalised library constructed from bovine ovary."
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100.0%; Pred. No. 7.6e+02;
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Matches 23; Conservative 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9823"
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Mammalia; Eutheria;
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Sus scrofa
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23 bp mRNA linear EST 14-AUG-2003 14FTL--05-H12.gl Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-H12, CF279238
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Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S., Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C. Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni
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                                                                                                                                                                                                                                                                  /clone="SmlC30h01.q1k"
/dev stage="lung schistcsomulum"
/clone lib="Schistcsoma mansoni lung schistcsomulum"
/note="country: Puerto Rico"
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/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AM047142 Schistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA clone SmlC26b06.qlk, mRNA sequence.
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the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
Contact: Ivens AC
Pathogen Microarrays Group
Wallcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
                                                                                                                                                                                                                                                                                                                                                                                       0.8%; Score 23; DB 1; Le
100.0%; Pred. No. 7.6e+02;
tive 0; Mismatches 0;
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/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
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Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 18A, UNITED KINGDOM.
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AM047142.1 GI:72293133
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                                                                 Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza.
1 (bases 1 to 23)
Kim.J.S., Jun.K.M., Cheong, P.J., Kim.M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim.J.K., Xim.Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                       Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggblo.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Yengin, Kyeonggi, Korea
Fax: 82 31 32 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
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100.0%; Pred. No. 7.6e+02;
Mismatches 0;
                                             Oryza sativa (japonica cultivar-group)
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/organism="Oryza sativa (japonica cultivar-group)"

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CF310501

23 bp mRNA linear EST 15-AUG-2003
ABF--05-C24.gl ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-C24, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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/dev_stage="7 days after germination"
/lab_host="R.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: ECORI; mRNA was capped with oligoribonuclectides and Then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Nahm B.H. Genemics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bloinformatics, MyongJi University
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/lab_bost="E.coli DH10B"
/clone lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
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/organism="Oryza sativa (japonica cultivar-group)"

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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Unpublished (2003)
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Pred. No. 7.6e+02;
0; Mismatches 0;
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/cultivar="Nackdong"
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/clone="ABF--05-C24"
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100.0%; Pre
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Mighlantae; Streptophyta; Embryophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

El (Bases i Lo 23)

El (Bases i Lo 23)

El (Masses i Lo 23)

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El (Masses i Lo 23)

Contact: Nam, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

YongIn, KyeongGi, Korea

Tel: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="callus"
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/dev stage="proliferated"
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                                                                    EST 15-AUG-2003
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                           L. J. J. J. L. D. OSHDACL-OVERSHIPS Innear EST 15-AUG-200 HD--09-K06.b1 OSHDACL-OVERSHIPS transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD-09-K06, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCR4-TOPO; Site_1: EcoR1; Callus was treated with ABA(10um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
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CF319212.1 GI:33690973
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Matches 23; Conservative
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CF319212/c
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
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/clone_lib="Callus"
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xhoɪ; cDNA was inserted into lambda Uni-zAP XR vector at
5' end with EcoRI and 3' end with Xhoɪ site. mRNA was
derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xrefer_taxon:33947"
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/lab_host="E_coli DH10B"
/clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida; Poales, Poaceae, BEP clade, Ehrhartoideae, Oryzeae, Oryza
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Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongGi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhaahm@pio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF329042 23 bp mRNA linear EST 18-AUG-NACL--04-D14.gl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-D14, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                               /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%; Score 23; DB 1; Le Similarity 100.0%; Pred. No. 7.6e+02; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF329042.1 GI:33806320
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RESULT 1013

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DEFINITION

KEYWORDS SOURCE ORGANISM

ACCESSION

VERSION

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

FEATURES

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/clone="B3CS00RL006F03"
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SfilA; Site_2: SfilB; Oriented library"
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, Vitacaeae, Vitis.

1 (bases 1 to 23)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vitis vinifers

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

1 (bases 1 to 23)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Handi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
                                                                                                                                                                                                                                                     Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.8%; Score 23; DB 1; Length 23; Best Local Similarity 100.0%; Pred. No. 7.6e+02; Matches 23; Conservative 0; Mismatches 0; Indels
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/organism="Vitis vinifera"
/mol type="mRNA"
/cultivar="Cabernet Sauvignon"
                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seg primer: T7
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Location/Qualifiers
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantes, Streptcophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae, Oryzae.

1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Xim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yogin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                         CF334657

JMT--04-Al4.gl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
                                                                                                        Gaps
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                                                      Length 23;
                                              Query Match
0.8%; Score 23; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0;
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CF334657
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Vitis vinifera
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 1014

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Surgaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

E. I (bases 1 to 23)

Salia, N.N.,
O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Benfey, P., Coruzzi, G. and Stevenson, D.
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory,
Po Box 100, Cold Spring Harbor Laboratory,
Tel: 516 367 8884
Fax: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cehl.org
Seq primer: -21M13UnivRev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="Cerebellum"
/dev_stage="3 month old normal canine"
/lab_host="XLIO Gold"
/lab_host="XLIO Gold"
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BEORI; Site 2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Mark Haskins VMD; Phb, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR063413 23 bp mRNA linear EST 06-JUN-2005 ip65809.gl Ginkgo megasporophyll (NYBG) Ginkgo biloba cDNA 3', mRNA
                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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Balija,V., Nascimento,L.U. and McCombie,W.R.
Britan Canis familiaris cerebellum (dog)
Unpublished (2004)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
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Pred. No. 7.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Canis familiaris"
/mol type="mRNA"
/db_xref="taxon:9615"
/esz="Unknown"
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100.0%; Pred. No. ...
0; Mismatches
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Ginkgo biloba
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mccombie@cshl.org.
Location/Qualifiers
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DR063413.1 GI:66986981
                                               CX004980.1 GI:56276396
                                                                                        Canis familiaris (dog)
Canis familiaris
mRNA sequence.
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Eukaryota; Parabasalidea; Trichomonada; Trichomonadida;
Trichomonadidae; Trichomonadinae; Trichomonasidae;
1 (bases 1 to 21)
2hou, Y., Shu, W.M., Huang, S.C.C., Huang, K.Y. and Tang, P.
Analysis of Gene Expression Profile in Trichomonas vaginalis by EST
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TvEST077D06 Tv30236_PT cDNA Library Trichomonas vaginalis cDNA 5',
                    /mol_type="mana"
/mol_type="mana"
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/duxref="taxon:29760"
/clone="BatGSSTRB007H08"
/clone="BatGSSTRB007H08"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_l: SfilA; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    // Organism="Trichomonas vaginalis"
/organism="Trichomonas vaginalis"
/mol_type="mRNA"
/dob xref="texon:5722"
/dev stage="Trophozoites at mid-log phase"
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/lab_host="Xil Blue-MRF"
/loof=ib="Trichomonas Pr cDNA Library"
/clone lib="Trichomonas Pr cDNA Library"
/note="Vector: Lambda ZAP-Express (Stratagene); Site_1:
ECORI; Site_2: Xhol"
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Molecular Regulation and Bioinformatics Laboratory, College of
                                                                                                                                                                                                                                                                                             Gaps
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259 Wenhwa 1st. Road, Kweishan, Taoyuan 333, Taiwan
Tel: +886 3 3283016 EXT5136
Fax: +886 3 3283031
                                                                                                                                                                                                                                          Query Match 0.8%; Score 23; DB 1; Length 23; Best Local Similarity 100.0%; Pred. No. 7.6e+02; Matches 23; Conservative 0; Mismatches 0; Indels
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llarity 100.0%; Pred. No. 7.6e+02;
Conservative 0; Mismatches 0;
  organism="Vitis vinifera"
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PCR PRimers
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Location/Qualifiers
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RESULT 1016

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E (bases I to 23)

E (cases I to 24)

E (contain, D. Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie

Lot Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8894

Email: mccombie@cshl.org
                                                                                     /mol_trye="mins" | /mol_trye="mi
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/note="Organ: leaf; Vector: :pBK-CMV; Site_1: Xhol;
Site_2: Eco RI; Stratagene ZAP Express CDNA Synthesis
The library was size-fractionated to enrich for large
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100.0%; Pred. No. 7.6e+02;
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                                                                  'organism="Ginkgo biloba"
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Ginkgo biloba
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   Location/Qualifiers
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Location/Qualifiers
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JOURNAL
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AUTHORS
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Ginkgo biloba

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

1 (Dases 1 to 23)

Brenner, E. D., Twigg, R. W., Runko, S. J., Katari, M. S., Dedhia, N. N.,

O'Shaughnessy, A. L., Balija, V., Martienssen, R. A., McCombie, R. W.,

Banfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 10 2020 8874
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Ginkgo biloba

Ginkgo biloba

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Ginkgophyta; Ginkgoaceae; Ginkgo.

E 1 (bases 1 to 23)

Sarenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,

O'Shaughnessy, A.L., Balija, W., Martienssen, R.A., McCombie, R.W.,

Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo male leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie

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PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8884

Email: mccombie@cshl.org

Seq primer: -21M3Uuivieso.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gex="female" Clone lib="dinkgo female leaf (NYBG)" Clone lib="dinkgo female leaf (NYBG)" /note="Organ: leaf; Vector: :pBK-CMV; Sire 1: XhoI; Site 2: Eco RI: Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DR074008 23 bp mRNA linear EST 08-JUN-2005 ik92a08.gl Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
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/db_xref="taxon:3311"
                                                                    Ginkgo biloba (maidenhair tree)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mccombie@cshl.org
Seg primer: -21M13UnivRev.
DR073135.1 GI:67050986
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DR074008.1 GI:67051937
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murcidea; Murinae; Mus.

1. (Lases I to 23)

2. I (Lases I to 23)

2. Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

2. Unpublished (2000)

3. Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah Genome Center
/sex="male"
/clone_lib="Ginkgo male leaf (NYBG)"
/clone_lib="Ginkgo male leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site_l: XhoI; Site_2:
Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large
inserts."
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1M0013G08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Moustant by plasmid UUGCIM library"
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musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
Laboratory Mouse DNA Resource
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                                                                                                                                                                                 tch 0.8%; Score 23; DB 1; Length 23; al Similarity 100.0%; Pred. No. 7.6e+02; 23; Conservative 0; Mismatches 0; Indels
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert Length: 10000 Std Error:
Plate: 0013 row: G column: 08
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 23.
Location/Qualifiers
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84112, US
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Best Local
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Wector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                  AZ309851 29-SEP-2000 1M0017L12F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0017L12 F, genomic survey sequence.
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inducible derivative of plasmid R1. The vector was ligated
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Pred. No. 7.6e+02;
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23; Conservative 0; Mismatches
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Insert Length: 10000 Std Error:
Plate: 0017 row: L column: 12
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
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Location/Qualifiers
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                                                                                                                                                       0.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: plasmid ends
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Fax: 801 585 7177
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84112, USA
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KEYWORDS
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli K110-GGld (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ312314 23 bp DNA linear GSS 29-SEP-2000 1M0028006F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0028006 F, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 23)

Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC1M0028006"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The
Mas hydrodynamically sheared by repeated passage through a
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., UT
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., UT
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Rm. 301 SS 5406
Fax: 801 SS 5406
Fax: 801 SS 5406
Fax: Boll SS 7177
Email: ddunn@genetics.utah.edu
Insert Lengul. 10000 Std Brror: 0.00
Plate: 0030 row: A column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0030A02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0030A02 R, genomic survey sequence.
AZ313922
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Eukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
Lases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Miderhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                Length 23;
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/organism="Mus musculus"
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/Bab.maie...
/Jab hoste.me. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/documents/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
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E 1 (bases 1 to 23)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokkes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R. Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R. Understand inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels
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Fax: 801 585 717.
Fax: 801 585 717.
Fax: 802 585 717.
Insert Length: 10000 Std Error: 0
Plate: 0.089 row: D column: 19
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0089D19"
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GSS.
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84112, USA
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TITLE

COMMENT

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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi | 4732114 | gb | AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 23)
Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Niederhausern, A. and Wright, D., Weiss, R.

Unpublished (2000)
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1M0099C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic CODE UUGC1M0099C23 F, genomic survey sequence.
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Pred. No. 7.6e+02;
); Mismatches 0;
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Insert.bength: 10000 Std Error:
Plate: 0099 row: C column: 23
Seg primer: CGTTGTAAAACGACGGCCAGT
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Mus musculus
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Best Local Similarity 100.0%; Pr
Matches 23; Conservative 0;
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Fax: 801 585 7177
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptore vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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23 bp DNA linear GSS 03-OCT-200
1M0195H07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0195H07 R, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
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/note="Twetcor: PWD42nv; Purified genomic DNA from M.musculus C57BL/60 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                                                                                                                                                                                 Length 23;
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                                                                                                                                                                                           0.8%; Score 23; DB 1; Le
100.0%; Pred. No. 7.6e+02;
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1411: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                   Mismatches
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/mol_type="genomic DNA"
fstrain="CS7BL/6"
/db_xref="taxon:10090"
/clone="UUGCIM0195H07"
/sex="Male"
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University of Utah Genome Center
University of Utah
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100.0%; Prec
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Mus musculus
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Best Local Similarity
Matches 23; Conserv
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84112, US
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0267D05F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0267D05 F, genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Murcidea; Muridae; Muriaes; Musiae; Mus.
1 (bases 1 to 23)
1 (bases 2 to 23)
1 (bases 2
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 1000

Rm. biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, 84112, USA
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Fax: 801 585 7177
Email: ddunnegenetics.utah.edu
blatt.Length: 10000 Std Error: 0.00
Plate: 0267 row: D column: 05
Seq primer: CGTTGTAAAACGACGGCCAGT

    .23
    /organism="Mus musculus"

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/strain="C57BL/6J"
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High quality sequence stop: 23.
Location/Qualifiers
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AZ461220.1 GI:10619345
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Best Local &
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plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X11.0-GOld (Stratagene) cells and selected for ampicillin resistance."
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1M0275K12F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0275K12 F, genomic survey sequence.
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Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Rax: 801 585 717
Rax: 801 585 717
Raz: 801 585 717
Insert Length: 10000 Std Error: 0
Plate: 0275 row: K column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0275K12"
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AUTHORS
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TITLE

COMMENT

FEATURES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 23)

2 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Reilly,M., Rose,M., Stockes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Unpublished (2000)

L Unpublished (2000)

L Contact: Robert B. Weiss
University of Utah Genome Center
inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-GGJd (Stratagene) cells and selected for ampicillin resistance."
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1M0306E11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0306E11 F, genomic survey sequence.
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Insært Length: 10000 Std Error:
Plate: 0306 row: E column: 11
Seg primer: CGTFGTAAAACGACGCCAGT
Class: plasmid ends
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/strain="C57BL/63"
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                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 23; Conservative
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Fax: 801 585 7177
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84112, US
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for amplicillin resistance."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wetcor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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Pred. No. 7.6e+02;
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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Best Local Similarity 100.0%; Pr
Matches 23; Conservative 0;
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Plate: 0396 row: O
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Fax: 801 585 7177
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COMMENT

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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-GGld (Stratagene) cells and selected for ampicillin resistance."
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1M0405C07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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/clome_lib="Mouse_10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic_DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0405 row: C column: 07
Seq primer: CGTYGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
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/organism="Mus musculus"
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/clone="UUGC1M0405C07"
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Best Local S:
Matches 23,
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0436N07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic CORE UUGCIM0436N07 F, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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                                                                                                                                                                                                  0.8%; Score 23; DB 1; Length 23; 100.0%; Pred. No. 7.6e+02; ive 0; Mismatches 0; Indels
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Fax: 801 585 7177
Fax: 801 585 7177
Fax: 802 585 7177
Insert Length: 10000 Std Error: 0
Plate: 0435 row: N column: 07
Seg primer: CGTTGTAAAACGACGCCCAGT
Class: plasmid ends
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Best Local Similarity 100.0
Matches 23; Conservative
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84112, USA
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/clone lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
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E 1 (bases 1 to 23)
S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacres,S., Mahmoud,M., Menen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Strokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-GOld (Stratagene) cells and selected for ampicillin resistance."
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Pred. No. 7.6e+02;
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100.0%; Pred. No. '...
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Insert Length: 10000 Std Error:
Plate: 0514 row: E column: 09
Seg primer: CGTYCTAAAACGACGGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0514E09"
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Location/Qualifiers
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Fax: 801 585 7177
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84112, USA
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli K110-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Pred. No. 7.6e+02;
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Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: D column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0529D03"
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Fax: 801 585 7177
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Best Local Similarity
Matches 23; Conserv
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (Jocuments/Anares/). The DNA
was hydrodynamically sheared by repeated passage through a
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0.005 inch orifice at constant velocity. The sheared DNA
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adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
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E (bases) 1 to 23)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

L Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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100.0%; Pred. No. 7.6e+02;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0014 row: O column: 08
Seq primer: CGTGTAAAACGACGCCAGT
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Elemanyota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bummalla, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognachi, Murcidea, Murinae, Mus.

Sciurognachi, Murcidea, Muridae, Mus.

El (Bases I to 23)

El (Bases I to 23)

El (Bases I to 23)

Balam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Noterhausern, A. and Wright, D. Wasse, R., Tingey, A., von Niederhausern, A. and Wright, D. Wasse, R., Tingey, A., von Niederhausern, A. and Wright, D. Wasse, R., Tingey, A., von University

L Ontuck: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X1.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0033C07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0033C07 F, genomic survey sequence.
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0033 row: C column: 07
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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clone="UUGC2M0033C07"
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Best Local Similarity
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FEATURES

REFERENCE AUTHORS

TITLE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Eutheria; Burarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

E. 1 (Dases 1 to 23)
S. Dum, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Unpublished (2000)
L. Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-GGJd (Stratagene) cells and selected for ampicillin resistance."
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2M0045K24F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0045K24 F, genomic survey sequence.
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/clone lib="Mouse lokb plasmid UUGCIM library."
/note="Vector: PWD42nr; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 7.6e+02;
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Plate: 0045 row: K column: 24
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/63"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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AZ792751.1 GI:12937005
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Best Local Similarity 100.
Matches 23; Conservative
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84112, US
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0165B14F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0165B14 F, genomic survey sequence.
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1 (bases 1 to 2)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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84112, USA
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                                                                                                                                                                                   0.8%; Score 23; DB 1; Length 23; 100.0%; Pred. No. 7.6e+02; rative 0; Mismatches 0; Indels
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// gtrain="C57BL/6J"

/db.xref="taxon:10090"

/clone="UUGC2M0165B14"

/sex="Male"
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Plate: 0165 row: B
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Fax: 801 585 7177
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AZ859570
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ORGANISM
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KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Murinae; Mus.

E (bases 1 to 23)

Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stockes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Meuuse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated by season from the constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0198107R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0198 row: I column: 07
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Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
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/strain="C57BL/6J"
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/clone="UUGC2M0198I07"
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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/lab host="B. coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria; Euarchontoglires, Glires, Rodentia, Sciurognathi, Murcidea, Muridae, Murinae, Mus.

1 (Joses 1 to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Resilly, M., Rose, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Waiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH000534 27-APR-200 2M028BB03R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M028BB03 R, genomic survey sequence.
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.0
Plate: 0288 row: B column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC2M0288B03"
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84112, US/
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BH000534/c
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Exastica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

I (bases I to 23)

Rang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,

Rang, T.J., Kwon, S.J., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,

Hahn, J. H. and Park, B.S.

End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

In Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1672

Fax: +82-31-299-1672
            with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
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/clome_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
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forganism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/culTivar="Chiifu"

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100.0%; Pred. No. 7.6e+02;
ative 0; Mismatches 0;
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/db_xref="taxon:51351"
/clone="KBrS006B23"
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Class: BAC ends.
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Brassica rapa subsp. pekinensis
Brassica, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids, eurosids II, Brassicales, Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="ground the sump; perimensis
/mol_type="ground the"
/sub_species="perimensis"
/sub_aref="taxon:51351"
/lab_host="Resolishis"
/clone="kBs:051 Bhi0B"
/clone="bector: pCUGIBAC1; Site_1: Sau3A1; Brassica rapa
/note="Vector: pCUGIBAC1; Site_1: Sau3A1; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
KBrS013E12R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS013E12, genomic survey sequence.
DUB34017
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Contact: Beom-Seok Park
Brassica Genomics Team
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100.0%; Pred. No. 7.6e+02;
ative 0; Mismatches 0;
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Class: BAC ends.
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DX071679.1 GI:84765975
                                                             DU834017.1 GI:83870613
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Unicity Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 18A, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TRED927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution of trypanosoma brucei (TRED927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@cligr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB081H24"
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/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TA151C02Q 23 bp DNA linear GSS 13-DEC-2000 T. brucei sheared genomic DNA clone 151c02, reverse sequence, genomic survey sequence.
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      225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1670
Fax: +82-30-20-1672
Bad 1: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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1 (bases 1 to 23)
Hall,N., Bownan,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Direct Submission
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                   1. .23
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiffu"
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National Institute of Agricultural Biotechnology
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="151c02"
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Class: BAC ends.
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AZ786257
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Rall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project. Sanger Center, The Wellcome Trust Genome Campus, Hinxton,

Cambridge Callo 1SA, E-mail: barrell@sanger.ac.uk and

nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA, isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayedetigr.org

petails of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.
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                                                                                                                                                                                                                           TA274B03P 23 bp DNA linear GSS 13-DEC-2000 T. brucei sheared genomic DNA clone 274b03, forward sequence,
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Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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1 (bases 1 to 23)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
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100.0%; Pred. No. 7.6e+02;
tive 0; Mismatches 0; Indels
  DB 1; Length 23; 7.6e+02;
                               0; Indels
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/clone="274b03"
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AL494456.1 GI:11870913
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GSS.
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Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTAt 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
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2M0031H11R Mouse 10kb plasmid UUGCIM library Mus musculus genomic close UUGC2M0031H11 R, genomic survey sequence.
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
Location/Qualifiers
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Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
I (basea I to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weise,R.
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100.0%; Pred. No. 7.6e+02;
ative 0; Mismatches 0; Indels
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/organism="Trypanosoma brucei"
/mol type="genomic DNA"
/strain="TREU927"
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Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CACAGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Best Local Similarity 100.0
Matches 23; Conservative
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Rm. 308, Bj
84112, USA
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                                                                                                                                                                                                        원
                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil47321141gb]AR12977.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xili0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhatroideae; Oryzeae; Oryza.

1 (bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-gcale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, KyeongGi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                             /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:39947"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                                                                          'lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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/mol_type="mRNA"
/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.8%; Score 23; DB 1; Length 24; 100.0%; Pred. No. 7.7e+02;
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                                                                                                                                                                                Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Preα. αν..
tive 0; Mismatches
/db_xref="taxon:10090"
/clone="UUGC2M0031H11"
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                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.8%
Best Local Similarity 100.0
Matches 23; Conservative
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CF301712
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DEFINITION
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COMMENT
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polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ386891 25 bp DNA linear GSS 02-OCT-2000 1M0146A08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (basea 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Niederhausern,A. and Wright,D., Weiss,R., Tingey,A., von
Niederhausern,A. and wright,D., Weiss,R.
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and Then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                          Query Match 0.8%; Score 23; DB 1; Length 25; Best Local Similarity 100.0%; Pred. No. 7.9e+02; Matches 23; Conservative 0; Mismatches 0; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0146 row: A column: 08
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0146A08"
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Location/Qualifiers
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AZ386891.1 GI:10500591
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Unpublished (2000)
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/lab host="E. Coli strain X110-Gold, T1-resistant, F-"
/lab host="E. Coli strain X110-Gold, T1-resistant, F-"
/clone lib="Wouse l0kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (Jocuments/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
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adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglines; Glires; Rodentia;
Sciuropathi; Murcidea; Muridae; Musinae; Mus.

1 (bases 1 to 25)
10 (bases 1 to 25)
11 (bases 1 to 25)
12 (bases 1 to 26)
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Pred. No. 7.9e+02;
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Insert Length: 10000 Std Error: 0.00
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/mol type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC2M0113M21"
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University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Fax: 801 585 7177
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84112, USA
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COMMENT

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26 bp mRNA linear EST 06-DEC-2002 CDNA clone 024-006-E10-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris BQ583199 GDNA clone 024-006-E10 5-PRIME, mRNA sequence.
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/orde="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
/orde="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
/orde="Vector: pcm sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
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(aryophyllates; Amaranthaceae; Beta.

(bryophylates; Amaranthaceae; Beta.

(caryophyllates; Amaranthaceae; Beta.

(bryophylates; Maranthaceae; Beta.

(caryophylates; Maranthaceae; Beta.

(caryophylates; Maranthaceae; Beta.

(caryophylates; Maranthaceae; Maranthaceae; Steinfath, M., Menze, M., O'Brien, J., Lehrach, H. and Radelof; Jungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof; Jungomylates; Maranthaceae; Construction of a 'uniqene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant, J. 32 (5), 845-857 (2002)
adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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    26
        /organis="Beta vulgaris"
/mol type="mRNA"
/culTivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                             Gaps
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 26 Std Brror: 0.00
Plate: 6 row: E column: 10
Seq primer: SP6; CATAGATTAGGTGACACTATAG.
                                                                                                      Query Match 0.8%; Score 23; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 23; Conservative 0; Mismatches 0;
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/db_xref="taxon:161934"
/clone="024-06-EID"
/lisue_type="inflorescence"
/lab_host="EMDH10B"
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Beta vulgaris
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RESULT 1054 R26779/c

DEFINITION

SOURCE

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

ACCESSION VERSION KEYWORDS

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Wilson, R.

The WashU-Merck EST Project
Unpublished (1955)
Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.watl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, Linn.
This clone is available rolly free through Linn.; contact the IMAGE Consortium (info@image.linl.gov) for further information.
Trace considered overall poor quality
Seq primer: mil-40 forward
High quality sequence stop: 1.

Liocation/Qualifiers
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yw86h10.s1 Soares placenta 8to9weeks 2NbHP8to9W Homo sapiens cDNA
clone IMAGE:259171 3' similar to gb:X64559 TETRANECTIN PRECURSOR
                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                        Hominidee, Homo.

1 (bases 1 to 27)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.8%; Score 23; DB 1; Length 27; 100.0%; Pred. No. 8.2e+02; ive 0; Mismatches 0; Indels
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                                                                HUMAN);, mRNA sequence.
                                                                                                      N29432.1 GI:1147952
                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N34459.1 GI:1155601
EST.
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Matches 23, Conservative
                                                                                                                                                                                                                                   Homo sapiens
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   DEFINITION
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                                                                                                  ACCESSION
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RY
WashU-March EST Project
Contact: Wilson RY
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Email: estGwatson wustl.edu
Insert Size: 1384
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@miage.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1384
Insert Length: 1384
Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 1.
                                                                                                                             EST 24-APR-1995
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae, Homo.

1 (bases 1 to 26)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                76 pp mRNA linear BST 24-yh44f06.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:132611 3' similar to gb:M85164 SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1A (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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8e+02;
hes 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .26
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:53823"
/db_xxef="taxon:9606"
/clone="IMAGE:132611"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 bp
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Homo sapiens
                                                                                                                                                                                                                                                                                          R26779.1 GI:782914
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source

FEATURES

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Gaps ö

23

ð a RESULT 1055 N29432/c LOCUS

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Nene, V., O'Neil, S., Price, C., Quail, M.A., Rabbinowitsch, E., Rawlings, N.D., Rutter, S., Saunders, D., Seeger, K., Shah, T., Squares, S., Tivey, A., Walker, A.R., Woodward, J., Dobbelaere, D.A.E., Langsley, G., Rajandraam, M.-A., McKeever, D., Shiels, B., Tait, A., Barrell, B. and Hall, N.

The genome of the host-cell transforming parasite Theileria annulate and a comparison with T. parva
annulate and a comparison with T. parva
The Pathogen Sequencing Unit
The Pathogen Sequencing Unit
The Wellcome Trust Sanger Institute
Genome Campus, CB10 15A, UNITED KINODOM
Piroplasm CDNA library: Frank Katzer and Brian Shiels, Division of Veterinary Infection and Immunity, ICM, University of Glasgow, UK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
I (bases I to 28)
Yang, T.J. Kwon, S.J. Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Bnd sequence of Brassica rapa BamHI (KBrB) BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DX072773 28 bp DNA linear GSS 10-JAN-;
KBrB082023F KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB082023, genomic survey
sequence.
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/organism="Brassica rapa subsp. pekinensis"
/organism="Genomic DNA"
/cultivar="Chifu"
/sub species="pekinensis"
/db_xref="taxon:51351"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="Theileria annulata piroplasm"
/note="country: Turkey:Ankara"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodum-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23; DB 1; Le
Pred. No. 8.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                              organism="Theileria annulata"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:5874"
/clone="TAC20908_g1ka"
/dev_stage="piroplasm"
/lab_host="Bos taurus (cow)"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/isolate="Ankara (clone D7)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.8%; Score 23; DB
Best Local Similarity 100.0%; Pred. No. 8.3
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Class: BAC ends.
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DX072773
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stops: 16 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theileria annulata
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                      Hominidae; Homo.

1 (bases I to 27)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                       Chordata; Craniata; Vertebrata; Euteleo
Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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Pred. No. 8.2e+02;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="GDB:3880756"
/db_xref="taxon:9606"
/clone="IMAGE:271114"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer: m13 -40 forward
High quality sequence stop: 16.
Location/Qualifiers
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AJ922998
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                                                                                                                                                                                                                                                              The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AJ922998.1 GI:67493340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
                                       Eukaryota, Metazoa,
Mammalia, Eutheria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Theileria annulata
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                                                                                                                                                                                                                                            Wilson, R
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Best Local Simi
Matches 23;
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Bource

FEATURES

LOCUS DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

RESULT 1057

AJ922998/c

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Gaps

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GSS 10-JAN-2006

est.res

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Email: cobellis@tigem.it
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CW020478/c
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DEFINITION
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ORGANISM
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PUBMED
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|/organism="Sus scrofa"
|/mol_type="mRNa"
|/db_xref="taxon:9823"
|/db_xref="taxon:9823"
|/db_xref="taxon:9823"
|/db_xref="taxon:9823"
|/db_xref="toxon:9823"
|/db_xref="toxon:98
                     /lab_host="E.coli DH10B"
/clone lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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BX563414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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Adelson, D.L. and Gill, C.A.

Porcine ESTS
Unpublished (2002)
Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
                                                                                                                                                                                                                                                                    Gaps
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LQG602768282.R1 CSEQFXL36 fetal brain Sus scrofa cDNA, mRNA
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Fax: 9798456970
Email: david.adelson@tamu.edu.
Location/Qualifiers
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Glossina morsitans morsitans
/clone="KBrB082023"
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Matches 24; Conserv
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Best Local 9
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BM658913/c
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Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CBIO 15A, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor Lis7 2UW
All clones with suffix qlc are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="country: Zimbabwe; EST from adult gut infected with
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GCO745 TIGEM gene trap library Mus musculus CDNA clone A015.B4,
mRNA sequence.
CW020478
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                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neopera; Endoperygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidea; Glossinidae; Glossina.

1 (Dases 1 to 26)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, M. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1...26.
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/mol_type="mRNA"
/sub_species="morsitans"
/db xref="taxon 37546"
/clone="Tse66605_plc"
/tissue type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0.8%; Score 22.8; DB 1;
Best Local Similarity 92.3%; Pred. No. 8.2e+02;
Matches 24; Conservative 0; Mismatches 2;
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Glossina morsitans morsitans
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Mus musculus
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Tel: +390816132205
Fax: +390815790919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T.brucei"
                                                                                                                                                                                                                                                                     response genes
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Vaccinium corymbosum
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// dev stage="adult"
// dev stage="adult"
// dev stage="adult"
// done lib="4018 - RescueMu Grid X"
// done lib="adult"
// done lib="adult"
// done lib="adult"
// done lib="adult"
// RescueMu is a 4.9 kb, modifide maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
// Mu elements insert preferentially into transcription
// designed romer information on RescueMu, go to the was
site 'http://www.mutransposon.org/project/RescueMu/'. Grid
X was grown at UCSD in 2003. DNA was extracted from leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CZ908520 2S. 08-AUG-2005 4018003G05.2EL_y1 4018 - RescueMu Grid X Zea mays genomic, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from TIGEM. Annotation information available from TIGEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: walbot@eranford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4018003 row: G column: 05
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/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.8%; Score 22.8; DB 1; Length 26; Best Local Similarity 92.3%; Pred. No. 8.2e+02; Matches 24; Conservative 0; Mismatches 2; Indels
                                                                                                                                                          /organism="Mus musculus"
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/clone="A015.B4"
/sex="male"
/cell_type="Embryonic stem cell"
/clone_lib="E14"
/clone_lib="TIGEM gene trap library"
/note="Vector: pFLIP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
TTE1: 650 723 2221
Fax: 650 725 8221
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                                                                          avallau...
Class: Gene Trap.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burvey sequence.
CZ908520
CZ908520.1 GI:71920521
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Walbot, V.
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Zea mays
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T. brucel sheared genomic DNA clone 327d04, forward sequence, AL497297
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/tissue_type="Flower buds including bud scales"
/dev stage="Mature plants"
/clone_lib="cDNA non acclimated Bluecrop library"
/note="Vector: pBluescript SK-; cDNA clones from Vaccinium corymbosum cv. Bluecrop, RNA for preparation of library was extracted from flower buds collected in the fall from
strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
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NA1103 R cDNA non acclimated Bluecrop library Vaccinium corymbosum cDNA 37, mRNA sequence.

CV091538
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Monitoring gene expression changes during cold acclimation of blueberry (Vaccinium corymbosum L.) using a cDNA microarray Unpublished (2004)
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Bldg 010A, 10300 Baltimore avenue, BARC West, Beltsville,
20705-2350, USA
Tel: 301-504-6654
Fax: 301-504-5653
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                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Vaccinium corymbosum"
/mol_type="mRNA"
/cultivar="Bluecrop"
                                                                                                               0.8%; Score 22.8; DB 1; 92.3%; Pred. No. 8.4e+02; ative 0; Mismatches 2.
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                                                                                                                                                                                                                                                                         1 AAAAATAAAGAAAAAAAAAAAAA 26
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GSS.
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Tue Nov

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Relvillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Mahlingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Mahlingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Mahlingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Direct Submission

Nobmitted (10-DEC-2000) Trypanosoma brucei genome sequencing project. Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA, isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Barrell of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers
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/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
Trypanosoma brucei
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 22.8; DB 1; Length 28;
Pred. No. 8.5e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="TREU927"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:5691"
/clone="327d04"
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Best Local Similarity 92.3%
                                              Irypanosoma.
(bases 1 to 28)
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CF281313
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KEYWORDS
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National Institutes or Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other_ESTs: 2819627.5prime
Contact: Robert Straubberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llhl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center.
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 24
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 24 contiguous distrinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LLCM2 row: B column: 12
High quality Sequence: Stop: 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW247159 24 bp mRNA linear EST 07-JAN-2000
2819627.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819627 3',
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                             /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="NIH MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5;
adaptor: GGCAGARG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
      /tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
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                                                                                                                                                                                                                                                                                                 ch 0.8%; Score 22.4; DB 1; Length 24; l Similarity 95.8%; Pred. No. 8.4e+02; 23; Conservative 0; Mismatches 1; Indels
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/tissue type="small cell carcinoma"
/cell line="MGC3"
/lab_host="DH10B (phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="14ETL--08-F05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 AAAAAAAGAAAAAAAAAAAA 1
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Homo.
1 (bases 1 to 24)
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AW247159
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AW247159/c
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Laboratory Mouse DNA Resource
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                   GSS 03-OCT-2000
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(basea 1 to 24)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Divaniand inserts
Unpublished (2000)
the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                           AZ438069
1M0228A10F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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                                                                                                            Score 22.4; DB 1; Length 24; Pred. No. 8.4e+02;
                                                                                                                                                                   1; Indels
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                   0; Mismatches
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C578L/6J"
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University of Utah Genome Center
University of Utah
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/clone="UUGC1M0228A10"
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Location/Qualifiers
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Plate: 0228 row: A c
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Best Local Similarity 95.8%;
Matches 23; Conservative
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blund or-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMM92 (gil 4732114 |gb| AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone_lib="Mouse_lokb_plasmid_UUGCNM_lbrazy"
/note="Vector: PWD42nv; Purified genomic DNA from M.
muscullus C57BL/6J (male) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah
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                                                                                                                  Length 24;
                                                                                                                                                                           1; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0261 row: E column: 24
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/63"
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/clone="UUGC1M0261E24"
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                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
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AZ458112/c
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AUTHORS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (ggl 4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 24)

1 bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Nouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
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                                                                                                                   Length 24;
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                                                                                                                   Score 22.4; DB 1;
Pred. No. 8.4e+02;
0; Mismatches 1;
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Insert Length: 10000 Std Error: (
Blate: 0429 row: G column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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Location/Qualifiers
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                                                                                                                   0.8%;
                                                                                                                                              Best Local Similarity 95.8
Matches 23; Conservative
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Fax: 801 585 7177
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KEYWORDS
SOURCE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 gbl/AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complamentary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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24 bp DNA linear GSS 13-DEC-2000
1M0454E23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0454E23 F, genomic survey sequence.
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adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Mus maculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (basea 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stockes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                  Length 24;
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                                                                                                               0.8%; Score 22.4; DB 1;
95.8%; Pred. No. 8.4e+02;
tive 0; Mismatches 1;
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Insert Length: 10000 Std Error: 0.00
Plate: 0454 row: E column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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AZ621257.1 GI:11743447
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Unpublished (2000)
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Fax: 801 585 7177
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RESULT 1071

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DU835497/c

DEFINITION

ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

TITLE JOURNAL COMMENT

FEATURES

AUTHORS REFERENCE

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Brassica rapa subsp. pekinensis
Brassica, Vizidiplantas, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

I (bases I to 24)
Syang, T.J.; Kwon, S.J.; Kim, J.A. Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y.; Lim, M.H.; Kim, H.I.; Choi, B.S.; Seol, Y.J.; Park, D.S.;
Brassica Genomics of Brassica rapa BamHI (KBrB) BAC clone
Brassica Genomics Team
National Institute of Agricultural Biotechnology
25 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1670
Bmail: pbeom@rda.go.kr
BmC and sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab host="E.coli DH10B"
/clone lib="KBrB, Brassica rapa BamH1 BAC library"
/note="vector: pCuGIBAC1; Site_1: BamH1; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear EST 30-DEC-1995
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1. (base; Homo.)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
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yw50g06.sl Weizmann Olfactory Epithelium Homo sapiens CDNA clone
IMAGE:255706 3' similar to gb:J05032 ASPARTYL-TRNA SYNTHETASE
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8889549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
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/db_xref="taxon:51351"
/clone="KBrB047B17"
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                           DX045709.1 GI:84740006
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Brassica rapa subsp. pekinensis
Bukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
1 (bases I to 2J)
Yang, T.J. Kwon, S.J. Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pbeom@rda.go.kr
d sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
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/clone lib="KBr5, Brassica rapa Sau3AI BAC library"
/note="Vector: pcUGIBACI; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBr5 BAC) is
avallable at NIAB."
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/mol_type="genomic DNA"
/culTivar="Chiffu"
                                                                                                           Length 24;
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                                                                                                                                                             1; Indels
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seedun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
                                                                                                         Query Match 0.8%; Score 22.4; DB 1; Best Local Similarity 95.8%; Pred. No. 8.4e+02; Matches 23; Conservative 0; Mismatches 1;
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/db_xref="taxon:51351"
/clone="KBrS016M18"
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Class: BAC ends.
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RESULT 1072 DX045709/c LOCUS

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DX082097.1 GI:84776393
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EST (Bloecker, et al.)
Unpublished (1999)
Contact: MIPS
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongln, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                              Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infc@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: and 3-40 forward
High quality sequence stop: 1.
Location/Qualifiers
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ABF--05-J07.gl ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--05-J07, mRNA sequence.
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.8%; Score 22.4; DB 1; Length 25; 95.8%; Pred. No. 8.5e+02; ve 0; Mismatches 1; Indels
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Location/Qualifiers
                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                     /mol type="mXNA"
/db_xref="GDB:3866115"
/db_xref="taxon:9606"
/clone="IMAGE:255706"
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                                                                                                                                                                                                                                                                                                                                                                /sex="Female"
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JAN-2006 KBEB095E02F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB095E02, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL039138 28 bp mRNA linear EST 06-JUL-2004 DKFZp566L164_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566L164, mRNA sequence.
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Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                             /note="Vector: pcR4-TOPO, Site_1: EcoRI; Leaf was dried for Zhrs. Oligo-capped mRNA was reverse transcribed and then used for ERC. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                              /tissue_type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABR9-overexpressing transgenic rice plasmid
cDNA library (ABF)"
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                                                                                                                                                                                                                                                                                                                                             0.8%; Score 22.4; DB 1; Length 27; 95.8%; Pred. No. 8.8e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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/db_xref="taxon:39947"
/clone="ABF--05-J07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2707 CTAAAAAAAAAAAAAAAAAAA 2730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="DKFZp566L164"
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/dev_stage="fetal"
/lab_host="Xl-2blue"
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Location/Qualifiers
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Query Match
Best Local Similarity
Matches 24; Conserv
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.
E 1 (bases 1 to 27)
S Kim,J.S., Jun,K.M., K.M.,Y.K., and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
L Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin; Kyeonggi, Korea
Tel: 82 31 330 6135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7LEAF--01-G09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-G09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E.coli DH10B"
/clone lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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              Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 28)
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M. H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
                                                                                                                                                                                                                                                                                 National Institute of Agricultural Biotechnology
225 Secdun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Exa: +82-31-299-1670
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.8%; Score 22.4; DB 1; Length 28; 95.8%; Pred. No. 8.9e+02;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB095E02"
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Location/Qualifiers
1. .28
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                                                                                                                                                                                                                                                                  Brassica Genomics Team
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Best Local Similarity 95.8
Matches 23; Conservative
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Seq primer: T7
Class: BAC ends
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EST 18-AUG-2003
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/clone="NACL--03-009"
/clone="NACL--03-009"
/drswue_trype="callus"
/lab_host="E.coli DH10B"
/clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: Ecol; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Nahm B.H.
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bioinformatics, MyongJi University
YongIn, KyeongGi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Eax: 92 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee, T.H., Shin, Y.C.,
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    .27
/organism="Oryza sativa (japonica cultivar-group)"

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Pred. No. 9e+02;
0; Mismatches 3; Indels
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Unpublished (2003)
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0; Mismatches
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88.9%; Pred. No. 9e+
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/cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                    0.8%;
88.9%;
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Best Local Similarity 88.9<sup>3</sup>
Matches 24; Conservative
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Query Match
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DEFINITION
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CL654516/c
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TITLE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="leaf"
/dev_stage="14 days after germination"
/dev_stage="14 days after germination"
/dev_stage="15 days after germination"
/dab_nost="E.coli DH108"
/clone lib="ActMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"-overexpressing transgenic rice plasmid
/note="Vector: pCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
pepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
                                       EST 18-AUG-2003
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                                                                                                                                                             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                    J bp mRNA linear EST 18-AUG-20 JMT--02-H05.gl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone CF331719.
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27 bp mRNA linear EST 02-APR
zb23e12.s1 Soares fetal lung NbHL13W Homo sapiens cDNA clone
HMAGE:302926 3' similar to gb.X59066 ATP SYNTHASE ALPHA CHAIN,
MITOCHONDRIAL PRECURSOR (HUMAN);, mRNA sequence.
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1 (bases 1 to 27)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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Pred. No. 9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:39947"
/clone="JMT--02-H05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 TTTTTAAAAAAAAAAAAAAA
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The WashU-Merck EST Project
                                                                                                                             CF333518.1 GI:33815326
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                    Contact: Nahm B.H.
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Best Local Similarity
Matches 24; Conserv
                                                                                                        CF333518
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RESULT 1079
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KEYWORDS
SOURCE
ORGANISM
                    CF333518/c
                                                     DEFINITION
                                                                                                                                                                                  ORGANISM
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DEFINITION
                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
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JOURNAL
COMMENT
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CL654516 100 DNA linear GSS 09-JUL-2004 PRI0120d B08 - PRI0120d.B21 (27) Note: Recurring String Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Unpublished (1995)

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 315 286 1810
Fax: 315 286 1810
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 27)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bmail: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 22.2; DB 1; Length 27; Pred. No. 9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Max-Planck-Institute for Developmental Biology
Spemanustr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2706 ACTABABABABABABABABABABA 2732
                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 AATGCAAAAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                           High quality sequence stop: 8
Location/Qualifiers
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Class: fosmid ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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FEATURES

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Oryza sativa (japonica cultivar-group)

Eukaryota, Viridiplantea; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryzae; Oryzae; Oryzae; Smi, J.S., Jun, K.M., C.K., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF300133 22 bp mRNA linear EST 15-AUG-2003 7LEAF--04-G19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-G19, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Orgia sativa (japonica cultivar-group)
Orgia sativa (japonica cultivar-group)
Orgia sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Wagnoliophyta; Lilioppida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases I to 23)
1 (klame J. C. Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Upubblished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:39947"
/clone="TLEAFO-:39F06"
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/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Wector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yonglin, KyeongJi, Korea
Yenglin, KyeongJi, Korea
Fax: 82 31 33 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/culTivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 100.0%; Score 22; DB 1; Length 22; Similarity 100.0%; Pred. No. 8.5e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     /db xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF300133.1 GI:33671894
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Best Local (
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KEYWORDS
SOURCE
ORGANISM
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                                     ORGANISM
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                                                                                                                                                                                                                 TITLE
JOURNAL
COMMENT
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JOURNAL
COMMENT
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                                                                                                                                                                    AUTHORS
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                                                                                                                                            REFERENCE
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Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 22)
Hopwood, P.A., Zhang, F., Lowden, S., Talbot, R., Burt, D., Archibald, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Hopwood PA

Contact: Hopwood PA

Dept. of Preclinical Veterinary Sciences

Royal School for Veterinary Studies

Summarhall, Edinburgh, EH9 10H, UNITED KINGDOM

Sequencing was performed by ARK genomics. This clone is available from ARK- Genomics, Roslin Institute, Roslin, Midlothian EH25 9PS, UK. See www.ark- genomics.org or contact info@arkgenomics.org.
                                     1...27
/organisms="Pristionchus pacificus"
/organisms="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AJ747407
AJ747407 forward - stimulated minus unstimulated macrophage Sus scrofa cDNA clone F_C0001825b_A06, mRNA sequence.
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Sus scrofa"
/mol type="mRNA"
/db xref="texon:9823"
/cloine="F_C0001825b_A06"
/tissue_type="lung"
/cloine="toype="lung"
/cloine_lib="forward - stimulated minus unstimulated macrophage"
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0
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100.0%; Pred. No. 8.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                   Query Match

0.8%; Score 22.2; DB 1; Length
Best Local Similarity 88.9%; Pred. No. 9e+02;
Matches 24; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Development of a porcine cDNA microarray Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                        2709 AAAAAAAAAAAAAAAAAAAAAAAAA 2735
                                                                                                                                                                                                                                                                                                                                                                                                                            27 AGAAAAAAATAGAAAAAAAAAA 1
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               Location/Qualifiers
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CF299342,1 GI:33671103
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ747407.1 GI:49917653
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa,
Mammalia, Eutheria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Dixon, L.
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VERSION KEYWORDS SOURCE ORGANISM

TITLE

COMMENT

FEATURES

REFERENCE AUTHORS

DEFINITION

AJ747407

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DEFINITION

CF299342/c

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ACCESSION VERSION KEYWORDS

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Gaps

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10:41:28 2006

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Tue Nov

RESULT 1085

ò 요 CF310366/c DEFINITION

ORGANISM

SOURCE

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS JOURNAL COMMENT

TITLE

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CF311269 22 bp mRNA linear EST 15-AUG-2003
ABF--06-G21.gl ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade, Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza,
I (bases 1 to 22)
I (bases 1 to 22)
I (kim,J.S., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Xim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University of Chorin, Kyeongji, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pCR4-TOPO, Site_1: EcoRI, Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
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/lab_bost="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
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ABF--07-B13.gl ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--07-B13, mRNA sequence.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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tive 0; Mismatches
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/clone="ABF--06-G21"
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                                                                                      ABF--06-G21, mRNA sequence.
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CF311269.1 GI:33683030
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Spermatophyta; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 22)
Kim,J.S., Uun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
/clone="7LEAF--04-G19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Nahm B.H.

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Tel: 82 31 330 6193
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Location/Qualifiers
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for 2hrs. Olig-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
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//nol type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                                                                                   0.8%; Score 22; DB 1; Length 22;
100.0%; Pred. No. 8.5e+02;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 8.5e+02;
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                                                                                                                                                                                                                                                                                                                                          2709 AAAAAAAAAAAAAAAAA 2730
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CF310366.1 GI:33682127
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Best Local Similarity luv...
Best 22; Conservative
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Matches 22; Conserv
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/organism="Oryza sativa (japonica cultivar-group)"
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/mol_type="mRNA"
/culfivar="Nackdong"
/db xref="taxon:39947"
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/note="Vector: pCK4-TOPO; Site 1: EcoNI; mRNA was capped
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 bp mRNA linear EST 18-AUG-2003 JMT--02-F04.gl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--02-F04, mRNA sequence.
                                                                                                                                                                                                                                                                                                                  CF330679 22.bJ Rice callus plasmid cDNA linear EST 18-AUG-2003 NACL--06-H22.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--06-H22, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Enrhartoideae; Oryzeae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Yengin, KyeongJi, Korea
Fax: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                             Length 22;
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                                             0.8%; Score 22; DB 1; Le
100.0%; Pred. No. 8.5e+02;
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100.0%; Pred. No. 8.5e+02;
tive 0; Mismatches 0;
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  line."
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CF333430/c
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CF330679/c
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

E (bases 1 to 22)
S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6135
Fax: 82 31 321 6355
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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
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/organism="Oryza sativa (japonica cultivar-group)"

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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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8.5e+02;
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    Location/Qualifiers
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100.0%; Pred. No. 8.5
:ive 0; Mismatches
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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--07-B13"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                  The service of the se
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/clone="JWT--02-F04"
/tiosuse type="leaf"
/dev_stage="14 days after germination"
/lab_host="B.coli DH10B"
/clone lib="AtJMT-overexpressing transgenic rice plasmid
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, YeyongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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/mol type="mRNA"
/cultivar-Nackdong"
/db xref="taxon:39947"
/clone="JMT--04-D05"
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Location/Qualifiers
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0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels
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/cultivar="Nackdong"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

(bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJWT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeongqi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA_library (JMT)"
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/mol_type="mRNA"
/cultivar="Nackdong"
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Location/Qualifiers
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/clone="JMT--06-D20"
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Enrhartoideae; Oryzaa.

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El (bases 1 to 22)

El (kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)

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Genenics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

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Email: bhnahm@ggio.com, bhnahm@bio.myongji.ac.kr.
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22 bp mRNA linear EST 18-AUG-2003
Library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--08-B11, mRNA sequence.
CP337580
CF337580.1 GI:33823547
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta, Bermatcophyta; Papermatcophyta; Papermatcophyta; Dagonica, Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.L., Kim,J.K., Win,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:39947"
/clone="JMT--08=Bl1"
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/dev_stage="lasf"
/dev_stage="lasf"
/lab_host="R.coli_DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA_library (JMT)"
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
YongJi, Kyeonggi, Korea
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|mol_type="mRNA"
|cultivar="Nackdong"
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U.00;

Best Local Similarity 100.0%; Pred. No. 8.5

Conservative 0; Mismatches
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/lab_host="E. coli"
/clone lib="AGS-1"
/clone lib="AGS-1"
/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
P. carinii organisme (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"
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                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2: XhoI; CDNA was inserted into lamda Uni-ZAP KR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"
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                                                                                                                                                                                                                                                                                  /tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
                                                                                                                                                                                                                                                                                                                                                       /clone lib="Regenerated callus lambda phage cDNA library
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                                                                                                                                            'organism="Oryza sativa (japonica cultivar-group)"
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University of Rentucky
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0255, USA
Tel: 606 257 2161
Fax: 606 257 1717
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SEC7 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
AW332181
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Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Entermocystidaceae; Pneumocystis.

1 (bases 1 to 22)
Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Sl
Edman, J.C., Kovacs, J. and Cushion, M.
Expressed sequence tags from Pneumocystis carinii
Umpublished (2000)
Contact: Staben C
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Tel: 82 31 330 6193
Fax: 82 31 321 635
Email: bhrahm@gpbio.com, bhrahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.8%; Score 22; DB 1; Length 22; 100.0%; Pred. No. 9.5e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                 /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--01-P07"
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Location/Qualifiers
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Universite de Bordeaux I, Institut National de la Recherche
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AW332399
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/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
/note="Vector: Lambda ZAP II; Site_1: ThoI; Site_1
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1 (bases 1 to 22)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
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1 (Dases 1 to 22)
Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C., Edman,J.C., Kovacs,J. and Cushion,M.
Baryressed sequence tags from Pneumocystis carinii
Unpublished (2000)
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University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
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UMR 619 - Equipe Biologie de la Vigne
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Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.
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Pneumocystis carinii
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetophyta; Gnetophyta; Gnetaceae; Gnetum.
1 (bases 1 to 22)
S brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., S o'Shaughnessy, A.L., Ballia, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Hazhor Laboratory
PO Box 100, Coll Spring Harbor, NY 11724, USA
Tel: 516 367 8874
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Gnetum gnemon cDNA 3', mRNA
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/note="Organ: mature, unfertilized reproductive strobill;
/note="Torgan: mature, unfertilized reproductive strobill;
Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"
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/cultivar="Cabernet Sauvignon"
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it83g12.g1 Gnetum female cone (NYBG)
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                                                                           Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7
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/db_xref="taxon:3382"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Gnetophyta; Gn
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/rolone="Organ: mature, unfertilized reproductive strobili;
/note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express CDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"
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El (bases 1 to 22)

Expenser, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

Lontact: W. Richard McCombie Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8884
                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="Ginkgo megasporophyll (NYBG)"
/note="Organ: megasporophyll; Vector: pBK-CMV; Site_1:
/note="Organ: megasporophyll; Vector: pBK-CMV; Site_1:
Shol; Site_2: Eco RI; Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts."
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Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cehl.org
Seq primer: -21Ml3UnlyRey.
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/mol_type="mRNA"
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Ginkgo biloba
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/db_xref="taxon:3311"
/sex="Female"
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El (Josses I to 22)

Es to 22)

Estemer, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

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Email: mccombie@cshl.org

Seq primer: -21M13UnivRev.
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E 1 (bases 1 to 22)

Spermatophyta; Ginkgoahva; Ginkgoaceae; Ginkgo.

Spermatophyta; Coruzai, G. and Stevenson, D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

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Contact: W. Richard McCombie

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PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884
                                                                                22 bp mRNA linear EST 08-JUN-2005
ik82h12.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
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//db.xref="texcon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf, Vector: :pBK-CMV; Site_1: Xho1;
Site_2: Eco_R1; Strategene ZAP Express CDNA Synthesis Kit.
The library was size-fractionated to enrich for large
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ik86b01.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
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tive 0; Mismatches 0; Indels
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/organism="Ginkgo biloba"
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Ginkgo biloba

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Cinkgophyta; Ginkgoo.

Eukari, M.S., Dedhia, N.N.,

Enferse; Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie

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Tel: 516 367 8884

Fax: 516 367 8874

Email: mccombie@cshl.org

Seq primer: -2ml3UnivRev.
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/dol_xref="texcon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/clone_lorgan: leaf; Vector: :pBK-CMV; Site 1: Xhol;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
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ik86g07.gl Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
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/db xref="texon:3311"
/db xref="texon:3311"
/db xref="texon:3311"
/esx="female"
/clone lib="Ginkgo female leaf (NYBG)"
/clone lib="Ginkgo female leaf (NYBG)"
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/nce="Organ: leaf; Vector: 19BK-CMV; Site 1: XhoI;
/nce="Organ: leaf; Vector: 2BK-CMV; Site 1: XhoI;
/nce="Organ: leaf; Vector: 19BK-CMV; Site 1: XhoI;
/nce="Organ: leaf; Vector: 19BK-CMV;
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/organism="Ginkgo biloba"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eyerantophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

E (bases 1 to 22)

S Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,

G'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,

Benfey, P., Corizzi, G. and Stevenson, D.

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E 1 (bases 1 to 22)

S Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnesy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.

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L Ontact: W. Richard McCombie

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Fax: 516 367 8874

Email: mccomble@cshl.org

Seq primer: -21M13UnivRev.
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/note="Organ: leaf; Vector: :pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
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ik79e05.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
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100.0%; Pred. No. 8.5e+02;
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/db_xref="taxon:3311"
/sex="female"
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Original 3 prime EST has been
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Matches 22; Conservative
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AZ310066 22 bp DNA linear GSS 29-SEP-2000 1M0018D18R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0018D18 R, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone_lib="Mouse lokb plasmid UUGCNM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                           /clone lib="Ginkgo male leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI; Site
BCo RI; Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large
inserts."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von
plasmid inserts
Ouppublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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Fax: 801 585 717
Eax: 801 585 717
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: D column: 18
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
'organism="Ginkgo biloba"
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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                    /mol_type="mRNA"
/db_xref="taxon:3311"
/sex="male"
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murcidea; Murinae; Mus.

E 1 (bases 1 to 22)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWN42 (gi|4732114 |gb|AF129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0089E07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0089E07 R, genomic survey sequence.
AZ351527
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0089E07"
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Matches 22; Conservative
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Fax: 801 585 7177
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Musmanlia; Butheria; Buarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Mus.

E (bases 1 to 22)

B Junn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacze,S., Mahmoud,M., Menen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.,

Mouse whole genome scaffolding with paired end reads from 10kb

L Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah
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/clone_lib="Mouse_lokb plasmid UGCIM library"
/note="Wector: PWB4ZLY; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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ligated to the blunt ends in high molar excess. The
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100.0%; Pred. No. 8.5e+02;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: M column: 15
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/organism="Mus musculus"
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-compatent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ388103 22 bp DNA linear GSS 02-OCT-200 1M0147N14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0147N14 R, genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus
1 (bases 1 to 22)
10 (bases 1 to 22)
11 (bases 1 to 22)
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi[4732114]gb[AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Whouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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1M0168P24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Insert Length: 10000 Std Error: 0.00
Plate: 0168 row: P column: 24
Seg primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0168P24"
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Fax: 801 585 7177
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0203A24R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0203A24 R, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Monse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0203A24"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored wector DNA, and transformed into chemically-competent E. coli XLIO-Godd (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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100.0%; Pred. No. 8.5e+02;
ative 0; Mismatches 0; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: A column: 05
Seq primer: CACAGGGAAACAGCTATGACC
Class: plasmid ends
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114 |gb|AF129072.1). a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0264G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0264G12 R, genomic survey sequence.
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G78BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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100.0%; Pred. No. 8.5e+02;
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Fal: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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AZ459654.1 GI:10617779
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Best Local Similarity
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-composernt B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0272E24F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niderhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid innerts
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Insert Length: 10000 Std Error: 0.00
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Seq primer: CGTGTAAAACGACGCCAGT
Class: plaemid ends
High quality sequence stop: 22.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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/clone="UUGC1M0272E24"
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Fax: 801 585 7177
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi[4732114]gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone_lib="Mouse lokb plasmid UUGCIM library"
/note="Vector: PW1942nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jacksor
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insert Length: 10000 Std Error: 0.00
Plate: 0272 row: E column: 12
Seg primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
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Mus musculus
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AZ463652.1 GI:10621777
GSS.
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Matches 22; Conservative
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Fax: 801 585 7177
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AZ463652/c
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi]4732114|gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptoretent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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22 bp DNA linear GSS 13-DEC-2000 1M0174J15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0374J15 R, genomic survey sequence.

AZ582403. GI:11701249
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherita; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Murcidea; Muridae; Mus.

1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Menen, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
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University of Utah Genome Center
University of Utah
Nm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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100.0%; Pred. No. 8.5e+02;
tive 0; Mismatches 0; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.(
Plate: 0374 row: J column: 15
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Unpublished (2000)
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Best Local Similarity
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AZ582403
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Mus musculus uncuse mouse;

Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Eurechontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

El (bases 1 to 22)

Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacree, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Man. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

Mallon, Contact
adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114 |gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0430A13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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/clone_lib="Mouse_10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculs C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0430 row: A column: 13
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/strain="C57BL/6J"
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/clone="UUGC1M0430A13"
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AZ607658.1 GI:11729848
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Fax: 801 585 7177
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gl[4732114] pl[AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Mederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid innerts
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1M0529D05F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0529D05 F, genomic survey sequence.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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/clone_lib="Mouse 10kb plasmid UUGCNM library."
/noce="Voctor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: D column: 05
Seg primer: cGTTGTAAAACGACGCCAGT
Class: plasmid ends

    .22
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/strain="C57BL/6J"

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/clone="UUGC1M0529D05"
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Mus musculus
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Fax: 801 585 7177
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114 |gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                    0.8%; Score 22; DB 1; Le
100.0%; Pred. No. 8.5e+02;
tive 0; Mismatches 0;
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grrain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCIM0554A24"
/gex="Male"
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Plate: 0554 row: A column: 24
Seq primer: CGTGTAAAACGACGGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Best Local Similarity 100.0
Matches 22, Conservative
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84112, USA
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AZ760533
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KEYWORDS
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10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA 1910/10.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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adaptored DNA was purified and size-selected for a 9.5 to
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Mus musculus
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciurognachi; Muroidea; Muridae; Murinae; Mus.

1 (basea 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stockes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0016112"
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 22, Conservative
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmanla; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

E 1 (bases 1 to 22)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah
Diversity of Utah
University of Utah
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                    10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number of inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0028E04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0028E04 R, genomic survey sequence.
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adaptored DNA was purified and size-selected for a 9.5 to
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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/clone="UUGC2M0028E04"
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Best Local Similarity
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84112, USA
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0033A05F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0033A05 F, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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1 (Dases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, R., Schokes, R., Pedersen, T., Niederhausern, A. and Whight, D., Weise, R., Tingey, A., von Niederhausern, A. and Whight, D., Weise, R., Tingey, A., von Diasmid inserts.
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                    Length 22;
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Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0033 row: A column: 05
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Fax: 801 585 7177
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AUTHORS
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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musculus C57BL/6J (male) was obtained from the Jackson laboratory Mouse DNA Resource
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1 (basea 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Relally, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Muse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
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100.0%; Pred. No. 8.5e+02;
tive 0; Mismatches 0;
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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: G column: 12
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Mus musculus
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AZ787606.1 GI:12926565
                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0
Matches 22; Conservative
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ORGANISM
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Diamid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW042 (gi|4732114 [94] AFL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and with adaptored wester DNA, and transformed into adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse_lokb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
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2M0045A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0045A24 F, genomic survey sequence.
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
I (basea I to 23.
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, M., Rose, R., Stockes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Disert Length: 10000 Std Error:
Plate: 0045 row: A column: 24
Seq primer: CGTTGTAAAACGACGGCCAGT
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High quality sequence stop: 22.
Location/Qualifiers
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114 [9h]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZB10674 2M0076E19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0076E19 F, genomic survey sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muroidea; Muridae; Musinae; Musinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Rejlay, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von.
Niederhausern, A. and Wright, D., Weiss, R.
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musculus C57BL/6J (Male) was obtained from the Jackson
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100.0%; Pred. No. 8.5e+02;
ttive 0; Mismatches 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: R ......
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Class: plasmid ends
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Location/Qualifiers
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/clone="UUGC2M0076E19"
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AZ810674.1 GI:12978158
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Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                               22; Conservative
                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                           Query Match
Best Local S:
Matches 22,
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DEFINITION
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gl[4732114] pgl[AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ820439
2M0092K13R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0092K13 R, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Nouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                       Length 22;
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                                                                                                                                                                                                                                                                                                                             Score 22; DB 1; Le
Pred. No. 8.5e+02;
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Insert Length: 10000 Std Error: 0.00
Plate: 0092 row: K column: 13
Seg primer: CACACAGGAAACAGCTAATGACC
                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches

    .22
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"

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University of Utah Genome Center
University of Utah
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/clone="UUGC2M0092K13"
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High quality sequence stop: 22.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                              Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Fax: 801 585 7177
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Best Local Simil
Matches 22; C
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW142 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-GOJd (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ralam, B., Aoyagi, A., Stokes, M., Meenen, E., Pedersen, T., Reily, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb Unpublished (2000)
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                       0.8%; Score 22; DB 1; Le
100.0%; Pred. No. 8.5e+02;
ttive 0; Mismatches 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: I column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
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University of Utah Genome Center
University of Utah
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/clone="UUGC2M0139118"
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Fax: 801 585 7177
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Best Local Similarity
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AZ841661
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AUTHORS
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse lobb plasmid UUGCIM library"
/clone lib="Mouse lobb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources(documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
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Sciurognath; Murcidea; Muridae; Murinae; Mus.
1 (bases 1 to 22)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
                          10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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adaptored DNA was purified and size-selected for a 9.5 to
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/67"
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Seq primer: CGTTGAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
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Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Eutheria; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Mus.

E 1 (bases 1 to 22)

B Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

L Contact: Robert B. Weiss
University of Utah Genome Center
adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ946102
2M0207D13R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0207D13 R, genomic survey sequence.
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Seg primer: CACACAGGAAACAGCTATGACC
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/strain="C57BL/6J"
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Location/Qualifiers
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Mus musculus
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AZ946102.1 GI:13812911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: plasmid ends
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Fax: 801 585 7177
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatorphyta; magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

I (bases 1 to 22)
Strang-T.-V. Kwon, S.-J. Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Swon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptore B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone lib="E. coli DH10B"
/note="Vector: DCUGIBAC1; Site 1: Sau3A1; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
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llarity 100.0%; Pred. No. 8.5e+02;
Conservative 0; Mismatches 0; Indels
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/cultivar="Chift"
/sule species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS014507"
                                                                                                                                                                                                                                                                                                                                                                               2709 AAAAAAAAAAAAAAAAAA 2730
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Class: BAC ends
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ENKaryorta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
ENKaryorta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

Tosids; eurosids II; Brassicales; Brassicaceae; Brassica.

Strangt. J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tell: #83.31-299-1670
Fax: #82-31-299-1670
Email: pbeom@rda.go.kr
BMC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
                                                               DU835320 22-DEC-2005
KBrS016H03F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS016H03, genomic survey
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Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Eucheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases I to 22)
Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim, M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrSolid DH10B"
/lab host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBACI; Site 1: Sau3AI; Brassica rapa Sap pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."
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/mol_type="genomic DNA"
/cultivar="Chiifu"
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Class: BAC ends.
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KBrS016H03
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                     RESULT 1132
DU835320
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/ gub_species="pekinensis"

/ db_xref="taxon:51351"

/ clone="KBrB031121"

/ lab_host="E.coli DH108"

/ clone lib="KBrB, Brassica rapa BamHI BAC library"

/ note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp

pekinensis var. Chiffu BAC library (KBrB BAC) is provided

by Yong-Pyo Lim (CNU)."
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End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
Contact: Beom-Seve Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1670
Fax: +82-11-299-1672
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB031121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica rapa subsp. pekinensis
Brassica rapa subsp. grreptophyta; Brassicatophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

I (bases I to 22)
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M. H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
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Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Secdun-Dong, Suwon, 441-707, Korea
111-182-11-299-1670
Fax: +82-11-299-1670
Email: pbeom@rda.go.kr
Email: pbeom@rda.go.kr
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/mol type="genomic DNA"
/cultivar="Chiifu"

    .22
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/mol type="genomic DNA"
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100.0%; Pred. No. 8.5e+02;
tive 0; Mismatches 0; Indels
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Class: BAC ends.
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Class: BAC ends
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/sub species="pekinensis"

Tue Nov

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Query Match
Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                                                                                         AUTHORS
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by Yong-Pyo Lim (CNU)."
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pekinensis var. Chiltu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                             DX056961 CSS 10-JAN-2006 KBEB062A19F KBrB, Brassica rapa BumHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB062A19, genomic survey
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Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 22)
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M. H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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                                                                                                                                                                   0.8%; Score 22; DB 1; Length 22;
100.0%; Pred. No. 8.5e+02;
iive 0; Mismatches 0; Indels
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Secdun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
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                                                                                                                                                                                                                                                     2709 AAAAAAAAAAAAAAAAAAA 2730
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Class: BAC ends.
Location/Qualifiers
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Best Local Similarity 100.0%
Matches 22; Conservative
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RESULT 1136 DX069868

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UXUBUG94
KBIBO93A2OR KBIB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBIBO93A2O, genomic survey
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by Yong-Pyo Lim (CNU)."
                     GSS 10-JAN-2006
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (Bass I to 22)
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
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Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantaes Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB079A22
DNA linear GSS 10-JAN-2 KBEB079A22F KBFB, Brassica rapa Bamil BAC library Brassica rapa subsp. pekinensis genomic clone KBrB079A22, genomic survey sequence.
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Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Yang, T.J., Kwon, S.J., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.8%; Score 22; DB 1; Le
ilarity 100.0%; Pred. No. 8.5e+02;
Conservative 0; Mismatches 0;
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Class: BAC ends.
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Page 441

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Matches 2
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                                                                                                                                                                                                                                                                                                              / sub_species="taxon: 5131"

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pekinensis var. Chiffu BAC library (KBrB BAC) is provided

by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submitseion

Direct Submitseion

Submitted (07-3AN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
S., Oun-dong, Yusong-gu, Daejeon 305-333, Korea

(E-mail:redstonedmail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
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Pan troglodytes DNA, clone: RP43-072N05.TJ, genomic survey
sequence.
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Brassica Genomics Team

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Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
Email: pacom@rda.go.kr
Stangolaro
KBrB093A20
Seg primer: M13 Reverse
Class: BAC ends.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. BAC end sequences of Library RP-43 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                          organism="Brassica rapa subsp. pekinensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.8%; Score 22; DB 1; Length 22; Best Local Similarity 100.0%; Pred. No. 8.5e+02; Matches 22; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/cultivar="Chiifu"
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                                                                                                                                                                                                                 Location/Qualifiers
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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AGI94579.1 GI:45226755
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Constructed at the Institute for Genomic Research (TIGR),
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Trypanosoma brucei (TRED927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution of
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Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.corg
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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1 (bases 1 to 22)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 18A, E-mail: barrell@sanger.ac.uk and
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T. brucei sheared genomic DNA clone 131b09, forward sequence,
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                         /cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
                                                                                                                                               Query Match 0.8%; Score 22; DB 1; Length 22; Best Local Similarity 100.0%; Pred. No. 8.5e+02; Matches 22; Conservative 0; Mismatches 0; Indels
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/clone="RP43-072N05.TJ"
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/strain="TREU927"
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AL492691.1 GI:11868830
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                                   /sex="male"
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Length 22; 0; Indels

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TA380A07P 22 bp DNA linear GSS 13-DEC-2000 T. brucei sheared genomic DNA clone 380a07, forward sequence, genomic survey sequence.
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LOCUS CF329694 23 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-B19.b1 Rice callus plasmid cDNA library (NACL) Oryza
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Rockville, MD. Genomic DNA isolated from a cloned population of
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Barrell, Oxford University Press, 1999).
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Location/Qualifiers
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Location/Qualifiers
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project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 22)
Hall, N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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100.0%; Pred. No. 8.5e+02;
ve 0; Mismatches 0; Indels
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Pred. No. 8.5e+02;
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                                                                                                                           /mol_type="genomic DNA"
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/strain="TREU927"
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/organism="Trypanosoma
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                                                                                                                                                                                                                                                      project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
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Cillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
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Bukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae,
                          Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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100.0%; Pred. No. c...
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Email: nelsayed@tigr.org
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AL454256
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| (bases 1 to 22)
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Best Local Similarity 100.
Matches 22; Conservative
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       rrypanosoma brucei
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TA35C12Q/c
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Query Match
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Clade; Ehrhartoideae; Oryzea; Oryza.

E I (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6155
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                                                                                                        Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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/clone="NACL--05-B19"
/clone="NACL--05-B19"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/dev_stage="proliferated callus plasmid cDNA library (NACL)"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoR1; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                       Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Bativa (japonica cultivar-group) cDNA clone NACL--05-B19, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Location/Qualifiers
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/cultivar="Nackdong"
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                                                                   CF329694.1 GI:33807601
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Beet Local Similarity luc.
22; Conservative
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23 bp mRNA linear EST 29-AUG-2005
WS0112.BR_L03 PT-P-FL-A-2 Populus trichocarpa cDNA clone WS0112_L03
5', mRNA sequence.
DT495201
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Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y., Kirkpatrick,R., Liu,J., Pallmquist,D., Stott,J., Barber,S., Yang,G., Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A., Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A., Bohlmann,J.
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/clone lib="PT-P-FL-A-2"
/note="Vector: pBluescript I1 SK (+) XR; Site 1: SstI (5'
end of cDNA); Site 2: XhoI (3' end of cDNA); Phloem and
cambium from 8 year old trees harvested within the Boise
Cascade region of Washington state on May 15th, 2001. CDNA
was prepared from 20 micrograms of mRNA according to the
full-length cDNA library construction method described by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                  /tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rico callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with Oligoribonucleotides and then used as templates for RT-PCR."
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Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Joerg Bohlmann
Genome BC forest genomics program .
Genome BC forest genomics program .
University of British Columbia .
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237, Vancouver, British Columbia, Canada, V6T 123
Tel: 1-604-822-2214
Email: bohlmann@msl.ubc.ca
Blate: W50112 row: L column: 03
High guality sequence stop: 132
POLYA=Yes.
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    23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"___

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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 23;

    .23
    Coganism="Populus trichocarpa"
/mol type="mRNA"
    /cultivar="383-2499 (Nisqually-1)"

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Similarity 100.0%; Pred. No. 8.7e+02;
22; Conservative 0; Mismatches 0;
                                                                                                                         /db_xref="taxon:39947"
/clone="NACL--08-N21"
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/clone="WS0112_L03"
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone llb="Mouse lokb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
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23 bp DNA linear GSS 03-OCT-200
1M0205L23R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0205L23 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
Carninci P. et al. (2000), Genome Research 10(10):1617-1630 and directionally ligated into the pBluescript IS SK (+) XR vector digested with SstI (5' end) and Xhoi (3'). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for
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1 (Dases I. t. 22)
1 (Dases I. t. 22)
1 (Dases I. t. 23)
1 (Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Nouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                       Query Match 0.8%; Score 22; DB 1; Length 23; Best Local Similarity 95.7%; Pred. No. 8.7e+02; Matches 22; Conservative 0; Mismatches 1; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0205 row: L column: 23
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0205L23"
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Location/Qualifiers
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                                                                                                                                                                   propagation.
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84112, USA
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0059J16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 22; Conservative 0; Mismatches 0;
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Plate: 0059 row: J column: 16
Seq primer: CTTGTAAAACGACGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC2M0059J16"
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Fax: 801 585 7177
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ABF--07-P12, mRNA sequence.
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/organism="Glycine max"
/moltype="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="112A03"
/tissue_type="Roctors"
/dev stage="Seedlings"
/clone lib="CDNA Peking library 12hr SCN3"
/clone lib="CDNA Peking library 12hr SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript SK- phagemid. "
inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptore boxer or DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicocyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA
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100.0%; Pred. No. 8.8e+02;
tive 0; Mismatches 0; Indels
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Location/Qualifiers
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"-hea 22; Conservative
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Fax: 301 504 5728
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Matches 22; Conserv
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                                                                                                                                                             Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@pio.myongji.ac.kr.
Location/Qualifiers
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone lib="ABF9-overexpressing transgenic rice plasmid
cDNA library (ABF)"
                                                                                     Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryopta; Viridiplantea; Streptophyta; Embryophyta; Tracheophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryzae,
1 (bases 1 to 24)
1 (kases 1 to 24)
Song, S.I., Kim, J.K., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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100.0%; Pred. No. 8.8e+02;
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/clone="ABF--07-P12"
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/cultivar="Nackdong"
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CF312319
CF312319.1 GI:33684080
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Class: transposon-tagged
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Walbot, V.
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                                                                                                                                                                                                             source
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CZ914626/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwapto (gill 4)732114 (gbl AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XILO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N59260 25 bp mRNA linear EST 23-FBB yz82d11.81 Soares multiple sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:289557 3' similar to gb:M77693 DIAMINE ACETYLTRANSFERASE (HUMAN);, mRNA sequence.
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1 (Dases 1 to 25)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hillier,L., Clark,N., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.8%; Score 22; DB 1; Length 24; Best Local Similarity 100.0%; Pred. No. 8.8e+02; Matches 22; Conservative 0; Mismatches 0; Indels
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0079 row: A column: 23
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                           /organism="Mus musculus"
mol_type="genomic DNA"
| strain="C57BL/60"
|db xref="taxon:10090"
|/clone="UUGC2M0079A23"
                                                                                                                                                                                High quality sequence stop: 24. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
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4013007H05.2EL_y1 4013 - RescueMu Grid O Zea mays genomic, genomic
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Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013007 row: H column: 05
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: mil -40 forward
High quality sequence stop: 1.
Location/Qualifiers
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/dev stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
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Stanford University
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/mol_type="mRNA"
/db_xref="GDB:3905397"
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/clone="IMAGE:289557"
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/organism="Zea mays"
//oultype="genomic DNA"
/cullivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/de_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/clone_lib="4013 - RescueMu is to 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu', Grid
O was grown at Stanford in 2001. DNA was extracted from
leaf strips, double digested using BamHI and BglII, and
ligated to form circular plasmids. DH10B cells were
transformed and then screened on LB plates with
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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/dev stage="adult"
/lab_host="DH10B"
/lab_host="DH10B"
/clone lib="40101 - RescueMu Grid V"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
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855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 725 8221
Bmail: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021002 row: C_column: 08
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/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution of
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@digt.corg
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using Bamili and Balli, and ligated to form circular plasmids. DH10B cells west transformed and then screened on LB plates with ampicillin."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TA154D03P 25 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 154d03, forward sequence,
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AM046273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
                                                                                                                                                                                                                                                                                                 Gaps
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1 (bases I to 25)
Hall, N. Bowman, S., Lennard, N. J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trypanosoma brucei
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 9e+02;
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100.0%; Pred. No. 9e+02;
vative 0; Mismatches 0
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100.0%; Pred. No. ...
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="154403"
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Best Local Similarity
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Query Match
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                                                                                                                                                                                                                                      Jacob J. Coulson, P.D., Coulson, P.S., Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C. Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C. Micoarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni Unpublished (2005)

Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CBJO 15A, UNITED KINGDOM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CZ914111 27 bp DNA linear GSS 08-AUG-2009
4013005E12.1EL x1 4013 - RescueMu Grid O Zea mays genomic, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Beparnatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
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Unpublished (2001)
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Tel: 650 723 2227
Fax: 650 725 8227
Fax: 650 725 8227
Fax: 650 726 8227
Fax: 650 728 8228
Fax: 650 728 8228
Fax: 650 728 8228
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Fax: 650 728
                                                                 Schistosoma mansoni
Schistosoma mansoni
Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosoma.
1 (bases 1 to 27)
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/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"
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/cultivar="mixed background w23/A188/B73/K55"
/cultivar="mixed background w23/A188/B73/K55"
/tissue_type="leaf"
/dev_stage="adult"
/dev_stage="b1108"
/clone_lib="4013 - RescueMu Grid O"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.8%; Score 22; DB 1; Length 27; Best Local Similarity 100.0%; Pred. No. 9.3e+02; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Schistosoma mansoni"
|mol_type="mkNA"
|db_xref="taxon:6183"
|clone="SmlC32a10.q1k"
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Department of Biological Sciences
Stanford University
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   AM046273.1 GI:75969955
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Zea mays
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SOURCE
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/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu alements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/. Grid O was grown a Stannford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

El (bases 1 to 25)
SKM, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/dav stage="proliferated"
/dab_host="E.Coll DH108"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.8%; Score 22; DB 1; Lk Best Local Similarity 100.0%; Pred. No. 9.3e+02; Matches 22; Conservative 0; Mismatches 0;
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RESULT 1158

AW249476/c

seguence

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Contact: Robert Strausberg, Ph.D.

Bmail: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PRRED from University of Washingtion Genome Center. Vector

Trimming: cross match from University of Mashingtion Genome Center.

Drosophila Genome Project. University of Washingtion Genome Center:

http://www.genome.washington.edu Low Quality Sequence: 25

contiguous PHRED high quality bases following vector sequence. Very

Low Quality Sequence: Trace file contained 25 contiguous distinct

peaks following vector sequence. Polyadenylation: Based upon the

presence of a XhoI site followed by a run of 14 or more T residues

at the beginning of the sequence, this CDNA insert was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"

/mol_type="mRNA"

/mol_type="mRNA"

/do=xref="Laxon:9606"

/clone="LMAGE:282131"

/tissue_type="small cell carcinoma"

/tissue_type="small cell carcinoma"

/tissue_type="small cell carcinoma"

/clone lib="MGG3"

/lab_host="DH10B (phage-resistant)"

/clone lib="NIH MGC 7"

/note="Organ: lung; Vector: pOTB7; Site 1: Xho1; Site 2: Bcot1, cDNA made by oligo-dr priming Directionally cloned into EccH/Xho1 sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
AW249476 281131.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821131 3',
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                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                Hominidae, Homo.

1 (bases 1 to 25)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other_ESTs: 2821131.5prime
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tive 0; Mismatches 2;
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Best Local Similarity 92.0°
Matches 23, Conservative
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                                                                  mRNA sequence.
                                                                                                                                                                                                                                Homo sapiens
                                                                                             AW24947
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KEYWORDS
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                          DEFINITION
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Gnetum gnemon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Gnetume.

Spermatophyta; Gnetophyta; Gnetopsida; Gnetales; Gnetume.

Spermatophyta; Gnetophyta; Gnetopsida; Gnetume.

Expressed to 25)

Expressed to 25)

Expressed tag sequences from Gnetum female cone (NYBG)

Expressed tag sequences from Gnetum female cone (NYBG)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8874

Email: mccombie@cshl.org

Seq primer: -21Ml3UnivRev.
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/clone_loggan: mature, unfertilized reproductive strobili;
/hote="Corgan: mature, unfertilized reproductive strobili;
/bctor: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for Sequencing 02/12/02.
Library: Stratagene ZAP Express CDNA Synthesis Kit. The
Library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84
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Mus musculus
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rose, M., Rose, M., Rose, R., Stockes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid inserts
Contact: Robert B. Weiss
University of Utah Genome Center
Nunversity of Utah
Nm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/organism="Gnetum gnemon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
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                               DN954014.1 GI:63026152
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Matches 23; Conservative
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Fax: 801 585
          DN954014
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                                                                                                                                                                                                                                                                                                                                                                               /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares/). The DNA
was hydrodynamically sheared by repeated epassage through a
0.005 inch orifica at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated were
ligated to rifica at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1M0234H18R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchonicoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
I (bases I to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Waiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: F column: 09
Seg primer: cGTTGTAAAACGACGCCAGT
Class: plasmid ends

    .25
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
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                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0056F09"
                                                                                                                                        High quality sequence stop: 25.
Location/Qualifiers
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AZ442170.1 GI:10566183
                                                                                                                                                                                                                                                                                                                                                                    /sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
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VERSION
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ઠે 셤

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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares/). The
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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KBrB057C20R KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB057C20, genomic survey
sequence.
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Rukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeomérda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 25)
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
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                                       Std Error: 0.00
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.0
Plate: 0234 row: H column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0234H18"
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Brassica Genomics Team
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DX053323.1 GI:84747620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
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Best Local Similarity 92.0°
Matches 23; Conservative
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Query Match
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DR072900/c
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ORGANISM
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                                                                                                                                                      DEFINITION
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VERSION
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COMMENT
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Organ sativa (japonica cultivar-group)
Organ sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermarophyta; Midplantae; Streptophyta; Embryophyta; Tracheophyta; Spermarophyta; Midplantae; Oryzae.

I (bases I to 26)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@ggibio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                             / dub_species="pekinensis"

/db_xref="taxon:51351"

/clone="kEnENG57C20"

/lab_host="E.coli DH108"

/clone_lib="KBrB, Brassica rapa BamHI BAC library"

/clone_loctor: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp

pekinensis var. Chiifu BAC library (KBrB BAC) is provided

by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CF337311 26 bp mRNA linear EST 18-AUG-2003 JMT--07-L06.gl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone CF337311
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/clone="JMT--07-1.06"
/tiosus="Lagh" -07-1.06"
/dev_stage="lagh" days after germination"
/lab_host="B.coll DH10B"
/clone lib="ALJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
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/mol_type="mRNA"
/cultivar="Nackdong"
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0
                                                                                  /organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiffu"
                                                                                                                                                                                                                                                                                                                                             0.8%; Score 21.8; DB 1; Length 25; 92.0%; Pred. No. 9.2e+02; tive 0; Mismatches 2; Indels
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                                          Location/Qualifiers
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Seq primer: M13 Reverse
Class: BAC ends.
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Best Local Similarity 92.0
Matches 23; Conservative
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Matches 23; Conserv
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                                                                     source
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VERSION
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/tissuc_type="last"
/dev_stage="14 days after germination"
/dev_stage="14 days after germination"
/dev_stage="14 days after germination"
/dev_stage="15 coli DH108"
/clone lib="Atyr-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
                                                                                                                                                                                                                    EST 18-AUG-2003
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ik78f03.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryoca, viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade, Ehrhartoideae, Oryzea, Oryza.
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Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
I (bases I to 23)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                             JMT--03-D17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 23)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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95.7%; Pred. No. 9.4e+02;
tive 0; Mismatches 1;
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23 bp
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/clone="JMT--03-D17"
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Ginkgo biloba
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CF334077.1 GI:33816466
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organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0138M14"
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84112, US
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Populus trichocarpa x Populus deltoides
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, endicotyledons, core eudicotyledons,
rosids, eurosids I; Malpighiales, Salicaceae, Saliceae, Populus.
I (bases I to 23)
Kalph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y.,
Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G.,
Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A.,
Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A.,
Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and
                                                                                                                                                                                                                                                                                                                                                              /sex="female" //sex="female" //sex="female" //sex="female" //clone_lib="Ginkgo female leaf (NYBG)" //clone_lib="Ginkgo female leaf (NYBG)" //sex="Grgan: leaf; Vector: :pBK-CMV; Site_l: Khol; Site_leaf; Vector: :pBK-CMV; Site_l: Xhol; Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts."
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Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 123
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Expressed tag sequences from Ginkgo female leaf (NYBG) Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.8%; Score 21.4; DB 1; Length 23;
95.7%; Pred. No. 9.4e+02;
tive 0; Mismatches 1; Indels
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Email: bohlmann@msl.ubc.ca
Plate: WS01313 row: M column: 18
                                                                                                                                                                                                                                                                        1. .23
/organism="Ginkgo biloba"
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/db_xref="taxon:3311"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 123
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/db_xref="taxon:3695"
/clone="WS01313_M18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2708 TAAAAAAAAAAAAAAAAAAAAA 2730
                                                                                                                                                                                                 Email: mccombie@cshl.org
Seg primer: -21M13UnivRev.
Location/Qualifiers
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DT501689.1 GI:73898951
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Best Local Similarity 95.7%
Matches 22, Conservative
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DT501689
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/lab host-="E. coli DH10B T1 phage resistant cells"
/clome_lib="PTxD-IL-FL-A-4"
/clome_lib="PTxD-IL-FL-A-4"
/clome_lib="PtxD-IL-FL-A-4"
/clome_lib="PtxD-IL-FL-A-4"
/clome_lib="Petcor: pBluescript II SK (+) XR; Site_1: SstI (5')
end of cDNA); Site_2: Xhol (3' end of cDNA); Sapling trees
one metre in height and grown under greenhouse conditions
were exposed to continuous feeding by Malacosoma disstria
Hubner (forest tent caterpillar) mid-instar larvae caged
on the sapling using mesh bags. Mature leaves from within
the caged region were collected 4 hours a B hours and 24
hours after the onset of treatment. Mature leaves were
also collected above the caged region (systemic response)
4 hours, 12 hours and 48 hours after the onset of
treatment. mRNA was isolated from each tissue were then pooled. cDNA was prepared from 20
micrograms of mRNA acisolated from each tissue were then pooled. cDNA was prepared from 20
micrograms of mRNA according to the full-length cDNA
library construction method described by Carninci P. et
al. (2000), Genome Research 10(10):1617-1630 and
directionally ligated into the Bluescript II SK (+) XR
vector digested with SstI (5' end) and Xhol (3'). Plasmid
DNA was then transformed by electroporation into DH10B
cells (Invitrogen) for propagation."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
Sciurognathi; Muroidea; Muridae; Mus.
Sciurognathi; Muroidea; Muridae; Mus.
Sciurognathi; Muroidea; Muridae; Mus.
Sciurognathi; Longacre, Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Unjublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
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23 bp DNA linear GSS 02-0CT-2000
1M0138M14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0138M14 R, genomic survey sequence.
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Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0138 row: M column: 14
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
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(http://www.iax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwapt (gqi 4732114 [gb] AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Twetcor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: M column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
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University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC1M0315M14"
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Best Local Similarity 95.7%
....hea 22; Conservative
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Fax: 801 585 7177
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84112, USA
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1M0474E01F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0474E01 F, genomic survey sequence.
AZ627841
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1 (Dases 1 to 23)
1 (Dases 1 to 23)
1 Islam, L., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Moose whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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Insert Length: 10000 Std Brror: 0.00
Plate: 0474 row: E column: 01
Seg primer: CGTYCTAAAACGACGCCAGT
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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Location/Qualifiers
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Mus musculus .
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Fax: 801 585 7177
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Sciurognathi; Muroidea; Muridae; Mus.
CE I (bases 1 to 23)
RS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unyublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Fex: 801 585 5606
Fex: 801 585 5606
Fex: 801 585 5606
/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bylorynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polyrucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: O column: 05
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="c57BL/6"
/db xref="taxon:10090"
/clone="UUGCIMO510005"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gilfa712114[gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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23 bp DNA linear GSS 10-JUL-2004
PRI0160b B06 2 - PRI0160b.BR (23) Note: Recurring String Mixed
stage fosmid library of P. pacificus var. California Pristionchus
pacificus genomic, genomic survey sequence.
/lab host="B. Coli strain XLIO-Gold, Tl-resistant, F-" /clone lib="Mouse lOkb plasmid UUGCIM library" /note=""Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/63 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Pristionchus pacificus
Pristionchus pacificus
Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Noodiplogasteridae; Pristionchus.

(bases 1 to 23)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppabB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tal: 00497071601371
Fax: 00497071601498
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/mol_type="genomic DNA"
/strain="California"
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Email: adana@nd.edu
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                                                                                                                                                                                                                                                                                                                Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 23)
Yang, T.-J. Kwon, S.-J. Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="KBrS003LL6"
/lab_host="E. coli DH10B"
/clone_lib="KBrS. Brassica rapa Sau3AI BAC library"
/clone_lib="KBrS. Brassica rapa Sau3AI BAC library"
/note="Vector: pcUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC_library (KBrS BAC) is
available at NIAB."
                         Gaps
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/mol_type="genomic DNA"
/cultivar="Chiifu"
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 Pred. No. 9.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Beom-Seck Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Secdun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sub_species="pekinensis"
/db_xref="taxon:51351"
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AL455778
AL455778.1 GI:11856729
Similarity 95.7%;
22; Conservative
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Best Local Similarity
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KBrS003L16
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Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www sanger.ac.uk/projects/T_brucei/
Location/Qualifiers
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Anopheles gambiae
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.

1 (bases 1 to 24)
Dana,A.N., Lobo,N.F., Hillenmeyer,M.E. and Collins,F.H.
Hematophagy-associated gene expression patterns in adult female Anopheles gambiae mosquitoes
Unpublished (2003)
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1 (bases 1 to 23)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
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PCR PRimers
FORWARD: ctcgggaagcgccattgtgttgg
BACKWARD: atacgactcactataggcgaattggc
Seq primer: ctcgggaagcgcgcttgtgttgg.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
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Tel: 574 - 631 - 3241
Fax: 574 - 631 - 3996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:5691"
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용
                                                                    /tdsue__ypc__mountains.
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/lab_host=="E. coli XLI-Blue"
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/site_2: Sfi IB; Plasmodium berghel-infected rat blood-fed
adult female An. gambiae mosquitoes were flash frozen
after a 30 hour incubation of adult mosquitoes at 19
degrees Celsius. Total RNA extracted from abdomens
separated from remaining carcass. CDNA inserts >500 bp
cloned directionally into lTriplEx2; Sfi IA site is 5'.
Non-normalized and Non-amplified phagemid library. Single
pass sequencing reactions from 5' end."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B. H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Torgin, Kyeongqi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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with oligoribonucleotides and then used as templates for RT-PCR."
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91.7%; Pred. No. 9.5e+02;
tive 0; Mismatches 2; Indels
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    Location/Qualifiers
                                              tissue_type="Abdomens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2709 AAAAAAAAAAAAAAAAAAAA 2732
db_xref="taxon:7165"
sex="female"
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/cultivar="Nackdong"
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//organism="musculus"
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//doin="1057BL/6J"
//d
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Rodentia;
Sciurognathi; Murcidea; Murinae; Mus.
1 (bases 1 to 24)
1 (bases 2 to 24)
1 (bases 2 to 24)
1 (bases 3 to 24)
1 (bases 3 to 24)
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1M0173J14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Insert Length: 10000 Std Error: 0.0
Plate: 0173 row: J column: 14
Seq primer: CACACGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
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/organism="Mus musculus"
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23 TTGTCCTAAAAAAAAAAAAAAAA
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Fax: 801 585 7177
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Gaps

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AZ486788/c LOCUS RESULT 1177

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DEFINITION

ACCESSION VERSION ORGANISM

REFERENCE AUTHORS

JOURNAL

TITLE

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Email: hideko@biol.tsukuba.ac.jp.
Location/Qualifiers
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/clone_lib="VS"
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/clone="VSF713"
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          23 TAAATAAAAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="AX4"
                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum
Dictyostelium discoideum
                                                                                                                                                                                                                                                          AU265663.1 GI:20524461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clon= lib="wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nr; Purified genomic DNA from M.
musculus C57BL/6/ (male) was obtained from the Jackson
laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4772114|gp|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                               ndago/ww 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0315122 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Solurognathi; Muroidea; Murinae; Musinae; Mus. 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Neelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: I column: 22
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.

    .24
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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Contact: Robert B. Weiss
University of Utah Genome Center
Nuiversity of Utah
Rm. 308, Blomedical Polymers Rese
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/clone="UUGC1M0315122"
2 CTCAAAAAAAAAAAAAAAAA 24
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Best Local Similarity
Matches 22; Conserv
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source

FEATURES

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Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
1 (bases 1 to 25)
Urushihara, H., Morio, T., Saito, T., Kohara, Y., Koriki, E., Ochiai, H., Amaeda, M., Williams, J. G., Takeuchi, I. and Tanaka, Y.
Analyses of cDNAs from growth and slug stages of Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV737092 CB Homo sapiens cDNA clone CBFBIB11 5', mRNA sequence.
AV737092
AU265663 25 Ap mRNA linear EST 26-APR-2004 AU265663 VS Dictyostelium discoideum cDNA clone VSF713 5', mRNA
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1 (bases 1 to 25)

Zhang, Q., Ye,M., Wu, X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
Chen,S., Mao,M. and Chen,Z.

Homo sapiens CB library cDNA clones
Unpublished (2000)

Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital

197 Rui-Jin II Road, Shanghai 200025, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Fax: 86-21-6474206
Email: mbshi@ms stn.sh.cn
This clone is available at Shanghai Hematology Institute in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Institute of Biological Sciences
University of Tsukuba
1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614

    .25
    /organism="Dictyostelium discoideum"

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of clone tracking errors
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AG194089.1 GI:45226265
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R.Site 1
R.Site 2
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Matches 2
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/dol type="mixed background W23/A188/B73/K55"
/db xxefe="text".
/tissue type="leaf"
/tissue type="leaf"
/dev stage="adult"
/dev stage="adult"
/done lib="lil9" - RescueMu Grid AA"
/clone lib="lil9" - RescueMu Grid AA"
/clone lib="lil9" - RescueMu Grid AA"
/clone lib="backbone); Site li BamHl; Site_2: BglII;
/RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements innert preferentially into transroription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CG726337 25 bp DNA linear GSS 20-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 25)
                                                                                                                                                                                                                                            /clone lib="CB"
/note="Vector: pBluescript; Site 1: EcoRI; The insert is
cloned randomly with the EcoRI dIgestion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119089 row: E column: 12
Class: transposon.tagged.
                                                                                                                       /mol_type="mRNA"
/db_xref="taxon.9606"
/clone="CBFBB11"
/clsue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
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Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
Location/Qualifiers
1. 25
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                              Query Match 0.8%; Score 21.4; DB 1; Length 25; Best Local Similarity 88.0%; Pred. No. 9.7e+02; Matches 22; Conservative 0; Mismatches 3; Indels
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Tel: 650 723 2227
Fax: 650 725 8221
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Stanford University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              survey sequence.
CG726337
CG726337.1 GI:37764992
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1180
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DEFINITION
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AM043942 Chistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA clone SmlCllb03.qlk, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submission

Submitted (07-JMN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail:kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                              26 bp DNA linear GSS 06-MAR-2004
Pan troglodytes DNA, clone: RP43-071013.TJ, genomic survey
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                Gaps
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Upublished
2 (bases 1 to 26)
DH10B cells were transformed and then screened plates with ampicillin."
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/clone lib="RP-43 Chimpanzee Male BAC Library"
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                                                                                     Length 25;
                                                                                                                                             1; Indels
                                                                                  0.8%; Score 21.4; DB 1;
95.7%; Pred. No. 9.7e+02;
tive 0; Mismatches 1;
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/organism="Pan troglodytes"
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/db_xref="taxon:9598"
/clone="RP43-071013.TJ"
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: EcoRI
: ECORI.
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Tue Nov

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Organ sativa (japonica cultivar-group)
Organ sativa (japonica cultivar-group)

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

El (bases I to 26)
El (bases I to 26)
El (bases I to 26)
El (Man,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongGJ, Korea
Tel: 82 31 321 6155
Email: bhaahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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14ETL--07-H09.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-H09,
                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlClib03.qlk"
/dev_stage="lung schistosomulum"
/clone lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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/cultivar="Nackdong"
/db xref="taxon:39947"
/tlone="l4FIL--07-H09"
/tlssue type="leaf"
/dev stage="14 days after germination"
/lab host="E.coli DH10B"
/clone lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'organism="Oryza sativa (japonica cultivar-group)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.8%; Score 21.2; DB 1; Length 26;
88.5%; Pred. No. 1e+03;
tive 0; Mismatches 3; Indels
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/organism="Schistosoma mansoni"
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 AM043942.1 GI:72292305
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                                         Schistosoma mansoni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
CF280688
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les 23; Conserv
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1M0101M24F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0101M24 F, genomic survey sequence.
A2358846.1 GI:10472546
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/clone_lib="%cs-1"
/note="Vector: Lambda ZAP II; Site_l: EcoRI; Site_2: Xhol
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                      Gaps
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Pneumocystis carinii
Pneumocystis carinii
Bukaryota; Pungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae: Pneumocystis.
1 (bases 1 to 26)
Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C., Edman,J.C., Kovacs,J. and Cushion,M.
Expressed sequence tags from Pneumocystis carinii
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Bullding, University of Kentucky, Lexington, KY
40506-0225, USA
                                                                                                                                                                                                                                                                                                                    AW333508 26 bp mRNA linear EST S22F8 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence. AW333508
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                                                                                                                                      3; Indels
                                                                                            ch 0.8%; Score 21.2; DB 1; Similarity 88.5%; Pred. No. 1e+03; 23; Conservative 0; Mismatches 3;
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/organism="Pneumocystis carinii"
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                                                                                                                                                                                                                  26 TTTCCCAAAAAAAAAAAAAAAA 1
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/db_xref="taxon:4754"
/lab_host="E.coli"
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Location/Qualifiers
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 0.8%; Sco
1 Similarity 88.5%; Pro
23; Conservative 0;
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Fax: 606 257 1717
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Best Local Similarity
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JOURNAL COMMENT

TITLE

FEATURES

REFERENCE AUTHORS

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In (DABES 1 to 21)

Anderson, S. I., Finlayson, H. A. and Archibald, A.L.

Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle

embryo development in pigs and cattle

Unpublished (2004)

Contact: Anderson SI

Genomics and Bioinformatics

Roslin, Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred

single pass sequencing. Vector is an another with the minscore 20

and —minmatch 12 options. Vector is match with the minscore 20

and —minmatch 12 options. Vector is maded library constructed

From pooled early embryos, from 8- cell stage to blastocysts.
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AJ658282
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                               Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
                                                                                                                                                                                                                                                                                                    Email: walbot@stanford.edu

Sossible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4021006 row: D column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 26
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon.4577"
/tiseue_type="leaf"
/lab_host="bH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.8%; Score 21.2; DB 1; Length 26;
88.5%; Pred. No. 1e+03;
Live 0; Mismatches 3; Indel8
                                                                                                                                               Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
TTE1: 650 723 2221
Fax: 650 725 8221
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                                                                                                                                                                                                                                                                                                                                                                                                                                Class: transposon-tagged.
Location/Qualifiers
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   (bases 1 to 26)
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Jean-Book Control Strain XL10-Gold, T1-resistant, F-"
/ Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/ Clone lib="wouse 10kb plasmid UUGCIM library"
/ note="Wetcor: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
was hydrodynamically sheared by repeated passage through a
was hydrodynamically sheared by repeated passage through a
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD47 (gil 4772114 [gb] AP129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chancally-complement E. coli Xil0-Gold (stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS 08-AUG-2005
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4021006D11.2EL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weise, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0101 row: M column: 24
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1e+03;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'organism="Mus musculus"
                                                                                                                                                                           plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 26.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="UUGC1M0101M24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'db_xref="taxon:10090"
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CZ917639
CZ917639.1 GI:71936614
                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
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RESULT 1186 CZ917639

Matches

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ACCESSION

VERSION KEYWORDS SOURCE ORGANISM

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Gaps ;

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Homo sapiens
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                                                                AL048777
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Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with the minscore 20
VO.020452.c. Vector identified by cross match with the minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
ECORI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institite,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
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Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
                                                                               1...21
/mol.type="mRNA"
/db_xref="taxon:9823"
/db_xref="taxon:9823"
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/clone="Vector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2: Not; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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/clone="C0000033 C15"
/clone lib="CSCRANO9"
/clone lib="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
Not1; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."
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Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
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100.0%; Pred. No. 9.5e+02;
/ative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                               Query Match 0.8%; Score 21; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 9.5e+02; Matches 21; Conservative 0; Mismatches 0; Indels
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Genomics and Bioinformatics
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Best Local Similarity
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ORGANISM
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1 ААААААААААААААААА 21

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DKF2D566N053 r1 566 (synonym: hfkd2) Homo sapiens cDNA clone ALO48777
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AM047262
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Schistosoma mansoni
Substrosoma mansoni
Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 21)
Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S.,
Nikolaidou-Katsaridou, N., Quall, M.A., Wilson, R.A., and Ivens, A.C.
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                               Hominidae; Homo.

1 (bases 1 to 21)

Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehrer, et al.)
Unpublished (1999)
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/clone=lib="Schistosoma mansoni lung schistosomulum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mgNA"
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/lab_host="x1-2blue"
/clone_lib="566 (gynonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: Sal1"
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100.0%; Pred. No. 9.5e+02;
ive 0; Mismatches 0; Indels
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Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                            Homo sapiens (human)
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Best Local Similarity 100.(
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: MIPS
MIPS
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Matches

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CF282216

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrbartcideae; Oryzeae; Oryza.

1 (Dases 1 to 21)

2 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Cryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

I (bases 1 to 21)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CF295642 11-AUG-2003 30DGS--05-K20.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--05-K20, mRNA
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Tal: 82 31 330 6193
Fax: 82 31 321 6355
Bmail: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/mol type="mRNA"
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/organism="Oryza Bativa (japonica cultivar-group)"
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/tissue_type="leaf"
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CF295642.1 GI:33664675
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AUTHORS
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Enthartoideae; Oryzaa.

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El (Dassea it o. 21)
El (Man, J. S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice BSTs
Unpublished (2003)
Contact: Nahm B.H.
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YongIn, Kyeonggi, Korea
Tel: 82 31 321 6155
Email: bhaahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                               21 bp mRNA linear EST 14-AUG-2003 14ETL--09-K01.gl Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-K01, mRNA sequence.
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(14ETL)"
                                                                                                               Gaps
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                                                          0.8%; Score 21; DB 1; Length 21; 100.0%; Pred. No. 9.5e+02; tive 0; Mismatches 0; Indels
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Oryza sativa (japonica cultivar-group)
               /note="country: Puerto Rico"
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RESULT 1194

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

JOURNAL COMMENT

TITLE

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REFERENCE AUTHORS

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Midiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Midiplantae; Oryza.

Clade; Ehrhartoideae; Oryzeae; Oryza.

El (Bases 1 to 21)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota; Viidiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhattoideae; Oryzaee; Oryza,
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:33947"
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/clone="TLEAF--01-K14"
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21 bp mRNA linear EST 15-AUG-27LEAF--05-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryzz sativa (japonica cultivar-group) cDNA clone 7LEAF--05-G20, mRNA
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100.0%; Pred. No. 9.5e+02;
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Tel: 82 31 330 6193
Fax: 82 31 321 6365
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/cultivar="Nackdong"
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        CF298322.1
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CF300809/c
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae.; Oryza.

El (bases 1 to 21)
S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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| Organism="Oryza sativa (japonica cultivar-group)"
| mol_type="mRNA"
| cultivar="Nackdong"
| db_xref="Laxon:39947"
| clone="30DGS--08-110"
| tissue_type="leaf"
| dev stage="30 days after
| dev stage="30 days after
| dev stage="10 bH10B"
| clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
| clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
| nith oligoribonucleotides and then used as templates for RT-PCR.
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/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for RT-PCR."
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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100.0%; Pred. No. 9.5e+02;
tive 0; Mismatches 0;
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Pred. No. 9.5e+02;
                                                                                                                                                         0.8%; SCol.
V 100.0%; Pred. No. >--
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Best Local Similarity
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CF297615
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RESULT 1195

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CF298322/c DEFINITION

ACCESSION

EST 15-AUG-2003 (7LEAF) Oryza

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Gaps

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EST 15-AUG-2003

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/dev stage="proliferated callus on 2N6 media for 2 weeks" /lab_host="E.coli DH10B" /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
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Oryza sativa (japonica cultivar-group)
Cyza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                          Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhattoideae; Oryzeae; Oryza,
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                      Laber news linear EST 15-AUG-200 mRNA linear EST 15-AUG-200 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--05-D16, mRNA sequence. CF316073
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University YongJi, KyeongJi, KyeongJi, Korea Tel: 82 31 330 6193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/culTivar="Nackdong"
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100.0%; Pred. No. 9.5e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                             CF316073.1 GI:33687834
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CF316073/c
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ABF--08-J10.gl ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--08-J10, mRNA sequence.
CF312715.1 GI:33684476
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 31 6155
Email: bhnahm@gDio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and Then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
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| / organism="Oryza sativa (japonica cultivar-group)"
| / organism="Oryza sativa (japonica cultivar-group)"
| / olitivar="Nackdong"
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| / tissue_type="leaf"
| / dev_stage="14 days after germination"
| / lab_host="E.coli DH108"
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                                                                                                                                                                                                                                                         Length 21;
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                                                                                                                                                                                                                                                         0.8%; Score 21; DB 1; Le Larity 100.0%; Pred. No. 9.5e+02; Conservative 0; Mismatches 0;
                        /db_xref="taxon:39947"
/clone="7LEAF--05-G20"
/tissue_type="leaf"
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Best Local Si
Matches 21
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TITLE JOURNAL COMMENT

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AUTHORS REFERENCE

LOCUS DEFINITION

CF312715

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Gaps

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Length 21;

source

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21 bp mRNA linear EST 18-AUG-2003 JMT--01-K14.bl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza stiva (japonica cultivar-group) cDNA clone JMT--01-K14, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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/dev stage="14 days after
/dev stage="14 days after
/lab_host="E.coli DH10B"
/clone lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongln, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Location/Qualifiers
             0; Indels
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100.0%; Pred. No. 9.5e+02;
tive 0; Mismatches 0;
             0; Mismatches
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/db_xref="taxon:39947"
/clone="JMT--01-K14"
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          21; Conservative
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CF332956/c
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(SM Oryza sativa (japonica cultivar-group)
(Sukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.

El (bases 1 to 21)

S (im, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                        /mol type="mRNA"

/unclivar="Nackdong"

/unclivar="Nackdong"

/db.xref="Laxon:39947"

/clone="NACL--01-D20"

/tissue_type="callus"

/dow stage="proliferated callus on 2N6 media for 30 days"

/dow stage="proliferated callus"

/dow stage="proliferated callus"

/dome_lib="Rice callus plasmid cDNA library (NACL)"

/noce="Vector: pCR4-TOPO; Site 1: EcoR1; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF327391 21 B-AUG-2003 NACL--01-N18.gl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-N18, mRNA
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University Yorongin, Kyeonggi, Korea Tel: 82 31 330 6193
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/lab_host="E.coli DH10B"
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    21
/organism="Oryza sativa (japonica cultivar-group)"

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                                                                                                                                 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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100.0%; Pred. No. 9.5e+02;
ative 0; Mismatches 0;
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Best Local Similarity
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CF327391
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RESULT 1200 LOCUS DEFINITION

ò 셤 CF327391

ORGANISM

ACCESSION VERSION KEYWORDS SOURCE TITLE JOURNAL

COMMENT

FEATURES

REFERENCE AUTHORS ö

Gaps

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Similarity 100.0%; Pred, NO. ...
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  'lab host="E.coli SOLR"
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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CN546489.1 GI:46911114
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Vitis vinifera
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Matches 21; Conserv
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
L Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
Vongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCR4-TOPO, Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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RCL1--01-P04.gl Regenerated callus lambda phage CDNA library (RCL1)
Oryza sativa (japonica cultivar-group) CDNA clone RCL1--01-P04,
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yonglin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:39947"
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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100.0%; Pred. No. 9.5e+02;
tive 0; Mismatches 0; Indels
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CF338522
CF338522.1 GI:33825432
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Best Local Similarity 100.0.
The Conservative
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KEYWORDS
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CN546504/c
LOCUS CN546504 21 bp mRNA linear EST 30-APR-2004
DEFINITION EST 18648 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
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                                                                        /note="Vector: pBluescript SK(+); Site_1: SstI, Site_2: Abol; cDNA was inserted into landa Uni-Zapa XR vector at S'end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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1 (bases 1 to 21)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
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| Clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
| Inde="Organ: Fruit without seeds; Vector: Lambda
| TriplEx2; Site_1: SfilA, Site_2: SfilB; Oriented library"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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100.0%; Pred. No. 9.5e+02;
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100.0%; Pred. No. 9.5e+02;
iive 0; Mismatches 0;
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clone B3CS57RB007G04 3', mRNA sequence.

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Query Match
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Vitis vinifera"
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TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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Vitis vinifera
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, Vitaceae, Vitis.

1 (bases I to 21)
Abbal, P., Agasse, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
                                                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
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Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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CDNA clone B3CS58RB008G02 3', mRNA sequence.
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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                                                                   Vitis vinifera
                                                                                         Vitis vinifera
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CO779794 21 bp mRNA linear EST 05-AUG-2004 BL007D E05 6-Day Axolotl Tail Blastema (6DAxBL) Ambystoma mexicanum cDNA 5' similar to hypothetical protein, mRNA sequence.
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/cultivar="cabernet Sauvignon"
/dultivar="cabernet Sauvignon"
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/dev stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
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/cell_type="rail Blastema"
/coll_type="rail Blastema"
/coll_type="rail Blastema"
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/clone_lib="6-Day Axolot1 Tail Blastema (6DAxBL)"
/note="vector: pCWNSport6; Site_l: Not1; Site_2: Sall;
/note="vector: pCWNSport6; Site_l: Not1; Site_2: Sall;
/note="vector pCWNSport6; Site_l: Not1; Site_2: Sall;
/note_rail rail along mRNA was polydT primed and cloned into
NMC1-Sall site of pCWNSport6. Bacterial host is
FMDH108-TONA. Average insert size is 1.67 kB.
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Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Email: tanakaa@mpi-cbg.de
Email: tanakaa.e
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Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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Ambystoma mexicanum
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Contact: Elly M. Tanaka
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ik79c11.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
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/note="Organ: megasporophyll; Vector: pBK-CMV; Site_1:
Xhol; Site_2: Eco RI; Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts."
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1 (bases 1 to 21)

Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
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/db_xref="taxon:3311"
/sex="Female"
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AZ348593 29-SEP-2000 1M0085A13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0085A13 F, genomic survey sequence.
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1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rajlam, H., Longacres, S., Mahmoud, M., Menen, E., Pedersen, T., Reily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
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/clone lib="Mouse 10kb plasmid UGGZIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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                                                                                                                                                                                                                                                                                                                                           /clone_lib="Ginkgo female leaf (NYBG)"
/note="Grgan: leaf; Vector: :DBK-CMY, Site_1: XhOI;
Site_2: ECO RI; Stratagene ZAP Express CDNA Synthesis
The library was size-fractionated to enrich for large
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Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 317 8874
Email: mccombie@cshl.org
Seq primer: -21Ml3UnlyRev.
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Insert Length: 10000 Std Error: 0.00
Plate: 0085 row: A column: 13
Seg primer: CGTTGTAAAACGACGGCCAGT

    1. .21
    forganism="Ginkgo biloba"
    mol_type="mRNA"
    db_xref="taxon:3311"
    sex="female"

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/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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High quality sequence stop: 21.
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Fax: 801 585 7177
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (basea 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb Unpublished (2000)
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1M0088C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M008BC14 F, genomic survey sequence.
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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tive 0; Mismatches 0; Indels
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Plate: 0088 row: C column: 14
Seg primer: CGTTAAAACGACGGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
84112, USA
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/strain="C57BL/6J"
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Mus musculus
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAD42 (gil-f172114[gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Murcidea; Muridae; Musinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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(Dipublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 108, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Fax: 801 585 7177

Email: ddunmegenetics.utah.edu

Fax: 804 5 70000 Std Error: 0.00

Flate: 0145 row: 0 column: 16

Seq primer: CACACAGGAAACAGCTATGACC
Laboratory Mouse DNA Resource

    .21
    /organism="Mus musculus"

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AUTHORS
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Page 470

Tue Nov

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In the control of the
                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalvel (gilly 4732114) [gb] AR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus
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Insert Length: 10000 Std Error: 0.00
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aboratory Mouse DNA Resource
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/strain="C57BL/6J"
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/clone="UUGC1M0145022"
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Fax: 801 585 7177
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TITLE

FEATURES

AZ386794

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(http://www.htm.er.gr.ncsolutes/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gql/4732114[gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLLO-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (Bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Duse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
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1M0149A13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic Conne UUGC1M0149A13 R, genomic survey sequence.
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0149A13"
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil47321141gb]AP129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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21 bp DNA linear GSS 02-0CT-2000
1M0150B10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0150B10 R, genomic survey sequence.
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1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rallay, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Waiss, R.
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/clone_lib="Mouse 10kb plasmid UnGclM library"
/note="Vector: FWD4Zuv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CACACAGGAAACAGCTATGACC
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0150B10"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4732114 [gb] AF129072.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Sciurognathi; Muroidea; Muridae; Mus.

(1) (bases 1 to 21)

Sunn,D., Aoyagi,A., Barber,W., Beach.T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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/clome_lib="Mouse_10kb_plasmid_UGCIM_library"
/note="Wector: PWD42ry; Purified_genomic_DNA_from M.
musculus C57BL/6J (male) was obtained from the Jackson
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100.0%; Pred. No. 9.5e+02;
rative 0; Mismatches 0; Indels
Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0176 row: E column: 24
Seq primer: CGTTGTAAAACGACGGCCAGT
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/organism="Mus musculus"
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/strain="C57BL/6J"
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/clone="UUGC1M0176E24"
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High quality sequence stop: 21.
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Matches 21; Conservative
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Fax: 801 585 7177
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KEYWORDS
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CE I (bases 1 to 21)

RS Dun, D., Acyagi, A., Barber, M., Beacor, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Nouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
B4112, USA
            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pubAld [94] #132114[9b] AP129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus
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ilarity 100.0%; Pred. No. 9.5e+02;
Conservative 0; Mismatches 0; Indels
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Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error:
Plate: 0186 row: D column: 23
Seprimer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
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/strain="C57BL/6J"
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/clone="UUGC1M0186D23"
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Fax: 801 585 7177
Email: ddunn@qenet
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Best Local Similarity
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VERSION KEYWORDS

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SOURCE

TITLE

FEATURES

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWMP2 (gil 4772114 [gb] AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Killo-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 21)

1 (bases 1 to 21)

1 (bases 1 to 21)

2 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Dunn, D., Borone scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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/clone lib="Mouse lokb plasmid UUGCNH library"
/note="Vector: PWB4Zny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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100.0%; Pred. No. 9.5e+02;
ive 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0186 row: N column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plaemid ends
High quality sequence stop: 21.
Location/Qualifiers
Laboratory Mouse DNA Resource
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Outs, correct Similarity 100.0%; Pred. No. 9.5

Best Local Similarity 100.0%; Mismatches
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/strain="C57BL/6J"
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/clone="UUGC1M0186N08"
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Mus musculus
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AZ412931.1 GI:10536944
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 47121141gbl AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xiii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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21 bp DNA linear GSS 03-OCT-2000
1M0189M07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0189M07 R, genomic survey sequence.
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1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Ztokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Unpublished (2000)
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Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0189 row: M column: 07
Seg primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0189M07"
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Marches 21; Conservative
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi |4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murcidea; Muridae; Murinae; Mus.

1 (bases 1 to 21)

El (bases 1 to 21)

Sciurognathi; Muscidea; Murinae; Mus.

Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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/clone_lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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100.0%; Pred. No. 9.5e+02;
rative 0; Mismatches 0; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0276 row: F column: 07
Seg primer: CGTTCTAAAACGACGCCCAGT
Class: plasmid ends
Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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/clone="UUGC1M0276F07"
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AZ465890.1 GI:10624015
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Best Local Similarity 100.0
Matches 21, Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4712114 [gb/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah Genome Center
University of Utah
Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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1M0436N02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0436N02 R, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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Laboratory Mouse DNA Resource
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Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0436N02"
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Location/Qualifiers
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Mus musculus
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AZ611116.1 GI:11733306
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Plate: 0436 row: N c
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Fax: 801 585 7177
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TITLE

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gil-fla1214[gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XII0-Gold (stratagene) cells and selected for ampicillin resistance."
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1 (basea 1 to 21)
1 Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Dasamid inserts
Plasmid inserts
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/clone lib="Mouse lokb plasmid UNGCN library"
/note="Vector: PWD47ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Insert Length: 10000 Std Error: 0.00
Plate: 0437 row: E column: 13
Seg primer: CACACAGGAAACAGCTAATGACC
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/mol type="genomic DNA"
/strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC1M0437E13"
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Location/Qualifiers
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Mus musculus
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Fax: 801 585 7177
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Matches 21; C
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwdet (gqi 4732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII0-GGld (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummanlai, Euteleia; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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/lab.host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 9.5e+02;
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Insert Length: 10000 Std Error: 0.00
Plate: 0444 row: M column: 19
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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AZ615628.1 GI:11737734
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Best Local Similarity 100.0
Matches 21; Conservative
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84112, USA
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAP2 (gil 47721141gb] AF125072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
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Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/note="Wector: PWD42Ivv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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Laboratory Mouse DNA Resource
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0474H03"
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Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Buntajia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognath; Murodaa; Muridae; Mus.

CE Lasses 1 to 21)

Rabon,D., Aoyagi,A., Barber,M., Beacon,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

Ball2, USA.
             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gil 4732114 [gb] AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0474G11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0474G11 F, genomic survey sequence.
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Insert Length: 10000 Std Error: 0.00
Laboratory Mouse DNA Resource
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Plate: 0474 row: G column: 11
Seg primer: CGTTGTAAAACGACGGCCAGT
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/strain="C57BL/63"
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/clone="UUGC1M0474G11"
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4712114[$D]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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E 1 (bases 1 to 21)
S Dum, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Reilly,M., Rose,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tungey,A., von Contacts

L Unpublished (2000)
L Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ657727 1000 21 bp DNA linear GSS 14-DEC-2000 1M0534B07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone_UUGCIM0534B07 F, genomic survey sequence.
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Insert Length: 10000 Std Error: 0.00
Plate: 0534 row: B column: 07
Seg primer: CGTTGTAAAACGACGGCCAGT
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/organism="Mus musculus"
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/strain="C57BL/6J"
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/clone="UUGC1M0534B07"
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Local 21; Conservative
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Fax: 801 585 7177
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was hydrodynalically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with TA DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-GGld (Stratagene) cells and selected for ampicillin resistance."
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/close_lib="Mouse_lokb plasmid UUGCIM library"
/note="Wector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
(http://www.jax.org/resources/documents/dnares/). The
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0564011"
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Best Local Similarity 100.0
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Fax: 801 585 7177
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84112, USA
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAPA2 (gil-f4732114 [gb]-RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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21 bp DNA linear GSS 16-FEB-2001
1M0571L11F Mouse 10kb plasmid UJGC1M library Mus musculus genomic
clone UJGC1M0571L11 F, genomic survey sequence.
AZ769976.1 GI:12890681
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
I (basea I to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
William Contact: Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Fax: 801 585 7177

Email: ddunmogenetics.utah.edu

losert Length: 10000 Std Error: 0.00

Plate: 0571 row: L column: 11

Seq primer: CGTIGTAAAACGACGGCCAGT
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/strain="C57BL/6J"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwAp42 (gil-#1432114|gbh-#129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacres, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, W., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Dupublished Genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 300, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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2M0046G18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0046G18 R, genomic survey sequence.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Mus.
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aboratory Mouse DNA Resource
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.
Plate: 0046 row: G column: 18
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC2M0046G18"
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TITLE

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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerses and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil/4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 21)

2 (bases 1 to 21)

3 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Unpublished (2000)

1 Unpublished (2000)

1 Contact: Robert B. Weiss

1 University of Utah Genome Center
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2N0056C09R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0056C09 R, genomic survey sequence.
AZ799327
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Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: C column: 09
Seg primer: CACACAGGAAACAGCTATGACC
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0056C09"
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Location/Qualifiers
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Fax: 801 585 7177
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xili0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (basea 1 to 21)

1 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Wiederhausern, A. and Wright, D., Weiss, R. Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
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/lab.host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
fronth: 10000 Std Brror: 0.00
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Plate: 0074 row: E column: 19
Seg primer: CGTGTAAAAACGACGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC2M0074E19"
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AZ810054
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWADA2 (gilfyla)[A12114[gh]AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone_lib="Mouse_10kb_plasmid UGGCIM_library"
/note="Wector: PWD42nv; Purified genomic_DNA_from m.musculus_C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0083 row: H column: 11
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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clone="UUGC2M0083H11"
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Anna 21; Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwdet (gil 4732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xiii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rammalais; Eutheria; Buarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Muridae; Musinae; Mus

1 (bases 1 to 21)

S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid innerts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

University of Utah
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2M0089110R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0089110 R, genomic survey sequence.
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/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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aboratory Mouse DNA Resource
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Fax: 801 585 7177
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM22 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-GGJd (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 21)
E 1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Reilly,M., Rose,M., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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2M0112P20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0112P20 F, genomic survey sequence.
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/clone_lib="Mouse_10kb plasmid UGCIM library"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Insert Length: 10000 Std Error: 0.00
Plate: 0112 row: P column: 20
Seg primer: CGTTGTAAAACGACGGCCAGT
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/strain="C57BL/6J"
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/clone="UUGC2M0112P20"
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High quality sequence stop: 21.
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Fax: 801 585 7177
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AR129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0142106R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0142106 R, genomic survey sequence.
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Unpublished (2000)
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Eax: 801 585 7177
Eax: 801 585 7177
Eax: 1 ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0142 row: I column: 06
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

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    /organism="Mus musculus"

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University of Utah Genome Center
University of Utah
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Best Local Similarity 100.0
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84112, USA
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gql #4732114 [gb] AR125072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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AZ960063. GI:13831290
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Mus musculus

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Sciurognathi; Muroidea; Muridae; Musinae; Mus.

I (basea 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stockes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Fax: 801 585 717
Fax: 801 585 717
Insert Length: 10000 Std Brror: 0.00
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Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Laboratory Mouse DNA Resource
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/organism="Mus musculus"
/mol_type="genomic DNA"
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/clone="UUGC2M0228A01"
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           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwaley (gql 4732114 [gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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S Dun, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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/clone llb="Mouse lokb plasmid UUGC2M library.
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
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Insert Length: 10000 Std Error: 0.00
Plate: 0288 row: O column: 20
Seg primer: CACACAGGAAACAGCTAATGACC
Laboratory Mouse DNA Resource
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High quality sequence stop: 21.
Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@qenet
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(http://www.jax.org/resourced documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with Ta DNA polymerase and Ta polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwhoz (gil 4732114|gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLL0-Gold (stratagene) cells and selected for ampicillin resistance."
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Brassica rapa subsp. pekinensis
Brassica, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Wagnoliophyta, eudicotyledons; core eudicotyledons; rosids, eurosids II, Brassicales, Brassicaceae, Brassica.

1 (bases 1 to 21)
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BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
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/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBACI; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
avallable at NTAB."
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End sequence of Brassica rapa Sau3AI (KBrS) BAC clone Unpublished (2005)
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Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0;
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Brassica Genomics Team
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Class: BAC ends
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DB 1; Length 21;

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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DU834573.1 GI:83871169
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KBrS006CO7R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS006CO7, genomic survey sequence.
DU830099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /eub_species"pekinensis"

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/clone="KBrS006C07"

/loh host="E. coli DH10B"

/clone lib="KBrS, Brassica rapa Sau3AI BAC library"

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ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
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tive 0; Mismatches 0; Indels
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Brassica rapa subsp. pekinensis
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Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
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DU832906.1 GI:83869502
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Best Local Similarity 100.
Matches 21, Conservative
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; cosids; eurosids II; Brassicales; Brassicacea; Brassica.

E 1 (bases 1 to 21)
S Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suvon, 441-707, Korea
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KBrS014K05F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS014K05, genomic survey
sequence.
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                                                                                                                                                                              End sequence of Brassica rapa Sau3AI (KBrS) BAC clone Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Scodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 21)
Yang/T.J., Kwon/S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,H.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
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BAC end sequence of Brassica rapa ssp. pekinensis Sau3Al BAC clone
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ssp.pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
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/mol_type="genomic DNA"
/cultivar="Chiifu"
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Class: BAC ends.
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
I (bases I to 21)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
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/organism="Brassica rapa subsp. pekinensis"
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Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
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Class: BAC ends.
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Class: BAC
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DX046130 21 bp DNA linear GSS 10-JAN-2006 KBrB047K19R KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB047K19, genomic survey sequence.

DX046130
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by Yong-Pyo Lim (CNU)."
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Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Brassica Genomics Team
Mational Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
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2709 AAAAAAAAAAAAAAAAAA 2729
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DX050095.1 GI:84744392
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Class: BAC ends.
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Best Local Similarity 100.0
Matches 21; Conservative
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Contact: Beom-Seok Park Brassica Genomics Team National Institute of Agricultural Biotechnology 225 Seodun-Dong, Suwon, 441-707, Korea National Institute of Agricultural Biotechnology 7e1: +82-31-299-1672

Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone KBrB052P02
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="B.coli DH10B"
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/clone lib="KBrB, Brassica rapa BamHI; Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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Brassica rapa subsp. pekinensis
Bukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (Dases 1 to 21)
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M. H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
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Contacts Beom-Seok Park

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225 Seodun-Dong, Suwon, 441-707, Korea

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/mol type="genomic DNA"
/cultivar="Chiifu"
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DX056929.1 GI:84751226
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Class: BAC ends.
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AUTHORS
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UANUSYYJ9 SERBOGEAOIF KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB066A01, genomic survey sequence.
                                                                                          db_xref="taxon:51351"

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pekinensis var. Chilib BAC library (KBrB BAC) is provided

by Yong-Pyo Lim (CNU)."
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pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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Brassica rapa subsp. pekinensis
Brassica, Virdiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaes; Brassica.
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BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
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100.0%; Pred. No. 9.5e+02;
tive 0; Mismatches 0; Indels
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
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                                                                        /sub_species="pekinensis"
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Class: BAC ends.
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Best Local Similarity
Matches 21; Conserva
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RESULT 1249
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/clone_lob="KBrB, Brassica rapa BamHI; Brassica rapa spp
/chote="Vector: Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                  DX075742 11 bp DNA linear GSS 10-JAN-2006 KBrB086M24F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB086M24, genomic survey
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Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
I (bases I to 21)
Yang, T.J. Kwon, S.J. Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Brassica faquence of Brassica rapa BamHI (KBrB) BAC clone
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Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 21)
Yang, T.J. Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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KBrB095F12F KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB095F12, genomic survey
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/mol_type="genomic DNA"
/cultivar="Chiifu"
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Class: BAC ends.
Location/Qualifiers
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Best Local Similarity 100.
Matches 21; Conservative
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DX082155/c
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pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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                                                                                                                   Contract: Beom-Seok Park
Brassica Genomics Team
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National Institute of Agricultural Biotechnology
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Tel: +82-31-299-1670
Fax: +82-31-299-1670
Fax: +82-31-299-1670
Fax: 482-31-299-1670
Fax: 482-31-299-16
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Wisidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (baess 1 to 21)
Yang, T.J., Kwon, S.J., Klm, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
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BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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Contact: Beom-Seok Park
Barssica Genomics Team
National Institute of Agricultural Biotechnology
255 Seedun-Dong, Suwon, 441-707, Korea
Fax: +82-31-299-1672
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)

    .21
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/mol type="genomic DNA"
/culEivar="Chiifu"
/culEivar="Chiifu"

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Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0;
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Class: BAC ends.
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Class: BAC ends.
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/clone="KBrB09524"
/lab_host="E.Coli DH108"
/clone lib="KBrB. Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBACI; Site_1: BamHI; Brassica rapa spp
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by Yong-Pyo Lim (CNU)."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF282024

22 bp mRNA linear EST 14-AUG-200
14ETL--09-F13.bl Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.
1 (bases 1 to 22)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol type="mgNA"
/db_xref="taxon:9606"
/clone="DRP2p566C1646"
/clone="DRP2p9e="kidney"
/dev stage="fetal"
/lab_host="X1-2blue"
/clone lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: Sal1"
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Location/Qualifiers
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Unpublished (1999)
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CF282024
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Best Local Similarity
Matches 21; Conserv
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AUTHORS
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JOURNAL
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E 1 (bases 1 to 22)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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1 (bases I to 22)
Habermann, B., Bebin, A.G., Herklotz, S., Volkmer, M., Eckelt, K.,
Habermann, B., Bebin, A.G., Schackert, H. K., Wiebe, G. and Tanaka, B.M.
Pehlke, K., Epperlein, H.H., Schackert, H. K., Wiebe, G. and Tanaka, B.M.
An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Fax: 0049 351 210 1489
Email: tanakaempi-cbg.de
Jate: BL003B row: 01 column: H
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
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100.0%; Pred. No. 9.7e+02;
tive 0; Mismatches 0;
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/organism="Ambystoma mexicanum"
clade; Ehrhartoideae; Oryzeae; Oryza.
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/db_xref="taxon:8296"
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Contact: Elly M. Tanaka
Tanaka Lab
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognachi; Murcidea; Murinae; Mus.

1 (bases 1 to 22)

2 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R. Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R. Dupublished (2000)

L. Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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/tissue_type="Tail Blastema"
/cell_type="regenerating tail blastema" (GDAxBL)"
/cell_type="regenerating tail blastema" (GDAxBL)"
/clone_lib="6-Day Axolot! Tail Blastema (GDAxBL)"
/note="Vector: pCMVSport6, Site_1: NotI; Site_2: Sall;
Unnormalized coDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydT primed and cloned into
NotI-Sall site of pCMVSport6. Bacterial host is
BMDH10B-TONA. Average insert size is 1.67 kB.
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
                                                                                                                                                                                                                                                                                                    Length 22;
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0.8%; Score 21; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 21; Conservative 0; Mismatches 0;
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0005K17"
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Location/Qualifiers
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GSS.
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Plate: 0005 row: K c
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KEYWORDS
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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi[4732114]gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ralam, H., Longacres, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Umouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ374487
1M0127H16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic Cone UUGCIM0127H16 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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100.0%; Pred. No. 9.7e+02;
ative 0; Mismatches 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0127 row: H column: 16
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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/clone="UUGC1M0127H16"
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                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
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Matches 21; C
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LOCUS
DEFINITION
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/documents/documents/latts). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
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1 (Dases 1 to 22)

2 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T., Niederhausern,A. and Wright,D., Weiss,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R., Unpublished (2000)

L Ontact: Robert B. Weiss
University of Utah Genome Center
10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) electrophoresis. Octor DNA was prepared from a derivative inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X1.10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZSOS769 1008 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0346A10R ouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0346A10 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                            Length 22;
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100.0%; Pred. No. 9.7e+02;
tive 0; Mismatches 0; Indels
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0346A10"
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
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Best Local Similarity 100.0
Matches 21, Conservative
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84112, USA
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciutognathi; Murcidae; Murinae; Mus.

1 (bases 1 to 22)

2 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2010)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymcelectide kinase. Adaptor oligonucleorides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
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/clone_lib="Mouse_l0kb plasmid UUGClM library"
/note="Vector: PWD4Zny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0098 row: K column: 07
Seq primer: CGTTGTAAACGACGCCAGT
class: plasnid ends

    .22
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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/clone="UUGC2M0098K07"
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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.11), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptorebent B. coli X110-GGJd (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                      DKF25560133 r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZP566N213, mRNA sequence.
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Populus trichocarpa x Populus deltoides
Populus trichocarpa x Populus deltoides
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 23)
Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehrer, et al.)
Unpublished (1999)
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/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: Sal1"
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Location/Qualifiers
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100.0%; Pred. No. 9.9e+02;
tive 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
/clone="DKFZp566N213"
/tissue_type="kidney"
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DT503381.1 GI:73900643
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Matches 21; Conservative
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Matches 21; Conserv
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1 (bases 1 to 23)
Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y.,
Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G.,
Babakaiff,R., Barbon,M., Chand,S., Featherstone,R., Masson,A.,
Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,
Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 bp mRNA linear EST 06-JUL-2004
DKF2D564L2164 rl 564 (synonym: hfbr2) Homo sapiens cDNA clone
AL037096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                  The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
Unpublished (2004)
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                   Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         l. .23
/organism="Populus trichocarpa x Populus deltoides"
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0
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100.0%; Pred. No. 9.9e+02;
vative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                               column: 19
                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:3695"
/clone="WS0136_G19"
                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/cultivar="H11-11"
                                                                                                                                                                                                                                                                                           Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Plate: WS0136 row: G colu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TAAAAAAAAAAAAAAA 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
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Gaps

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0; Indels

0; Mismatches

21; Conservative

Matches

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Trypanosoma.

If (bases 1 to 26)

If (bases 2 to 20)

If (bases 2 
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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                                                                          Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
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Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 1e+03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol type="mRNA"
/mol wref="taxon:9606"
/clone="DKRZp56412164"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="x1.2blue"
/clone_lib="564 (synonym: hfbr2)"
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Best Local Similarity 100.0%; Pred. No. 1e+
Matches 21; Conservative 0; Mismatches
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/strain="TREU927"
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/clone="321g11"
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                                                                                                    Wiemann, S.
EST (Duesterhoeft, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
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Hominidae, Homo.
1 (bases 1 to 26)
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0.8%; Score 21; DB 1; Length 26; 100.0%; Pred. No. 1e+03;

Query Match Best Local Similarity

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor
                                                                                                                                                                                                             GSS 13-DEC-2000
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                                                                                                                                                                                 AACOZOLUI
1M0466J07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0466J07 F, genomic survey sequence.
AZ626101
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1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von. Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 20.8; DB 1; Length 24; 91.7%; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rel: 601 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0466 row: J column: 07
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasnid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC1M0466J07"
   2729
                                                        1 AAAAAAAAAAAAAAA 21
                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
2709 AAAAAAAAAAAAAAAAA
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Matches

ઠે a RESULT 1262 AZ627850 DEFINITION

ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE JOURNAL COMMENT

TITLE

FEATURES

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Mismatches
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Pristionchus pacificus
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Class: fosmid ends
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22; Conservative
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DU829360/c
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                                                                                                                                                                                                             GSS 13-DEC-2000
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1M0474N20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0474N20 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 24)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
Gaps
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Indels
5
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Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: N column: 20
Seg primer: CGTTGTAAAACGACGGCCAGT
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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/strain="C57BL/6J"
                                             2709 AAAAAAAAAAAAAAAAAAAAA 2732
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                                                                        24 AAAAAAGAAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                               AZ627850.1 GI:11750136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: plasmid ends
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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Best Local Similarity
22;
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ö ö GSS 22-DEC-2005 GSS 10-JUL-2004 Brassica rapa subsp. pekinensis Brassica rapa subsp. pekinensis Brassica, viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. CL693181
PRIO160c_A02_2 - PRIO160c.BR (24) Note: Recurring String Mixed stage fosmid_library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence. DU829360 24-bp DNA linear GSS 22-DEC-20 KBrS004M04R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS004M04, genomic survey /db_xref="taxon:54126" /clone_lib="Mixed stage fosmid library of P. pacificus var. California" /note="Vector: pEpifos-5 Fosmid vector" Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

1 (bases 1 to 24)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. AppabB: an AcedB database for the nematode satellite organism Pristionchus pacificus Gaps Gaps Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Max-Planck-Institute for Developmental Biology
Speamannstr. 37-39, Tuebingen D-72076, Germany
Fai: 00497071601498
Email: rall-sommer@tuebingen.mpg.de
Fins library was generated at Caltech, Passadena, USA and end ö ö Length 24; Indels /organism="Pristionchus pacificus" /mol_type="genomic DNA" /strain="California" Nucleic Acids Res. 32 (1), D421-D422 (2004) , , DB 1; 0.8%; Score 20.8; DB 1 91.7%; Pred. No. 1e+03; ative 0; Mismatches

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Best Loc
Matches
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Swaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Murinae; Mus.

1 (bases 1 to 25)

S Dunn, D., Aoyagai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid innearts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

University of Utah
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                                                           Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
125 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Bmail: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3Al BAC clone
KBrS004M04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      / sub_speciee="pekinensis"
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spp_pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
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Hahn,J. H. and Park,B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
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                                                                                                                                                                                                                                                                                                                                                                                        organism="Brassica rapa subsp. pekinensis"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0294 row: M column: 10
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1. .25
                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
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Class: BAC ends.
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84112, USA
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KEYWORDS
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF12972.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-GG1d (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
855 California Ave, Palo Alto, CA 94304, USA
856 California Ave, Palo Alto, CA 94304, USA
857 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 8221
Email: walbockstanford.edu
Very probable ligation site of ends cut by single endonuclease.
Very probable ligation site of ends cut by single endonuclease.
Paverse complemented post-ligation sequence from source sequence.
Plate: 4012001 row: F column: 09
Class: transposon-tagged.
Location/Qualifiers
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musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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-hes 2; Indels
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Walbot V
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Zea mays
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DEFINITION
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Page 494

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ampicillin."

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/lab host="DH10B"
/clone lib="4012 - RescueMu Grid BB"
/clone lib="4012 - RescueMu Grid BB"
/note="Drgan: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/. Grid BB was grown at UC Barkeley in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
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/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHl; Site_2: BglII;
/RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHl and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
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4021004B07.2EL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 8221

Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021004 row: B column: 07
Class: transposon-tagged.
Location/Qualifiers
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CZ917081
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
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                                                            ö
                                                                                                                                                                                                                                                                                                       AZ437459 26 bp DNA linear GSS 03-OCT-2000 1M0225B15R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0225B15 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Murcoidea; Muridae; Murinae; Mus.
Sciurognathi; Murcoidea; Muridae; Murinae; Mus.
I (bases I to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Roilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note=""dector: PMP42nv; Purified genomic DNA from Musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                            Gaps
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0.8%; Score 20.8; DB 1; Length 25; 91.7%; Pred. No. 1e+03; tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email ddundgenetics.utah.edu
Insert Length: 10000 Std Error: 0.0
Plate: 0225 row: B column: 15
Seg primer: CACACAGGAAACACCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="taxon:10090"
/clone="UUGC1M0225B15"
                                                                                                                   2709 AAAAAAAAAAAAAAAAAAAAA 2732
                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                           AZ437459.1 GI:10561472
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                                                               Conservative
                                  Similarity
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Best Local Simir
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           Query Match
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AZ437459/c
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CF298427/c

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KEYWORDS SOURCE

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

ACCESSION VERSION

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/ Bex."Femals."
/ Jab host="E. coli DH10B T1 phage resistant cells."
/ clon=lib="MP-FL-A-2"
/ clon=lib="YP-P-FL-A-2"
/ note="Vector: pBluescript II SK (+) XR; Site 1: SstI (5')
end of cDNA); Site_2: XhoI (3' end of cDNA); Phloem and
cambium from 8 year old trees harvested within the Boise
Cascade region of Washington state on May 15th, 2001. cDNA
was prepared from 20 micrograms of mRNA according to the
full-length cDNA library construction method described by
Carninci P. et al. (2000), Genome Research
10(10):1617-1630 and directionally ligated into the
pBluescript II SK (+) XR vector digested with SeII (5')
end) and XhoI (3'). Plasmid DNA was then transformed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
Populus trichocarpa
Populus trichocarpa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachoophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachoophyta;
Fosida; eurosida I; Malpighiales; Salicaceae; Saliceae; Populus.
I (Bases I to 22)
Kalph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y.,
Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G.,
Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A.,
Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C. E., Siddigui, A.,
Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and
                            Ralph.S., Cooper.D., Kolosova,N., Oddy,C., Butterfield,Y.,
Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G.,
Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A.,
Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,
Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 bp mRNA linear EST 29-AUG-2005
WS01126.BR H02 FT-P-FL-A-2 Populus trichocarpa cDNA clone
DT497428
                                                                                                                                                                                                                   The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
Unpublished (2004)
  rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
                                                                                                                                                                                                                                                                                       onjubilished (2004)
Contact: Jocest Schlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 123
Tel: 1-604-822-082
Fax: 1-604-822-214
Email: bohlmann@msl.ubc.ca
Plate: WS01118 row: H column: 18
High quality sequence stop: 105
POLYAPYES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       electroporation into DH10B cells (Invitrogen) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20.4; DB 1; Length 22;
Pred. No. 1e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/cultivar="383-2499 (Nisqually-1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .22
/organism="Populus trichocarpa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:3694"
/clone="WS01118_H18"
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DT497428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/culfivar="Nackdong"
/culfivar="Nackdong"
/culfivar="3994"
/clone="7LEAF--01-M24"
/tissue_type="1eaf"
/tissue_type="7 days after germination"
/lab_host="E.coli DH10B"
/clone=11b="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Wector: pCR4-TOPO; Site 1: ECORI; mRNA was capped with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                               CF298427
7LEAF--01-M24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-M24, mRNA
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tobases 1 to 22)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
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                                                  Length 26;
and selected for ampicillin resistance."
                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bhnahm@bio.myongji.ac.kr.
                                                     DB 1;
                                                  0.8%; Score 20.8; DB 1;
91.7%; Pred. No. 1.1e+03;
                                                                                                  0; Mismatches
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                                                                                                                                                                                                           26 AAAAAAAAAGAAAAGAAAAA 3
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Location/Qualifiers
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                      Query Match
Best Local Similarity 91.72
Best Local 22, Conservative
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Best Local Similarity 95.5.
....hes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
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DT494457

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ACCESSION VERSION KEYWORDS SOURCE

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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Populus trichocarpa x Populus deltoides
Populus trichocarpa x Populus deltoides
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
1 (bases 1 to 22)
Ralph, S., Cooper, D., Kolposova, N., Oddy, C., Butterfield, Y.,
Rikpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G.,
Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A.,
Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A.,
Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DT502811 22 bp mRNA linear EST 29-AUG-2005 WS0134.BR_F03 PTxD-IL-FL-A-4 Populus trichocarpa x Populus deltoides cDNA clone WS0134_F03 5', mRNA sequence.
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Unpublished (2004)
The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
Unpublished (2004)
                                                                                                  Contract: Joer 120 to 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'organism="Populus trichocarpa"
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Genome BC forest genomics program
University of British Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2708 TAAAAAAAAAAAAAAAAA 2729
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Matches 21, Conservative
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/Bab host="E. coli DH10B T1 phage resistant cells"
/clone_lib="PTxD-IL-FL-A-4"
/clone_lib="Vetcor: pBluescript II SK (+) XR; Site I: SEI (5'
end of cDNA); Site 2: XhoI (3' end of cDNA); Sapling trees
one metre in height and grown under greenhouse conditions
were exposed to continuous feeding by Malacosoma disstria
Hubner (forest tent caterpillar) mid-instar larvae caded
on the sapling using mesh bags. Mature leaves from within
the caged region were collected 4 hours, 8 hours and 24
hours after the onset of treatment. Mature leaves were
also collected above the caged region (systemic response)
4 hours, 12 hours and 48 hours after the onset of
treatment. mRNA was isolated from each tissue source
independently and equal quantities of mRNA from each
tissue were then pooled. CDNA was prepared from 20
micrograms of mRNA according to the full-leapth cDNA
library construction method described by Carninci P. et
al. (2000), Genome Research 10(10):1617-1630 and
directionally ligated into the pBluescript II SK (+) XR
vector digested with SsII (5' end) and XhoI (3'). Plasmid
DNA was then transformed by electroporation into DH10B
cells (Invitrogen) for propagation."
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2M0287L21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
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1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
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Contact: Robert B. Weiss
Contract: Your Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
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                                                                                                                                                                                                                                                                                                                                                    /organism="Populus trichocarpa x Populus deltoides"
/mol_type="mRNA"
/cultivar="H11-11"
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Similarity 95.5%; Pred. No. 1e+03;
21; Conservative 0; Mismatches
                                                                                           Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Blate: WS0134 row: F column: 03
High quality sequence stop: 115
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3695"
/clone="WS0134_F03"
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Mus musculus
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Location/Qualifiers
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DX060105.1 GI:84754401
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                                                                        Seg primer: T7
Class: BAC ends.
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Class: BAC ends.
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DX060105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4712114[gb]AR12977.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLLO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNBJS072 SEPONA Linear GSS 22-DEC-2005 KBrS015P15F KBrS, Brassica rapa SaulAI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS015P15, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                               /lab_host="E. coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus CS7BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.7%; Score 20.4; DB 1; Length 22; 95.5%; Pred. No. 1e+03; tive 0; Mismatches 1; Indels
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Secdun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Tel: 801 585 5606
Fax: 801 585 7177
Fax: 801 585 7177
Fax: 802 585 7177
Fate: 0.00 Std Brror: 0.00
Flate: 0.287 row: L column: 21
Sea primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
                                                                                                                                                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="UUGC2M0287L21"
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                                                                                                                                                                                                                                                                                                                             /sex="Female"
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Best Local Similarity 95.5°
Matches 21, Conservative
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pekinensis var. Chiftu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
Fax: +82-31-299-1672
Email: pbecm@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS015P15
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Boermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Tosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (Bass II; Brassicales; Brassicaceae; Brassica.
I (Bass II; Brassicales; Brassicaceae; Brassica.
Bark, J. Y., Lim, M. H., Kim, J. A., Kim, J. S., Lim, K. B., Jin, M.,
Bark, J. Y., Lim, M. H., Kim, H. I., Choi, B. S., Seol, Y. J., Park, D. S.,
Hahn, J. H. and Park, B. S.
Unpublished (2005)
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BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. coli DH10B"
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/note="Vector: pcUGIBACI; Site 1: Sau3AI; Brassica rapa sap pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."
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22 bp DNA linear GSS 10-JAN-2 KBrB066D14F KBrB, Brassica rapa subsp. pekinensis genomic clone KBrB066D14, genomic survey sequence.
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/organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/culTivar="Chiffu"
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    22
/organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/cultivar="Chiftu"

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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
                                                                                                                                                                                                                                                                                                                                                                       /sub_species="pekinensis"
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/clone="KBrS015P15"
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Wiemann, S.
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Email: nalsayed@tigr.org

at http://www.sanger.ac.uk/Projects/T_brucei/.
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DKF2p566N082, mRNA sequence.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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T. brucei sheared genomic DNA clone 303g05, forward sequence,
genomic survey sequence.
#1497201
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Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                    0.7%; Score 20.4; DB 1; Length 22; 95.5%; Pred. No. 1e+03; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |mol_type="genomic DNA"
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Homo sapiens
              Query Match
Best Local Similarity 95.5%
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TA303G05P
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AL038592 23 bp mRNA linear EST 06-JUL-2004
DKFZp566G1446_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp56GG1446, mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 23)
Ottenwaelder,B., Obermaler,B., Mewes,H.W., Gassenhuber,J. and
1 (bases 1 to 23)
Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
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EST (Ottenwaelder, et al.)
Unpublished (1999)
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Unpublished (1999)
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Best Local Similarity 51...
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BX559898.1 GI:33367802
                                    21; Conservative
                 Best Local Similarity
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AL038609
DKFZp566G0946_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp566G0946, mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
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1 (bases 1 to 23)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
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/db_xref="laxon:9666"

/clone="DKFZp566G0946"

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/lab_host="X1-2blue"

/clone_lib="S66 (synonym: hfkd2)"

/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
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/note="Vector: pAMP1; Site_1: Not1; Site_2: Sall"
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Location/Qualifiers
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Location/Qualifiers
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/lab_host="X1-2blue"
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                                                                                                                                                                                                                    Wiemann,S.
EST (Ottenwaelder, et al.)
Unpublished (1999)
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Unpublished (1999)
                                                 AL038609
AL038609.1 GI:49682169
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                                                                                                  Homo sapiens (human)
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Homo sapiens
                                                                                                                                                                                                                                                                     Contact: MIPS
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23 bp mRNA linear EST 14-AUG-2003 14FIL--05-P06.bl Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-P06, mRNA sequence. CF279593. CF279593.1 GI:33656979
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                                                                                                                                                                                                                                                                                                        BX559898 Glossina morsitans morsitans adult infected gut Glossina morsitans cDNA clone Tse46d05_plc, mRNA sequence.
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T.brucei"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 All clones with suffix qlc are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insects; Pterygota;
Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.

1 (bases 1 to 23)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M. B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the teetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .23
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/mol_type="mNA"
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/clone=lib="Glossina morsitans morsitans adult infected
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Thinxton, Cambridge, CB10 18A, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
0.7%; Score 20.4; DB 1; Length 23; 95.5%; Pred. No. 1.1e+03; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    response genes
Genome Biol. 4 (10), R63 (2003)
                                                                                                            2705 TACTAAAAAAAAAAAAAAA 2726
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ORGANISM

SOURCE

TITLE JOURNAL COMMENT

AUTHORS

REFERENCE

Bource

FEATURES

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/ Jab host="E-majorary | Jab host="E-majorary | Jab host="E-coli DH10B T1 phage resistant cells" | Jab host="E-coli DH10B T1 phage resistant cells" | Jab host="E-coli DH10B T1 phage resistant cells" | /clos="lab" | /clos="Vector: pBluescript I1 SK (+) XR, Site_1: Sat1 (5' end of cDNA); Site_2: XhoI (3' end of cDNA); Phloem and cambium from 8 year old trees harvested within the Boise Cascade region of Washington state on May 15th, 2001. cDNA was prepared from 20 micrograms of mRNA according to the full-length cDNA library construction method described by Carninci P. et al. (2000), Genome Research 10(10):1617-1630 and directionally ligated into the pBluescript I1 SK (+) XR vector digested with Sat1 (5' end) and XhoI (3'). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae, Homo.

1 (bases 1 to 24)

Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALU48765
DKFZp566M233_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp566M233, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutelec
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="kidney"
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/lab_host="X1-2blue"
/clone llb="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.7%; Score 20.4; DB 1; Length 23; 95.5%; Pred. No. 1.1e+03; ative 0; Mismatches 1; Indels
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Location/Qualifiers
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                                                                                                    1. .23
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/cultivar="383-2499 (Nisqually-1)"
/db_xref="taxon:3694"
/clone="WS01125_A14"
  14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566M233"
                             High quality sequence stop: 108
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Best Local Simi
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Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y., Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G., Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A., Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A., Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and
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The poplar transcriptome: Analysis of expressed sequence tags from
multiple cDNA libraries
Contact: Nahm B.H.
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yogin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and Then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2004)
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 123
Tel: 1-604-822-0282
Fax: 1-604-822-2114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Oryza sativa (japonica cultivar-group)"
mol_type="mRNA"
cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
Populus trichocarpa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
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Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
0.7%; Score 20.4; D
Best Local Similarity 95.5%; Pred. No. 1.1e
Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:39947"
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RESULT 1283

δ 셤 DT496947

DEFINITION

ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

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Gaps

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EST 04-SEP-2003

Euteleostomi;

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Gaps

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/lab host="E. coli DH10B T1 phage resistant cells"
/clone lib="PT-P-FL-A-2"
/clone lib="PT-P-FL-A-2"
/note="Vector: pBluescript II SK (+) XR; Site 1: SStI (5'
end of cDNA); Site 2: XhoI (3' end of cDNA); Phloem and
cambium from 8 year old trees harvested within the Boise
Caccade region of Washington state on May 15th, 2001. cDNA
was prepared from 20 micrograms of mRNA according to the
full-length cDNA library construction method described by
Carninci P. et al. (2000), Genome Research
10(10):1617-1630 and directionally ligated into the
pBluescript II SK (+) XR vector digested with SetI (5'
end) and XhoI (3'). Plasmid DNA was then transformed by
electroporation into DH10B cells (Invitrogen) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lessiva/1 25 bp mRNA linear EST 15-AUG-2003 ABF-05-C07.gl ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--05-C07, mRNA sequence.
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  The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
Unpublished (2004)
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Nahm B.H.
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yogin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                            Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smitch Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Blate: WS01123 row: A column: 15
High quality sequence stop: 124
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 25)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale sequencing Analysis of Rice ESTs

Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="383-2499 (Niequally-1)"
/db xref="taxon:3694"
/clone="WS01123_A15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.7%; Score 20.4; DB 1; Best Local Similarity 95.5%; Pred. No. 1.1e+03; Matches 21; Conservative 0; Mismatches 1;

    .24
    /organism="Populus trichocarpa"

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                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            propagation.
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KEYWORDS
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                                                                                                                   CF326993 24 bp mRNA linear EST 18-AUG-2003 NACL--01-E17.gl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-E17, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 bp mRNA linear EST 29-AUG-2005
WS01123.BR A15 PT-P-FL-A-2 Populus trichocarpa cDNA clone
DT496307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnoliophyta; endicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.

1 (Bases I to 24)

Ralph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y., Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G., Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A., Bohlmann, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                               db xref="taxon:39947"

/clone="NACL--01-E17"

/tissue_type="callus"

/dev stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/lab_host="E.coli DH10B"

/lab_host="E.coli DH10B"

/lone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Populus trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yogin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.7%; Score 20.4; DB 1; Length 24; 95.5%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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CF326993.1 GI:33802241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Nahm B.H.
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Best Local Similarity
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                                                                   RESULT 1285
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                                                                                                                                       DEFINITION
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Gaps

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AMMACATOR 1020 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0209N21 R, genomic survey sequence.
                                                                                                                                                                                                                            CF300714 1inear EST 15-AUG-2003 7LEAF--05-E19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-E19, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Bhrhatroideae; Oryzeae; Oryza.
1 (bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, KyeongJi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Listue type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: BcoRI; mRNA was capped with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (basea 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="wackdong"
/db xref="taxon:3994"
/clone="71EAF-05-E19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.7%; Score 20.2; DB 1; Length 25; ilarity 88.0%; Pred. No. 1.1e+03; Conservative 0; Mismatches 3; Indels
Indels
  1;
  Mismatches
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                                                   2707 CTAAAAAAAAAAAAAAAAA 2728
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                                                                                                          4 CCAAAAAAAAAAAAAAAAAA
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GSS.
                                                                                                                                                                                                                                                                                                                                                                    CF300714.1 GI:33672475
  21; Conservative
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Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                      sequence.
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AZ427752
                                                                                                                                                                                   RESULT 1289
CF300714/c
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Yang, T.J. Kwon, S.J. Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,

Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,

Hahn, J.H. and Park, B.S.

End sequence of Brassica rapa BamHI (KBrB) BAC clone

Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team

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225 Seodun-Dong, Suwon, 441-707, Korea

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Fax: +82-31-299-1670

Email: pbeom@rda.go.kr

Email: pacemace of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      עאישפטבא GSS 10-JAN-2006 KBrB047019R KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB047019, genomic survey sequence.
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/lab_host="B.coli DH10B"
/lab_host="B.coli DH10B"
/clone lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosida II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                     /note="Vector: pcR4-TOPO, Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
                                                                                                                                                        /tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib==#BF9-overexpressing transgenic rice plasmid
cDNA library (ABF)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps

    .25
        Creanism="Orryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivat="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0

    25
/organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/cultivar="Chift"

                                                                                                                                                                                                                                                                                                                                                                                                                                              0.7%; Score 20.4; DB 1; Length 25; 95.5%; Pred. No. 1.1e+03; ive 0; Mismatches 1; Indels
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/db_xref="taxon:51351"
                                                                                                       db_xref="taxon:39947"/clone="ABF--05-C07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2709 AAAAAAAAAAAAAAAAAA 2730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: M13 Reverse
Class: BAC ends.
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Best Local Similarity 95.5;
Matches 21; Conservative
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Best Local Similarity
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LOCUS DEFINITION

DX046299

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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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Gaps

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Euteleostomi;

7 10:41:28 2006

Tue Nov

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil 4732114 [gb] ART29072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse_10kb plasmid UTGCIM library"
/note="Wector: PWD42lv; Purified genomic_DNA_from M.
musculus C57BL/6J (male) was obtained from the Jackson
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
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                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0.09 row. N column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="genomic DNA"
fstrain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC1M0209N21"
                                                                                                                                              Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male"
                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
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84112, USA
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of public [473214 gb] hR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
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T. brucei sheared genomic DNA clone 12f02, reverse sequence,
                                                                   plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
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Trypanosoma brucei
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Blate: 0177 row: F column: 23
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0177F23"
                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 25.
Location/Qualifiers
                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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1 (bases 1 to 25)
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Matches 22; Conserv
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Hominidae; Homo.
1 (bases 1 to 20)
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Best Local Similar
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Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 15A, E-mail: barrell@sanger.ac.uk and
hl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREUS27/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
A kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Barrell, Oxford University Press, 1999).
Email: nelsayed@etigr.org
petails of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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Genomics and Bioinformatics
Roslin, Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
V0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
ECORI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institite,
Location/Qualifiers
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Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Pevelopment of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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/organisme="Sus scrofa"
/mol_type="mRNA"
/clone="c0000033_c23"
/tissue_type="placenta"
/clone_lip="CSEQRANO"
/note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
Not1; Single pass sequencing. Normalised_library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 0.7%; Score 20.2; DB 1; Local Similarity 88.0%; Pred. No. 1.1e+03; nes 22; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2701 TTTGTACTAAAAAAAAAAAAAA 2725
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:5691"
/clone="12f02"
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AJ666402.1 GI:49350853
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Sus scrofa
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20 bp mRNA linear EST 06-JUL-2004 DKF2p566A1746 rl 566 (synonym: hfkd2) Homo sapiens cDNA clone DKF2p566A1746, mRNA sequence.
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DKF2p566A1946 r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKF2p566A1946, mRNA sequence.
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1 (Dases 1 to 20)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
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constructed from pooled tissue from day 30
                                             Length 20;
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/lab_host="k1-2blue"
/clone_lib="566 (synonym: hfkd2)"
                                           0.7%; Score 20; DB 1; Le
100.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 0;
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100.0%; Pred. No. 1.1e+03;
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/db_xref="taxon:9606"
/clone="DKF2p566A1746"
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Location/Qualifiers
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EST (Ottenwaelder, et al.)
Unpublished (1999)
Contact: MIPS
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Unpublished (1999)
Contact: MIPS
MIPS
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DKFZp566F1746_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
AL038570
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DKF2p566M1146_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKF2p566M1146, mRNA sequence.
AL038750.1 GI:49682199
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                    Gaps
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1 (bases 1 to 20)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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/db_xref="taxon:9606"
/clone="bkF2p566A1946"
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/lab_host="xX1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: SalI"
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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany. Location/Qualifiers
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Location/Qualifiers
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/lab_host="X1-2blue"
/clone_llb="566 (synonym: hfkd2)"
                                                                                                                                                                                                             Score 20; DB 1; Le
Pred. No. 1.1e+03;
                                                                                                                                                                                                             Query Match 0.7%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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Unpublished (1999)
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Matches 20; Conserv
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Bhrhatroideae; Oryzeae; Oryza.

1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (12.0.)
Unpublished (12.0.)
Contract: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF280913
14ETL--07-M07.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-M07,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                 Hominidae; Homo.
1 (bases 1 to 20)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
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                                                                                                                                                                                                                                                                                    Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
Location/Qualifiers
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0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
/clone="DKFZp566M1146"
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                                                                                                                                       Wiemann, S.
EST (Ottenwaelder, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
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CF280913
CF280913.1 GI:33658299
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Page

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

RESULT 1299

CF282035

Matches

8

DEFINITION

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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP calade; Enkhatrodideae; Oryzae.

1 (bases 1 to 20)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF299822 20 bp mRNA linear EST 15-AUG-2003 7LEAF--03-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-P22, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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100.0%; Pred. No. 1.1e+03;
iive 0; Mismatches 0;
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota, viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

E I (bases 1 to 20)

S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Genedics and Shoinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                           14-ZUC-203 14-AUG-2003 mRNA linear EST 14-AUG-2003 14FIL--09-F19.gl Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F19, CF282035
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Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-019,
CF282414
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(14Fll)"
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                                                           0.7%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.1e+03; tive 0; Mismatches 0; Indels
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             RT-PCR."
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Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Unpublished (2003)
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YongJin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                    Organ sativa (japonica cultivar-group)
Organ sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Mighlantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Mighlantae; Oryzaa.

Lade; Ehrhartoideae; Oryzaae; Oryza.

El (bases I to 20)

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El (bases I to 20)

Song, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H.

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Unpublished (2003)

Contact: Nahm B. H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
VongIn, Kyeonggi, Korea

Tel: 82 31 321 6355

Bmail: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa (japonica cultivar-group)"

mol type="mRNA"

/cultivar-a."Nackdong"

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/clone="7LEAF-0-1947"

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/dev stage="7 days after germination"

/dab_host="E.col DH108"

/clone=lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Yector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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iive 0; Mismatches 0; Indels
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lilopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

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Ekim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H.

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Tel: 82 31 321 6355
Bmail: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/lab host="8.coli DH108"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and Then used as templates for RT-PCR.
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7LEAF--06-L01.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza
8ativa (japonica cultivar-group) cDNA clone 7LEAF--06-L01, mRNA
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7LEAF--07-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-C16, mRNA
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20 bp mRNA linear EST 15-AUG-2003 HD--09-I13.bl OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--09-I13, mRNA sequence. CP319133. CF319133.1 GI:33690894
                                                                                                                       LEJIODY 20 DP MRNA linear EST 15-AUG-2003
HD--01-L22.bl OBHDAC1-overexpressing transgenic rice plasmid CDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--01-L22, mRNA sequence.
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Oryza sativa (japonica cultívar-group)
Oryza sativa (japonica cultívar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                                                                                                                                                                                                                                                                                                                                                                                                         Embryophyta; Tracheophyta;
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6155

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartcideae; Oryzeae; Oryza.

1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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                   1 AAAAAAAAAAAAAAA 20
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cDNA library (HD)"
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Oryza sativa (japonica cultivar-group)
Eukaryota, viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Torgin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF3131067 200 pm.RNA linear EST 15-AUG-200 LPD-01-BO2.91 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza gativa (japonica cultivar-group) cDNA clone HD--01-B02, mRNA sequence.
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Location/Qualifiers
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Oryza sativa (japonica cultivar-group)
Curza sativa (japonica cultivar-group)
Eukaryota, Viridiplancae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzae, Oryza,
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Song, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B. H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6155
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/organism="Oryza sativa (japonica cultivar-group)"
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100.0%; Pred. No. 1.1e+03;
ative 0; Mismatches 0;
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Oryza sativa (japonica cultivar-group)

Cryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Strepophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Strepophyta; Embryophyta; Tracheophyta;

Spermatcphyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 20)

S Kim, J. S., Juu, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,

Song, S. I., Kim, J. K., Kim, Y. - K. and Nahm, B. H.

Large-grane Scale Sequencing Analysis of Rice ESTS

Unpublished (2003)

Contact: Nahm B. H.

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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
/clone lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF328565 20 bp mRNA linear EST 18-AUG-2003 NACL--03-114.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--03-114, mRNA
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//clone_lib="Rice callus plasmid cDNA library (NACL)"
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/organism="Oryza sativa (japonica cultivar-group)"

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Pred. No. 1.1e+03;
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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0;
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/db_xref="taxon:39947"
/clone="NACL--03-114"
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Length 20;

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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone lib="AtcUMT-verexpressing transgenic rice plasmid
/clone lib="AtcUMT-verexpressing transgenic rice plasmid
/clone lib="AtcUMT-verexpressing transgenic mRNA
/note="Vercor: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
pepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
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Oryza sativa (japonica cultivar-group)
Bukaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongGi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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'organism="Oryza sativa (japonica cultivar-group)"

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/organism="Oryza sativa (japonica cultivar-group)"

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    Location/Qualifiers
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                                                                Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.
E 1 (bases 1 to 20)
S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
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JMT--03-F17.gl AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--03-F17, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Espermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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/clone="JMT--01-P11"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab host="s.coli DHIOB"
/clone lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yogin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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|mol_type="mRNA"
|cultivar="Nackdong"
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CF333173.1 GI:33814617
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line." ö Gaps ö Length 20; Query Match 0.7%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 20; Conservative 0; Mismatches 0; Indels 2709 AAAAAAAAAAAAAAAAA 2728 ઠે

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

RESULT 1313

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DEFINITION CF337494/c

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/clone_lib="AGS-1"
/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
P. carinii organisms (3x169) from a single rat (59-1-6, sacrificed on 3/17/9) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard conditions described by vendor, Stratagene. Further details see www.uky.edu/Project/Pneumocystis/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CN545446 2004 EST 17390 Green Grape Skin Triplex2 Library Vitis vinifera CDNA clone B3CS00GL005C02 3', mRNA sequence.
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Coone_libe-Green Grape Skin Triplex2 Library"
/note="Organ: Fruit skin: Vector: Lambda TriplEx2; Site_1:
SfilA; Site_2: SfilB; Oriented library"
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1 (bases 1 to 20)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp Or seeds) at Various Developmental Stages
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
                University of Kantucky
101 Morgan Building, University of Kentucky, Lexington,
40506-0225, USA
Tel: 606 257 1117
Eax: 606 257 1717
Email: staben@pop.uky.edu.
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    /organism="Pneumocystis carinii"

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/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
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/clone="B3CS00GL005C02"
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7
                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
School of Biological Sciences
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                                                                                                                                         CF337494 20 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--07-P04, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Cura sativa (japonica cultivar-group)
Eukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP.
clade, Ehrhartoideae, Oryzaee, Oryza.

1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJn, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
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Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
1 (bass I to 20)
Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,
Edman, J.C., Kovacs, J. and Cushion, M.
Expressed sequence tags from Pneumocystis carinii
Contact: Staben C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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S39F5 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
AW334823
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Location/Qualifiers
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100.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 0; Indels
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/clone="JMT--07-p04"
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                20 AAAAAAAAAAAAAAAAA
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EST 17445 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
COUR B3CS00GL005H02 3', mRNA sequence.
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/dev_stage="green stage"
/clone_lib="Green Grape Skin Triplex2 Library"
/clone_lib="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_l: SfilB; Oriented library"
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetophyta; Gnetopsida; Gnetales; Gnetaceae; Gnetum.
1 (basea 1 to 20)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
                                                                                                                                                                                                                                                                                                                                   Eukaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

1 (bases 1 to 20)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N. Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
                 Gaps
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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Pred. No. 1.1e+03;
0; Mismatches 0;
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/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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DN953918.1 GI:63026056
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Vitis vinifera
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Enctophyta; Gnetophyta; Gnetoph
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/note="Organ: mature, unfertilized reproductive strobili;
/notes"Cogan: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: ECO RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express CDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
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/note="Organ: mature, unfertilized reproductive strobili;
/notes="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express CDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"
O'Shaughnessy, A. L., Balija, V., Martienssen, R. A., McCombie, R. W., Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
Pp Box. 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 884
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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0;
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/mol_type="mRNA"
/db_xref="taxon:3382"
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/organism="Gnetum gnemon"
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/db_xref="taxon:3382"
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Seq primer: -21M13UnivRev.
Location/Qualifiers
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Seg primer: -21Ml3UnivRev
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Gnetum gnemon
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RESULT 1319

DN954289

Matches

ò g DEFINITION

ACCESSION VERSION KEYWORDS

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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Ginkgo biloba (matuelman) tree)

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatorphyta; Ginkgoales; Ginkgoaceae; Ginkgo.

1 (bases 1 to 20)

Shaughnessy,A.L., Ballja,V., Martienssen,R.A., Dedhia,N.N., O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W., Benfey,P., Coruzzi,G. and Stevenson,D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Hazbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="Ginkgo microsporophyll (NYBG)"
/note="Organ: microsporophyll; Vector: pBK-CMV; Site_1:
/note="Organ: microsporophyll; Vector: pBK-CMV; Site_1:
/note="Organ: microsporophyll; Vector: pBK-CMV; Site_1:
/note="Organ: Air The library was size-fractionated to enrich for large inserts."
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Ginkgo microsporophyll (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8884
Fax: 516 367 8884
Fax: 121413Univey
Seq primer: -21M13Univey
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ik85h04.gl Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
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/mol type="mRNA"
/mol type="mRNA"
/baxef="taxon:331"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/cl
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0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels
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/db_xref="taxon:3311"
/sex="male"
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Seg primer: -21M13UnivRev
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E. 1 (Dases 1 to 20)

S. Brenner, E. D. Trigg, R. W., Runko, S. J., Katari, M. S., Dedhia, N. N., O'Shaughnessy, A. L., Balija, V., Martienssen, R. A., McCombie, R. W., Banfay, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Gnetum female cone (NYBG)

Lita Annanberg Hazen Genome Sequencing Center

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Fal: 516 367 8884

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Fax: 516 367 8874

Emmail: mccombie@cshl.org

Seq primer: -21M13UnivRev.
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1994g12.gl Ginkgo microsporophyll (NYBG) Ginkgo biloba cDNA 3',
mRNA sequence.
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Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 20)
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       Sample: NYBG accession number #436/84"
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Pred. No. 1.1e+03;
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/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
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Ginkgo biloba
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20; Conservative
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Best Local
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FEATURES

RESULT 1320

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DR065440

LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ej (bases 1 to 20)
S Germatophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
S Grandpnessy, A. L., Balija, V., Martienseen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
L. Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
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5', mRNA Sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids I; Malpighiales; Salicacee; Salicace; Populus.

1 (bases 1 to 20)

Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y.,

Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G.,

Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A.,

Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,
                                                                                                                                                                                                         DR073130 20 bp mRNA linear EST 08-JUN-2005 ik86h03.gl Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA sequence.
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Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
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0; Mismatches 0;
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0.7%; Score 20; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0;
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/db_xref="taxon:3311"
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                                                             2709 AAAAAAAAAAAAAAAA 2728
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Seq primer: -21M13UnivRev
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100.0%;
Best Local Similarity 100.
Matches 20; Conservative
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/lab hoste."E. coli DH10B T1 phage resistant cells"
/clone lib="PT-P-FL-A-2"
/clone lib="PT-P-FL-A-2"
/note="Vector: pBluescript II SK (+) XR; Site 1: SEII (5'
end of cDNA); Site 2: XhoI (3' end of cDNA); Phloem and
cambium from 8 year old trees harvested within the Boise
Caccade region of Washington state on May 15th, 2001. cDNA
was prepared from 20 micrograms of mRNA according to the
full-length cDNA library construction method described by
Carninci P. et al. (2000), Genome Research
10(10):1617-1630 and directionally ligated into the
pBluescript II SK (+) XR vector digested with SelI (5'
end) and XhoI (3'). Plasmid DNA was then transformed by
electroporation into DH10B cells (Invitrogen) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T50579 20 bp mRNA linear EST 06-FEB-1995 yb76d04.rl Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:77095 5' similar to contains L1 repetitive element, mRNA
Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and
Bohlmann,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                              The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
Unpublished (2004)
Contact: Joerg Bohlmann
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smittish Columbia
Michael Smittish Columbia, Canada, V6T 123
Tel: 1-604-822-0282
Fax: 1-604-822-2114
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1 (bases 1 to 20)

1 (lases 1 to 20)

1 (lases 1 to 20)

2 (lases 2 to 20)

2 (lases 3 to 20)

3 (lases 4 to 20)

4 (lases 4 to 20)

4 (lases 5 to 20)

5 (lases 6 to 20)

6 (lases 7 to 20)

7 (lases 7 to 20)

8 (lases 7 to 20)

8 (lases 8 to 20)

8 (lases 8 to 20)

8 (lases 9 to 20)

9 (lases 9 to 20)

10 (lases 9 to 20)

11 (lases 9 to 20)

12 (lases 9 to 20)

13 (lases 9 to 20)

14 (lases 9 to 20)

15 (lases 9 to 20)

16 (lases 9 to 20)

17 (lases 9 to 20)

18 (lases 9
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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8889549
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| forganism="Populus trichocarpa"
| mol type="mRNA"
| cultivar="383-2499 (Nisqually-1)"
| db xref="taxon:3694"
| clone="w80111_L11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: bohlmann@meil.ubc.ca
Plate: WS0111 row: L column: 1
High quality sequence stop: 139
PoLYR=Yes.
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0063 row: K column: 10
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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Fax: 801 585 7177
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1M0009M20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0009M20 R, genomic survey sequence.
AZ307671
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7el: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Source: IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RP1
High quality sequence stop: 20.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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                                                                                                                                                                                                                           1. .20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:506824"
/db_xref="taxon:9606"
/clone="IMAGE:77095"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert Length: 10000 Std Error: C
Plate: 0009 row: M column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                         /sex="female"
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AZ307671/c
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SOURCE
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DEFINITION
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COMMENT
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(http://www.nduer.DNA resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp (14712114 [gb] AR125072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
I (basea 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                  /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse_lokb plasmid UGCIM library"
/note="Vector: PWD4Zlry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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0
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Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                           /db_xref="taxon:10090"
/clone="UUGC1M0009M20"
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Tue Nov

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High quality sequence stop: 20.
Location/Qualifiers
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Mus musculus
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GSS.
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Best Local Similarity 100.
Matches 20; Conservative
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Fax: 801 585 7177
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AZ343031
LOCUS
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                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

L Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2010 E., SLC, UT

84112, USA
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                         /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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/mol_type="genomic DNA"
/strain="C57BL/6J"

                                                                                                /db_xref="taxon:10090"
/clone="UUGC1M0063K10"
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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AZ341530.1 GI:10417873
                                                                                                                                                    /sex="Male
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Best Local Similarity 100.0
Matches 20; Conservative
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/Bab. maile...
/Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
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10.5 kb range using preparative agarose gel
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inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn,D., Aoyagi 1 to 20)
Dunn,D., Aoyagi,B., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Nucderhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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100.0%; Pred. No. 1.1e+03;
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Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: F column: 13
Seg primer: CGTTGTAAAACGACGGCCAGT
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University of Utah Genome Center
University of Utah
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7 10:41:28 2006

Tue Nov

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gil-4732114 [gb]-RR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murcidae; Murinae; Musinae; Musinae;
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                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
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Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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AZ357623.1 GI:10471335
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Fax: 801 585 7177
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Best Local Similarity
           source
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1M0089B18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0089B18 F, genomic survey sequence.
AZ351273
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1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XLIO-Gold, TI-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Pred. No. 1.1e+03;
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Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

0.7%; Score 20, L.1.

Best Local Similarity 100.0%; Pred. No. 1.1.

Matches 20; Conservative 0; Mismatches
(organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: 0089 row: B column: 18
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                         /db_xref="taxon:10090"
/clone="UUGC1M0076F13"
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Location/Qualifiers
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Plate: 0089 row: B c
                                                                                                                                                                                                                         'sex="Male"
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Fax: 801 585 7177
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84112, US
source
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AZ351273
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerses and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose get
adaptored using preparative agarose gfrom a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.7%; Score 20; DB 1; Length 20; 00.0%; Pred. No. 1.1e+03;
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Insert Length: 10000 Std Error: 0.00
Plate: O145 row: C column: 11
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.7%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 1.1. Matches 20; Conservative 0; Mismatches
                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                           /db_xref="taxon:10090"
/clone="UUGC1M0120024"
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Location/Qualifiers
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Mus musculus
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                               /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from Musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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1 Unn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plaemid inserts
Unpublished (2000)
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Insert Length: 10000 Std Error: 0.00
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100.0%; Pred. nv. _
"ive 0; Mismatches
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Plate: 0120 row: O column: 24
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                       /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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Pred. No.
                                                                                                              /db_xref="taxon:10090"
/clone="UUGC1M0099A20"
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GSS.
                                                                                                                                                                          /sex="Male'
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Best Local Similarity 100.0
Matches 20, Conservative
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Fax: 801 585 7177
     source
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of puble (4712114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 20)

1 (bases 1 to 20)

2 I (bases 1 to 20)

3 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Contact: Robert B. Weiss

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
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1M0236B11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0236B11 F, genomic survey sequence.
                                                                                                                                                                                        /sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G77BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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0.7%; Score 20; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0236 row: B column: 11
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
                                                             /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                          /db_xref="taxon:10090"
/clone="UUGC1M0161K02"
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                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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E 1 (bases 1 to 20)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rallam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center University of Utah Genome Center
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/clone lib="Mouse 10kb plasmid UUGClM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
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Pred. No. 1.1e+03;
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Insert Length: 10000 Std Error: 0.00
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V 100.0%; Pred. No. ...
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Plate: 0161 row: K column: 02
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0145C11"
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Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                        /sex="Male"
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Best Local Similarity 100.7
Matches 20, Conservative
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Fax: 801 585 7177
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Class: plasmid ends
Fligh quality sequence stop: 20.
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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was bylory-loww.jax.org/resources/documents/dnares/). The DNA
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was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
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electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi] 4732114 gb] kR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
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adaptored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0272 row: O column: 06
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC1M0236B11"
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Location/Qualifiers
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Mus musculus
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AZ463331.1 GI:10621456
                                                                                                                                                                                                                                                           'sex="Male
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84112, USA
    source
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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nr, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/): The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
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Insert Length: 10000 Std Error: 0.00
Plate: 0297 row: E column: 23
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
/mol_type="genomic DNA"
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                                                                   /db_xref="taxon:10090"
/clone="UUGC1M0272006"
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GSS.
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Best Local Similarity 100.0
Matches 20; Conservative
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwapto (gilly 14732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmanlia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Mus.

E (bases 1 to 20)

S lunn, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

L Unpublished (2000)

Conteact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2010 E., SLC, UT

84112, USA
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                                                                                                                                                                                                     /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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Pred. No. 1.1e+03;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: C column: 20
Seq primer: CGTGGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
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                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                   /db xref="taxon:10090"
/clone="UUGC1M0300P01"
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1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ralam, L., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Whose whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
                                                                                                                                                                                            /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Best Local Similarity 100.0%; Pred. No. 1.1
Matches 20; Conservative 0; Mismatches
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Plate: 0300 row: P column: 01
Seq primer: CGTTGTAAAACGACGGCCAGT
                           organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                                                          /db_xref="taxon:10090"
/clone="UUGC1M0297E23"
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Mus musculus
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source
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AZ479464/c
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5

FEATURES

TITLE

COMMENT

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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gil 4732114 gb | AF129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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E 1 (bases 1 to 20)
S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longaczes,S., Mahmoud,M., Menen,E., Pedersen,T., Reilly,M., Rose,M., Rose,M., Stoke,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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1M0361E11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0361E11 R, genomic survey sequence.
AZ514729
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Insert Length: 10000 Std Brror: 0.00
Plate: 0361 row: E column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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                                                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0336E05"
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Mus musculus
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                                                                                                                                                                                 /sex="Male"
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Matches 20; Conservative
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Fax: 801 585 7177
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AZ514729
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KEYWORDS
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                                                                                                                                                                                              /lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4732114 gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1M0336E05F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0336E05 F, genomic survey sequence.
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Mammalia, Eutheria, Euarchoncoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 20)
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Dunn,D., Acyagi.A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0336 row: E column: 05
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                          'mol_type="genomic DNA"
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                                                                                                                /db_xref="taxon:10090"
/clone="UUGC1M0315C20"
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Location/Qualifiers
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Best Local Similarity 100.0
Matches 20; Conservative
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source
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TITLE

COMMENT

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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clome_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was bydrodynamically sheared by repeated excess. The
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xi10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0396 row: A column: 13
Seg primer: CGTTCTAAAACGACGCCAGT
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                                                                                                      /db_xref="taxon:10090"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gil-4732114)gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0369P1SR Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0369P1S R, genomic survey sequence.
AZ581208
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                   /lab host="B. Coli strain XLIO-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"
/note=""Vector: PWD42nv; Purified genomic DNA from M. musculus C578467 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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Pred. No. 1.1e+03;
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Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

0.7%; SCOLE 20, ___
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 20; Conservative 0; Mismatches
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                                                    'mol_type="genomic DNA"
'strain="C57BL/6J"
                                                                                               /db_xref="taxon:10090"
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Location/Qualifiers
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Plate: 0369 row: P
                                                                                                                                                      sex="Male"
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Fax: 801 585 7177
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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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1 (Dases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.
Mouse, whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: K column: 05
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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                                                                                                                    /db_xref="taxon:10090"
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Mus musculus
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Best Local Similarity 100.0
Matches 20, Conservative
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Fax: 801 585 7177
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (Accuments/Anares). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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0.005 inch orifice at constant velocity. The sheared DNA
was blunt ender-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adappored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

E 1 (bases 1 to 20)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Mennen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid innerts

L Unpublished (2000)
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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1M0429A14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0429A14 R, genomic survey sequence.
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
.....th: 10000 Std Error: 0.00
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Plate: 0429 row: A column: 14
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Class: plasmid ends
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                                                                                                                        /db_xref="taxon:10090"
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AZ607328.1 GI:11729518
                                                                                                                                                                                              /sex≂"Male
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Best Local Similarity 100.0
Matches 20; Conservative
source
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gql/4732114/gbl/A123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Rammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murcidae; Murinae; Mus.
1 (bases 1 to 20)
S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weise,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
L Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                            /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-" /clome lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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0.7%; Score 20; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0;
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Fax: 801 585 7177

Email: ddunnggenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0507 row: D column: 18
Seg primer: CACACAGGAAACAGCTAATGACC
                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                     /db xref="taxon:10090"
/clone="UUGC1M0460L12"
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High quality sequence stop: 20.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb4732114[pb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
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1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Railly, M., Rose, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Muode wande genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZBZ1214 10Kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0460L12 R, genomic survey sequence.
                                                                                                                                                                                                      /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Pred. No. 1.1e+03;
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Insert Lengch: 10000 Std Brror: 0.00
Plate: 0460 row: L column: 12
Seq primer: CACACAGGAAACAGGTAATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.1.
Matches 20; Conservative 0; Mismatches
1. .20
/organism="Mus musculus"
                                                          /mol_type="genomic DNA"
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Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                sex="Male"
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Fax: 801 585 7177
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84112, USA
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AZ623214/c
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/gex="Male"
//lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
//lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
//clone lib="Mouse 10kb plasmid UUGCIM library"
//note="Wetcor: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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inducible derivative of plasmid R1. The vector was ligated
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purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XiiO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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Contact: Robert B. Weiss
Contversity of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederthausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.7%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 1.1e+03;
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Insert_Length: 10000 Std Error: 0.00
Plate: 0520 row: C column: 21
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Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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Fax: 801 585 7177
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E Sciurognathi; Muroidea; Muridae; Mus.

I (bases 1 to 20)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Dylasmid inserts

D Jasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                             /lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Weator: PWD42ry; Purified genomic DNA from M.
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Fax: 801 585 7177
Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: D column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends

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/strain="C57BL/6J"

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AZ645829/c DEFINITION

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KEYWORDS SOURCE ORGANISM ACCESSION VERSION

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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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E 1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Diamid inserts

L Unpublished 2010

Contact: Robert B. Weiss
University of Utah Genome Center University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                        /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus G79EL/6J (male) was obtained from the Jackson
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0.7%; Score 20; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0;
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Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                 /mol_type="genomic DNA"
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                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0554A24"
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                                                                                                                                                                                     /sex="Male
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         source
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                                                                                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwapto (gilly 14732114 [gb] AF125072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0554A24R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0554A24 R, genomic survey sequence.
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                  /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0554 row: A column: 24
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High quality sequence stop: 20.
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                                                                                                                                                                            /sex="Male"
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Fax: 801 585 7177
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Mus musculus (house mouse)

Mus musculus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Sciurognathi; Muroidea; Muridae; Murinae; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

CE 1 (bases 1 to 20)

Elam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weises, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weises, R., Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

##112, USA
                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwbl2 (gil 4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
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musculus G7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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121: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
.....t. 10000 Std Error: 0.00
1. .20
/organism="Mus musculus"
// organism=-"nenomic DNA"
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Plate: 0562 row: H column: 04
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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clone="UUGC1M0560M02"
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Location/Qualifiers
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AZ765211.1 GI:12880970
                                                                                                                                                       /sex="Male
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/Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated from an originate to the blunt ends in high molar excess. The
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coll XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Meacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menen, B., Pedersen, T., Mederhausern, A., and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Insert Length: 10000 Std Error: 0.00
Plate: 0574 row: A column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                    /db_xref="taxon:10090"
/clone="UUGC1M0562H04"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwdet (giff4732114 [gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Craniata; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"/clone_lib="Mouse_lokb plasmid UGCIM library."
/note="Vector: PWB4Zny; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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100.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 0;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: B column: 21
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource

    .20
    /organism="Mus musculus"

                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC2M0015M18"
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                                                                                                                                                                                   /sex="Male"
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Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                              / Jab host="Society strain XLIO-Gold, Tl-resistant, F-"
/ Jab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/ Clone lib="Whouse 10kb plasmid UNGCIM library
/ note="Vector: PWASINY: Purified genomic DNA from
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWAP2 (gql 4732114 gpl AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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E 1 (bases 1 to 20)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Kose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Unpublished (2000)
L Unpublished (2000)
L Contact: Robert B. Weiss
University of Utah Genome Center
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2M0015M18R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0015M18 R, genomic survey sequence.
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Pred. No. 1.1e+03;
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                        organism="Mus musculus"
                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                          /db_xref="taxon:10090"
/clone="UUGC1M0574A13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 20.
Location/Qualifiers
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Mus musculus
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Best Local Similarity 100.(
Matches 20; Conservative
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Fax: 801 585 7177
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84112, USA
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source
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AZ779425/c
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KEYWORDS
SOURCE
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Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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Best Local Similarity 100.0
Matches 20; Conservative
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Fax: 801 585 7177
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source
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KEYWORDS
SOURCE
ORGANISM
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LOCUS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalpd (gill #132114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ793467 2005 DNA linear GSS 16-FEB-2001 2M0046C16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0046C16 R, genomic survey sequence.
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                                                                                                                               /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0046 row: C column: 16
Seq primer: CACAGGGAAACAGCTATGACC
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clone="UUGC2M0026B21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 2
Location/Qualifiers
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AZ793467.1 GI:12938450
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Best Local Similarity 100.0
Matches 20; Conservative
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AZ793467/c
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ORGANISM
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/Bax=waie".
/Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated gassage through a
0.005 inch orifica at constant velocity. The sheared DNA
was hydrodynamically shared by repeated by separed by
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
polynucleotide kinase Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

plasmid inserts
Umpublished (2000)
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Insert Length: 10000 Std Error: 0.00
Plate: 0055 row: G column: 19
Seg primer: CGTTGTAAAACGACGGCCAGT
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University of Utah Genome Center
University of Utah
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                              /db_xref="taxon:10090"
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Mus musculus
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GSS.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gilfa) 14 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus

Bukartyota; Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mummalia; Butheria; Buarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

E. (bases 1 to 20)

E. (bases 1 to 20)

S. Junn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (200)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT

#4112, USA
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2M0068C08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0068C08 R, genomic survey sequence.
                                                                                                                                                                                                              /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Lonsert.length: 10000 Std Error: 0.00
Plate: 0068 row: C column: 08
Seq primer: CACACAGGAAACAGCTAATGACC
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/db_xref="--
                                                                                                                        /db_xref="taxon:10090"
/clone="UUGC2M0066L14"
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High quality sequence stop: 20.
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         source
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
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electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1 (bases 1 to 20)

Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse_10kb plasmid UUGClM library"
/note="Wector: PWD42Ivv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 1.1e+03;
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Insert Length: 10000 Std Error: 0.00
Plate: 0066 row: L column: 14
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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1. .20
/organism="Mus musculus"
"-----ic DNA"
                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0055G19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2709 AAAAAAAAAAAAAAAAAA 2728
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Mus musculus
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                                                                                                                                                                                     sex="Male"
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Fax: 801 585 7177
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Best Local Similarity
Matches 20; Conserv
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84112, USA
   source
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ACCESSION VERSION KEYWORDS

AZ805163

ઠે g REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

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High quality sequence stop: 20.
Location/Qualifiers
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Best Local Similarity 100.
Matches 20; Conservative
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Fax: 801 585 7177
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AZ809306
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source
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ORGANISM
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KEYWORDS
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                                                                                                                                                                                                                                                                       (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0068C1SR Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0068C15 R, genomic survey sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muroidea, Muridae, Musinae, Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Rally, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                           /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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1.1e+03;
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Resear
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Plate: 0068 row: C column: 15
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Pred. No.
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                                                                                        /db_xref="taxon:10090"
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Location/Qualifiers
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AZ806585.1 GI:12970081
GSS.
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Best Local Similarity 100.09
Matches 20; Conservative
                                                                                                                                            'sex≂"Male'
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_weetor: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated by seared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adapprored vector DNA, and transformed into
chemically-competent E. coli X110-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (bases 1 to 20)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Unpublished (2000)

L Unpublished (2000)

L Contact: Robert B. Weiss
University of Utah
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0
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Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: D column: 15
Seg primer: CGTTGTAAAACGACGGCCAGT
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/mol_type="genomic DNA"
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                                                                 /db_xref="taxon:10090"
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GSS.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwNaQ2 (gil-f4732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus

Bukartyota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmanlia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Mus.

E 1 (bases 1 to 20)

S Dunn, D., Aoyagi, A., Barber, M., Meanen, E., Pedersen, T.,

Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

L Unpublished (2000)

Conteact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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2M0081F21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0081F21 F, genomic survey sequence.
                                                                                                                                                                                                /lab host="B. Coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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Pred. No. 1.1e+03;
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Fax: 801 585 717
Eaxi: 801 585 7177
Eaxi: 801 585 7177
Insert Length: 10000 Std Error: 0.00
Plate: 0081 row: F column: 21
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
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Best Local Similarity 100.0%; Pred. No. 1.1.
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/strain="C57BL/6J"
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AZ813908.1 GI:12983804
                                                                                                                                                                           /sex="Male
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AZ813908
      source
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1 (bases 1 to 20)

2 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Waright, D., Weiss, R. Tingey, A., von Diasmid inserts

1 Diasmid inserts

1 Unpublished (2000)

1 Contact: Robert B. Weiss

1 University of Utah Genome Center

1 University of Utah

1 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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2M0076I20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0076I20 R, genomic survey sequence.
AZ810986
                                                                                                                                                               /sex="Male"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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100.0%; Pred. No. 1.1e+03;
rative 0; Mismatches 0;
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                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                            /db_xref="taxon:10090"
/clone="UUGC2M0073D15"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Plate: 0076 row: I
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Best Local Similarity 100.0
Matches 20; Conservative
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Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                        /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Weator: PWD42nry, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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E 1 (bases 1 to 20)

S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ralla, H., Longacre, S., Mahmoud, M., Mesen, E., Pedersen, T., Niederhausern, A. and Wright, D. Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R. Ungublished (2000)

L Unpublished (2000)

L Ontect: Robert B. Weiss
University of Utah Genome Center
University of Utah
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    .20
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

                                                                                                     /db_xref="taxon:10090"
/clone="UUGC2M0081F21"
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AZ817323.1 GI:12987327
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Fax: 801 585 7177
Email: ddunn@genet
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bylorymanically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymersae and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD402 (gil 4/732114/gpl AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA. and transformed into
chemically-competent E. coli XLL0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Wus.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Bilam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Railly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
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Insert Length: 10000 Std Error: 0.00
Plate: 0086 row: K column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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University of Utah Genome Center
University of Utah
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                               /db_xref="taxon:10090"
/clone="UUGC2M0086C20"
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GSS.
                                                                                                                                                  /sex="Male"
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source

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwapt (gilfy17121/4[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
1 (bases 1 to 20)
S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
University of Utah Genome Center
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2M0087K08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0087K08 F, genomic survey sequence.
                                                                                                                                                                                                                  /lab host="E. Coli strain XLIO-Gold, TI-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"
//note="Yestor: PWD42rv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0087 row: K column: 08
Seg primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
                                                                 /mol_type="genomic DNA"
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AZ817608.1 GI:12987516
                                                                                                                                                                                             /sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 20; Conservative
source
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AZ817608/c
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                                                                                                                                                                     / Jab_host="Solistrain XL10-Gold, T1-resistant, F-"
/ Jab_host="E. Colistrain XL10-Gold, T1-resistant, F-"
/ Clone lib="Mewose 10kb plasmid UUGCIM library
/ Inote="Vector: PWAPINY: Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD4 (gf | 4712114| gb] AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (Dases 1 to 20)

2 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R. Tingey, A., von Disamid inserts

1 Unpublished (2000)

2 Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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2M0086J15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0086J15 R, genomic survey sequence.
AZ817467
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0.7%; Score 20; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0;
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                    organism="Mus musculus"
                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                              /db_xref="taxon:10090"
/clone="UUGC2M0086K08"
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Plate: 0086 row: J c
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Fax: 801 585 7177
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RESULT 1365 AZ817467 DEFINITION

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ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

ACCESSION VERSION KEYWORDS SOURCE

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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: M column: 05
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
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Best Local Similarity 100.
Matches 20; Conservative
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Fax: 801 585 7177
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                                                                                                                                                                                 /Bab. Moste-"E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated by respected by
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adappored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognachi; Muroidea; Muridae; Mus.
E 1 (bases 1 to 20)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah Genome Center
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Length: 10000 Std Error: 0.00
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Plate: 008B row: K column: 01
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                          db_xref="taxon:10090"
clone="UUGC2M0087K08"
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Mus musculus
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Fax: 801 585 7177
Email: ddunn@genet
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84112, USA
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ઠે 셤 REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
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and selected for ampicillin resistance."
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Sciurognathi, Muroidea, Muridae, Murinae, Mus.

I (bases 1 to 20)

Dunn, D., Aoyagi, L. Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R.,

Miderhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
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2M0089M05F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0089M05 F, genomic survey sequence.
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                            /db_xref="taxon:10090"
/clone="UUGC2M0088K01"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gql 4732114 [gb] AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Musinae; Mus.

E. (bases 1 to 20)

E. (bases 1 to 20)

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Really,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

M. 2012. USA
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2M0139H16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0139H16 F, genomic survey sequence.
                                                                                                                                                                                  /sex="Male" / Albhost="E. Coli strain XL10-Gold, T1-resistant, F-" / Albhost="E. Coli strain XL10-Gold, T1-resistant, F-" / Clone lib="Mouse 10kb plasmid UUGCIM library" / Clone lib="Woctor: PWD4Znv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: H column: 16
Seq primer: CGTIGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
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100.0%; Pred. No. 1...
                                         organism="Mus musculus'
                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC2M0132K13"
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Fax: 801 585 7177
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Best Local Similarity
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwapt (gil-#4732114|gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Relan, M., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Dusse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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2M0132K13R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
                                                                                                                                                                                                     /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"/clone_lib="Mouse_lokb plasmid UUGCIM library"
/note=""Vector: PUMP4Znv; Purified genomic DNA from M. musculus G57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Pred. No. 1.1e+03;
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
.....h. 10000 Std Error: 0.00
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0.7%; Score 20, L

Best Local Similarity 100.0%; Pred. No. 1.1

Matches 20; Conservative 0; Mismatches
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                                                            /mol_type="genomic DNA"
/strain="CS7BL/6J"
                                                                                                         /db_xref="taxon:10090"
/clone="UUGC2M0089M05"
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                                                                                                                                                                                         sex="Male"
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84112, USA
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AZ837491
source
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High quality sequence stop: 20.
Location/Qualifiers
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Matches 20; Conservative
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Fax: 801 585 7177
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LOCUS
source
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SOURCE
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                                                                                                                                                          /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophorasis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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2M0119A10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0139A10 R, genomic survey sequence.
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1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.7%; Score 20; DB 1; Length 20; 00.0%; Pred. No. 1.1e+03;
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Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: A column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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i. .20
/organism="Mus musculus"
/organism="mus musculus"
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University of Utah Genome Center
University of Utah
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Mus musculus
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Best Local Similarity 100.0
Matches 20; Conservative
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Fax: 801 585 7177
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Laboracy Mouse DNA Kesource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb12 (gilfa712114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0163003F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0163003 F, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Relly, M., Rose, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid binserts
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Contact: Robert B. Weiss
Contversity of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                       /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Brror: 0.00
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. .20
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1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rislam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
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                                                                                                                                                                   /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
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musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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100.0%; Pred. No. 1.1e+03;
ative 0; Mismatches 0;
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Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
.. .20
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Plate: 0163 row: O c
                                                                                                                                                 /sex="Male"
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pward (gql 4732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciurcognathi; Murcidea; Muridae; Murinae; Mus.

1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
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Laboratory Mouse DNA Resource
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(Dubblished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Pred. No. 1.1e+03;
0; Mismatches 0; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0193 row: G column: 23
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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100.0%; Pred. No. ...
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AZ936914.1 GI:13795495
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Best Local Similarity
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High quality sequence stop: 20.
Location/Qualifiers
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Best Local Similarity 100.0
Matches 20; Conservative
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Fax: 801 585 7177
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                                                                                                                                                                    /Bab hose=E. coli strain XL10-Gold, T1-resistant, F-"

(clone_lib="wouse 10kb plasmid UUGC2M library"

/note=="vector: PWD42nv; Purified genomic DNA from M.

/note=="vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA

was hydrodynamically sheared by repeated more excess. The
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Sciurognathi; Burerchontoglires; Glires; Rodentia;

Sciurognathi; Murcidea; Muridae; Musiae; Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Scokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

Unpublished (2000)
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                   /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                    /db_xref="taxon:10090"
/clone="UUGC2M0193G23"
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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AZ949180.1 GI:13820407
                                                                                                                                                         /sex="Female"
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Best Local Similarity 100.0°
Matches 20; Conservative
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84112, USA
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/lab hose="Be coli strain XL10-Gold, T1-resistant, F-"
/lab hose="Be coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse lokb plasmid UUGC2M library"
/notes="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resources
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129772.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adappored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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E 1 (bases 1 to 20)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Mesen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Unpublished (2000)
L Unpublished (2000)
L Context: Robert B. Weiss University of Utah Genome Center University of Utah Genome Center University of Utah
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2M0233J01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0233J01 F, genomic survey sequence.
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Insert Length: 10000 Std Error: 0.00
Plate: 0233 row: J column: 01
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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    .20
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

                                                                                                                                           /db xref="taxon:10090"
/clone="UUGC2M0212I02"
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Mus musculus
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GSS.
                                                                                                                                                                                                                  /sex="Female"
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Gaps

source

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GSS 22-DEC-2005
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/lab host="E.coli DH10B"
/clone_lib="KBrH, Brassica rapa HindIII BAC library"
/note="Vector: pCUGIBacl; Site 1: HindIII; Brassica rapa
spp. pekinensis inbred line Chīifu BAC library (KBrH BAC)
is provided by Yong-Pyo Lim."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Wagnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 2), Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrs013J15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DUB34188 22-DEC-20 KRS013J15F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS013J15, genomic survey sequence.
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/db_xrefe="taxon:51351"
/clone="KBrS013415"
/lab host="R. coli DH10B"
/clone lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pUGIBAC1; Site 1: Sau3AI, Brassica rapa spekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."
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/organism="Brassica rapa subsp. pekinensis"
                                                                                                                                                                                                                                                                                         Query Match 0.7%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 20; Conservative 0; Mismatches 0; Indels
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Secdun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
     /sub_species="pekinensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/cultivar="Chiifu"
                                /db_xref="taxon:51351"
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Class: BAC ends.
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                                                                                                                                                           / Jab_host="Second strain XL10-Gold, T1-resistant, F-"
/ Jab_host="B. coli strain XL10-Gold, T1-resistant, F-"
/ clone_lib="Wouse 10kb plasmid UVGCSM library."
// note="Vector: PWD42Nv; Purified genomic DNA from M.
musculus G57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orfifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide Kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD4 (gi|H712114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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BAC end sequence of Brassica rapa ssp. pekinensis HindIII BAC clone
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Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, wagnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales, Brassicaceae, Brassica.
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Contact: Beom-Seok Park
Brassica Genomics Team
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/mol_type="genomic DNA"
/cultivar="Chiifu"
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Fax: +82-31-299-1670
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Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No.
l. .20
organism="Mus musculus"
                                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                              /db_xref="taxon:10090"
/clone="UUGC2M0233J01"
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CW979138.1 GI:56810425
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Class: BAC ends.
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Best Local Similarity
Matches 20; Conserv
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RESULT 1377

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CW979138

LOCUS DEFINITION

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TITLE JOURNAL COMMENT

REFERENCE AUTHORS

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DX055580
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DX055580
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                                              GSS 22-DEC-2005
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Contact: Beom-Seck Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
25 Secdun-Dong, Suwon, 441-707, Korea
Fil +82-31-299-1670
Fax: +82-31-299-1670
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
                                                                                                                                                                                             Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 20)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M. H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica i Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 20)
Yang, T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
                         10 by DNA linear GSS 22-DEC-20 by DNA linear GSS 22-DEC-20 Subsp. pekinensis genomic clone KBrS016A17, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / gub_species="pekinensis"

/db_xref="texon:51351"

/clone="KBrS016A17"

/lab_host="E. coli DH10B"

/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"

/note="vector: pcuGIBAC1; Site_1: Sau3AI; Brassica rapa

sp. pekinensis var. Chiifu BAC library (KBrS BAC) is

available at NIAB."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Brassica rapa subsp. pekinensis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/cultivar="Chiifu"
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DX045751.1 GI:84740048
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Matches 20; Conservative
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Class: BAC ends.
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DX045751
RESULT 1379
DU835125
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KBRBOGODOSR KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrBOGODOS, genomic survey
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/clone lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pcuGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Byermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.

1 (Bases I to 20)
Yangy T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
Bnd sequence of Brassica rapa BamHI (KBrB) BAC clone
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB047C15
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BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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/organism="Brassica rapa subsp. pekinensis"
/organism="Brassica rapa subsp. pekinensis"
/cultivar="Chiifu"
/sub species="pekinensis"
/db xref="taxon:51351"
/clone="KBrB047C15"

    .20
    /organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/culfivar="Chifu"
/sub species="pekinensis"
/db_xref="taxon:51351"

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Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Becom-Seck Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                        Seq primer: T7
Class: BAC ends.
Location/Qualifiers
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Class: BAC ends.
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/clone="KBrB060D05"
/lab_host="E.coli DH10B"
/clone llb="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                  UXU/0282 20 bp DNA linear GSS 10-JAN-2006 KBrB079J23F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB079J23, genomic survey sequence.
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/lab_host="E.coli DH108"
/clone lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCuGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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Brassica rapa subsp. pekinensis
Bukaryota, Virldiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
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/mol_type="genomic DNA"
/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
                                                                                                                              Length 20;
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1.1e+03;
                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Institute of Agricultural Biotechnology 225 Secdun-Dong, Suwon, 441-707, Korea Fel: +82-31-299-1670
Fax: +82-31-299-1670
Email: pbecom@rda.go.kr
                                                                                                                            Score 20; DB 1; Le
Pred. No. 1.1e+03;
                                                                                                                                100.0%; Pred. No.
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100.0%; Pred. No. 1.1
tive 0; Mismatches
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Brassica Genomics Team
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                                                                                                                              0.78;
                                                                                                                                                                  Conservative
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Best Local Similarity 100.
Matches 20; Conservative
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Class: BAC ends.
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Best Local Similarity
Matches 20; Conserv
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EST 10-OCT-2003

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mRNA

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BX556006

RESULT 1383 BX556006/c LOCUS

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/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoidae; Oryzeae; Oryza.

1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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BX556006 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse24c09_plc, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                Lehane, M.J., Akooy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Echane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are reverse primer reads starting at Each of the cDNA all plc reads are from
the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Glossina morsitans morsitans"
/mol_type="mRNA"
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/db_xref="taxon:37546"
/clone="Tec24c09 plc"
/tissue type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
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                                                                                                                                                                                                               Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Hippoboscoidea, Glossinidae, Glossina.
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100.0%; Pred. No. 1.1e+03;
ive 0; Mismatches 0; Indels
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Genome Biol. 4 (10), R63 (2003)
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Glossina morsitans morsitans
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CF276638.1 GI:33654024
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Canis familiaris (dog)
Canis familiaris
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhatroideae; Oryzeae; Oryza.

I (bases 1 to 21)
Kim,J.S., Jun.K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pcR4-TOPO, Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for RNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Boinformatics, MyongJi University
YongIn, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA_library (ABF)
                                                                                                                                                                                                                                                                                                    /clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
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|mol_type="mRNA"
|cultivar="Nackdong"
                                                                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
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of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 31 21 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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100.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 0; Indels
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Location/Qualifiers
                                                                                                                                                                                                              /db_xrefe"taxon:39947"
/clone="14ETL--01-N19"
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/cultivar="Nackdong"
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Best Local Similarity 100.00
Matches 20, Conservative
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LILDIOSA 21 bp mRNA linear EST 15-AUG-2003
HD--08-C11.bl OsHDAC1-overexpressing transgenic rice plasmid CDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--08-C11, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 320 6195
Fax: 82 31 320 6195
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/lab_host="E.coli DH10B"
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   Length 21;
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Location/Qualifiers
Query Match 0.7%; Score 20; DB 1; Le Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 20; Conservative 0; Mismatches 0;
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/clone="HD--08-C11"
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/cultivar="Nackdong"
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CF318152.1 GI:33689913
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WS01124.BR D19 PT-P-FL-A-2 Populus trichocarpa cDNA clone
DT496709
DT496709.1 GI:73893971
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /fiscue_type="Cardiac muscle"
/dev stage="3 month old normal canine"
/lab_host="Kil0 Gold"
/lab_host="Kil0 Gold"
/clone lib="Light Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site_I:
EcoR; Site_2: Mhol; Library constructed using pBluescript
XR kit from Stratagene. Cloned CDNA was size selected
between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,
Pathology and Medical Genetics, School of Veterinary
Medicine, University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y., Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G., Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A., Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A., Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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Unpublished (2004)
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons,
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Josep Bollmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-2114
Email: bohlmann@mel.ubc.ca
Plate: WS01124 row: D column: 19
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                                                            1 (bases 1 to 21)
1 (bases 1 to 21)
2 Saria from Canis familiaris left cardiac ventricle (dog)
2 Unpublished (2004)
2 Contact: W. Richard McCombie
Lita Annenberg Hazzor Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org.
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Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                       /organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
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Best Local Similarity 100.0
Matches 20; Conservative
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                                                  Canis
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KEYWORDS
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AUTHORS
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/done lib="PT-P-PLA-2"
//done lib="PLA-2"
//done lib="PLA-2
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn, D., Agodi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. coli DH10B T1 phage resistant cells"
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Pred. No. 1.1e+03;
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                                                                                                                                                                       /organism="Populus trichocarpa"
/mol type="mRNA"
/cultivar="383-2499 (Nisqually-1)"
/db_xref="taxon:3694"
/clone="WS01124_D19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
High quality sequence stop: 116 POLYA=Yes.
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Female"
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Best Local Similarity 100.
Matches 20, Conservative
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DX056270/c
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KEYWORDS
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                                                                                                                                                 Induction to 19 (Mark Besource (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared but of inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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E 1 (bases 1 to 21)

S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Londact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS 05-OCT-2000
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                                                   /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UNGCIM library"
/note="Vector: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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100.0%; Pred. No. 1.1e+03;
trive 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0328 row: C column: 11
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
clone="UUGC1M0267B23"
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Fax: 801 585 7177
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Matches
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VERSION
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwD42 (giffa732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector NNA, and transformed into chamically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 21)
Yang, T.J. Kwon, S.J. Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
End sequence of Brassica rapa BamHI (KBrB) BAC clone
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BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                     /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note=""Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/culcivar="Chifu"
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodum-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
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Best Local Similarity 100.0%; Fred. No. 1.10
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/db_xref="taxon:51351"
/clone="UUGC1M0328C11"
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Class: BAC ends
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Brassica rapa subsp. pekinensis

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatorophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

I (bases I to 21)

St Ang, T. W., Kum, J. A., Kim, J. S., Lim, K. B., Jin, M.,

Park, J. Y., Lim, M. H., Kim, H. I., Choi, B. S., Seol, Y. J., Park, D. S.,

Hahn, J. H. and Park, B. S.

End sequence of Brassica rapa BamHI (KBrB) BAC clone

Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1672

Email: pbeomedra.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

KBEB093P23
/lab_host="E.coli DH10B"
/clone lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"

/cultivar="Chiifu"

/cultivar="Chiifu"

/cultivar="Chiifu"

/db xref="reach":5131"

/clone="Werbar Barasica rapa BamHI BAC library"

/clone="Vector: pcUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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ABF--05-C16.gl ABF3-overexpressing transgenic rice plasmid cDNA
                                                                                                                                                                                                                                                                                                                                                    DX081159 21 bp DNA linear GSS 10-JAN-2
KBrB093P21R KBrB, Brassica rapa BamH1 BAC library Brassica rapa
subbp. pekinensis genomic clone KBrB093P23, genomic survey
sequence.
                                                                                                                                                                      Gaps
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                                                                                                                           Length 21;
                                                                                                                       0.7%; Score 20; DB 1; Length 21;
100.0%; Pred. No. 1.1e+03;
ative 0; Mismatches 0; Indels
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Matches 20; Conservative 0; Mismatches
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DX081159.1 GI:84775455
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Best Local Simi:
Matches 20;
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CF310486
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
E. (bases 1 to 22)
Brenner, E. D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfer, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
L. Unpublished (2005)
L. Richard McCombie Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
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ik82h05.gl Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
                                                                                                                                                     Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 22)
(Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Xin,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bloinformatics, MyongJi University
Yonglin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-C16, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--05-C16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ginkgo biloba (maidenhair tree)
Ginkgo biloba
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DR073660.1 GI:67051563
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RESULT 1396
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ALSB7621 GI:13192655
                                                                                                           /mol_type="mRNA"
/do xzef="texcon:3311"
/bex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/clone_logan: leaf, Vector: :pBK-CMV; Site_1: XhoI;
Site_2: Eco_RI; Strategene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: frazer.murray@bbsrc.ac.uk
GCGGCCCCTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
(*6854-
                          prime
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                                                                                                                                                                                                                                                                            Gaps
Email: mccombie@cshl.org
Original 3 prime EST has been reverse completed to be in 5
direction
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Pred. No. 1.1e+03;
0; Mismatches 1; Indels
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100.0%; Pred. No. 1.1e+03;
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                                                                                  1. .22
/organism="Ginkgo biloba"
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/organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dept. Genomics and Bioinformatics
Roslin Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                        3 TAAAAAAAAAAAAAAAAA 22
                                                    Seq primer: -21M13UnivRev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP Chicken Brain Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
Contact: Frazer Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                    inserts."
                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                              Query Match
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gilfal) [gp] [AR129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Glires; Rodentia;
Sciurognathi; Muroidae; Murinae; Mus.
1 (bases 1 to 23)
5 Dunn, D., Ayagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
                                                                                                                                                                                      A2315640
1M0033004F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0033004 F, genomic survey sequence.
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42Try; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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84112, USA
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0033 row: O column: 04
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
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/organism="Mus musculus"
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23 AAAAAAAAAAAAAAAAAAAA 3
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/clone_lib="wouse 10kb plasmid UUGCIM library"
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musculus G57BL/G/ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was blut safety flow, jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pWM2 (gil f4722114 gb] AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                             AZ621676
1M0455J07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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1 (bases I t
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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100.0%; Pred. No. 1.1
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Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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AZ621676.1 GI:11743962
GSS.
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Matches 20; Conserv
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SOURCE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwAp42 (gilfa712114[ph] hP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                 GSS 20-FEB-2001
                                                                                                                                                                                 AMBLINEZS 20-FEB-200 2MO087N09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0087N09 F, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sclurognathi; Muroidea; Muridae; Murinae; Mus.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
linsert Length: 10000 Std Error: 0.00
Plate: 0087 row: N column: 09
Seg primer: CGTTGTAAAACGACGGCCAGT
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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High quality sequence stop: 23.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
Mus musculus
AZ817623.1 GI:12987531
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Length 23; 0; Indels

DB 1; Le 1.1e+03;

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Gaps

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Length 23; Indels

0.7%; Score 20; DB 1; Let 100.0%; Pred. No. 1.1e+03; iive 0; Mismatches 0;

Query Match Best Local Similarity 100.(Matches 20; Conservative

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

RESULT 1399

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DX064291/c

DEFINITION

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Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
ECORI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institite,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
                                                                                                                                                                                                      Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
ECORI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Punctional Genomics in Farm Animals, Roslin Institite,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
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Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol type="mmk" out out of the property of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 24;
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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Sus scrofa"
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                                                                                                                              Contact: Anderson SI
Genomics and Bioinformatics
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AJ663467
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/clone lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosida, eurosida II; Brassicales, Brassicaceae, Brassica.
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BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                                                                                                                                                                                          UXU04291 CSS 10-JAN-2
KBrB071L16F KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB071L16, genomic survey
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
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/mol type="genomic DNA"
/cultivar="Chiifu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute of Agricultural Biotechnology 225 Seodun-Dong, Suwon, 441-707, Korea Tel: +82-31-299-1670 Fax: +82-31-299-1672
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1 (bases 1 to 24)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB071L16"
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                                                           1 AAAAAAAAAAAAAAA 20
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Brassica Genomics Team
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DX064291.1 GI:84758587
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (pig)
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Class: BAC ends.
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CF297907/c
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/clone lib="KBrB, Brassica rapa BamHI BAC library"
/clone lib="KBrB, Brassica rapa BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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BX568055.1 GI:33434952
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryora, Viridiplantae; Streptophyta; Eubryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 25)
Yang, T.J., Kon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H., and Park, B.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."
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/mol_type="genomic DNA"
/cultivar="Chiifu"
                                                        Length 25;
                                                                                            0; Indels
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Secdun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
                                                      Score 20; DB 1; Le
Pred. No. 1.2e+03;
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Pred. No. 1.2e+03;
                                                                     1 Similarity 100.0%; Fred. No. 1.2
20; Conservative 0; Mismatches
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/db_xref="taxon:51351"
/clone="KBrB081N24"
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Class: BAC ends.
Location/Qualifiers
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DX071965.1 GI:84766261
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Matches 20; Conserv
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/note="country: Zimbabwe; BST from adult gut infected with T.brucei"
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                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neopera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidea; Glossinidae; Glossina.

1 (Dases 1 to 23)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongGi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                      Contact: Hall N
Pathogen Sequencing Unit
Pathogen Sequencing Unit
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are reverse primer reads starting at 5 end of the cDNA all plc reads are from
the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol type="morsitans"
/sub_species="morsitans"
/db_xref="teaxon:37546"
/clone="Tee9160; plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
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Genome Biol. 4 (10), R63 (2003)
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Glossina morsitans morsitans
Glossina morsitans morsitans
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CF297907.1 GI:33669668
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

Skim, J.S., Jun, K.M., Cheong, D.J., Kim, J.V., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Lunpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
                                                         /organism="Oryza sativa (japonica cultivar-group)"
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/mol type="mRNA"
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/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
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with oligoribonucleotides and then used as templates for RT-PCR."
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cDNA library (HD)"
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  Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
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    Location/Qualifiers
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CF314322.1 GI:33686083
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Oryza sativa (japonica cultivar-group)

ISM Oryza sativa (japonica cultivar-group)

Eukaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

CE 1 (bases 1 to 23)

RS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 321 6195

Fax: 82 31 321 6195

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/dev stage="proliferated callus on 2N6 media for 2 weeks"
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/clone lib="dollhAcl-overexpressing transgenic rice plasmid cDNA library (HD)"
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23 bp mRNA linear EST 15-AUG-200
HD--08-F07.bl OsHDAC1-overexpressing transgenic rice plasmid cDNA
Library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--08-F07, mRNA sequence.
CF318266
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Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
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Smultan,A.G., Arnold,J., Weise,M., Wunderlich,J.,
Edman,J.C., Kovacs,J. and Cushion,M.
Expressed sequence tags from Pneumocystis carinii
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                                                              23 TGTATAAAAAAAAAAAAAAAA
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RESULT 1409
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                                                                                                                                                                                                                                                                                                                                                                                                      /organism="pneumocystis carini;"
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/note="Vector: Lambda ZAP II; Site_1: GoRI; Site_2: XhoI;
/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_1: EcoRI;
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1M0244E15F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0244E15 F, genomic survey sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Musinae, Mus.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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                                   Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2117
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Insert Length: 10000 Std Error:
Plate: 0244 row: E column: 15
Seg primer: CGTTGTAAAACGACGGCCAGT
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/clone="UUGCIM0244E15"
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High quality sequence stop: 23.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                 Email: staben@pop.uky.edu.
Location/Qualifiers
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   Unpublished (2000)
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Fax: 801 585 7177
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84112, USA
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/lab host="E. Coli strain Xil0-Gold, Tl-resistant, F-"
/lab host="E. Coli strain Xil0-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gil 4732114 | gb | AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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1 (Dases 1 to 23)
1 (Dases 1 to 23)
1 Islam, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Duouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

(Dipublished (2000)
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0.7%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 2; Indels
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Seq primer: CGTTGTAAAACGACGGCCAGT
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/strain="C57BL/6J"
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Insert Length: 10000 Std Errc
Plate: 0542 row: D column: 04
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Mus musculus
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Fax: 801 585 7177
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Unpublished (1999)
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Unpublished (1999)
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EST.
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EST (Otten
  RESULT 1411
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AL038839
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                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwblat (gilly 4732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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DKFZp566F0946_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp566F0946, mRNA sequence.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
1 (bases 1 to 21)
/lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculuw G7SBL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="vector: pAMP1; Site_1: Not1; Site_2: Sall"
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Location/Qualifiers
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0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.7%; Score 19.8; DB 1; Length 23; Best Local Similarity 91.3%; Pred. No. 1.2e+03; Matches 21; Conservative 0; Mismatches 2; Indels
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EST (Ottenwaelder, et al.)
Unpublished (1999)
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Homo sapiens
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AL038627 21 bp mRNA linear EST 06-JUL-2004 DKFZp566H2046 rl 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566H2046, mRNA sequence.
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DKFZp566P1346 x1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp566P1346, mRNA sequence.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 21)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
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1 (bases 1 to 21)
Ottenwaeider,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
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/mol type="mRNA"
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/clone="bype="kidney"
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/lab_host="x1-2blue"
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/note="Vector: pAMP1; Site_1: Not1; Site_2: SalI"
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/clone="DKF2p566p1346"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
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                                                                                                                                                                                                                                                          BX548564 Glossina morsitans morsitans adult infected gut Glossina morsitans clone Tsel01903_plc, mRNA sequence.
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1 (Dases 1 to 21)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M. B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the teetse fly Glossina morsitans morsitans and expression analysis of putative immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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/clone="Tselol1903_plc"
/tiseue_type="adult infected gut"
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/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: Sal1"
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The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
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                                                    Score 19.4; DB 1; Length 21;
Pred. No. 1.2e+03;
0; Mismatches 1; Indels

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    /organism="Glossina morsitans"

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School of Biological Sciences,
University of Wales,
                                                                                                                           2708 TAAAAAAAAAAAAAAAAAA 2728
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                                                    Query Match 0.7%;
Best Local Similarity 95.2%;
Matches 20; Conservative 0
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CF296213 21 bp mRNA linear EST 14-AUG-2003 30DGS--06-H19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--06-H19, mRNA
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                                                                    Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Tongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/mol_type="mRNA"
/cultivar="Nackdong"
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Location/Qualifiers
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Location/Qualifiers
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GI:33654133
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/db_xref="taxon:39947"
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/cultivar="Nackdong"
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                                                                                           HD--02-L11, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.
E (bases 1 to 21)
S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs.
Lupublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/cultivar="wackdong"
/db xref="taxon:13947"
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/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
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with oligoribonucleotides and then used as templates for RT-PCR."
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'organism="Oryza sativa (japonica cultivar-group)"
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Location/Qualifiers
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Matches 20; Conservative
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FEATURES

REFERENCE AUTHORS RESULT 1417

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/tissue_type="callus" /dev_stage="proliferated callus on 2N6 media for 2 weeks" /lab_nost=ns.coll DH10B" /clone_lib="CostDAC1-overexpressing transgenic rice plasmid cDNA library (HD)" ö DR073305 ik77a11.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA EST 15-AUG-2003 Bukaryota 1.00a Bukaryota 1.00a Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo. 1 (basea 1 to 21) Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Expressed tag sequences from Ginkgo female leaf (NYBG) Unpublished (2005) Contact: W. Richard McCombie Contact: W. Richard McCombie Lita Annemberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory Oryza sativa (japonica cultivar-group) Oryza sativa (japonica cultivar-group) Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza. CF314260
HD--02-L11.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone /note="Wector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression Gaps /organism="Oryza sativa (japonica cultivar-group)" ö 0.7%; Score 19.4; DB 1; Length 21; 95.2%; Pred. No. 1.2e+03; trive 0; Mismatches 1; Indel8

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: :pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
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Cold Spring Harbor, NY 11724, USA
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: J column: 02
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/organism="Ginkgo biloba"
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Seg primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0035J02"
/sex="Male"
                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
                                                                                       Email: mccomble@cshl.org
Original 3 prime EST has been
direction
                                                                                                                                                                                         Seq primer: -21Ml3UnivRev.
Location/Qualifiers
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20; Conservative
PO Box 100, Cold :
Tel: 516 367 8884
Fax: 516 367 8874
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Laboratory Mouse DNA Resources (documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophorasis. Vector DNA was prepared from a derivative of pwM22 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 21)
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11 (bases 1 to 22)
12 (bases 2)
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musculus C57BL/6J (male) was obtained from the Jackson
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/note="Vector: PWD42nv; Purified genomic DNA from M.
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Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Brror: 0
Plate: 0315 row: M column: 10
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0315M10"
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imboratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonicleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil 4732114 [gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptore complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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E 1 (bases 1 to 21)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Relly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Dasmid inserts
Unpublished (2000)
Context: Robert B. Weiss
University of Utah
University of Utah
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Fax: 801 585 7177
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from the Jackson
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musculus C57BL/6J (male) was obtained
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Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: M column: 12
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC2M0045M12"
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Location/Qualifiers
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Best Local Similarity
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AZ792613/c
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Laboratory Mouse DNA Resource Library Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM22 (gi|4732114|gb|RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0096I20F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0096I20 F, genomic survey sequence.
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S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia;
musculus C57BL/6J (male) was obtained from the Jackson
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/note="Vector: PWD42nv; Purified genomic DNA from M.
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC2M0096120"
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Insert Length: 10000 Std Err
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Fax: 801 585 7177
Email: ddunn@qenet
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KEYWORDS
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM22 (gi|4732114|gb|RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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  musculus C57BL/6J (male) was obtained from the Jackson
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/clone lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
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1 (bases 1 to 21)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J. Appabs: an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seg primer: T7
Class: fosmid ends.
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Max-Planck-Institute for Developmental Fology
Tel: 00497071601371
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Pred. No. 1.2e+03;
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Pred. No. 1.2e+03;
0; Mismatches 1;
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/strain="California"
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Pristionchus pacificus
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Matches 20; Conserval
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Matches 20; Conserv
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                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4732114[gb]AR12972.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0156D09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0156D09 R, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
  from the Jackson
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Pred. No. 1.2e+03;
0; Mismatches 1; Indels
musculus C57BL/6J (male) was obtained
Laboratory Mouse DNA Resource
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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: C
Plate: 0156 row: D column: 09
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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Location/Qualifiers
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note="country: Zimbabwe; EST from adult gut infected with
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Glossina moreitans morsitans
Glossina moreitans morsitans
Glossina moreitans
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Hippoboscoidea, Glossinidae, Glossina,
1 (bases 1 to 22)
1 (bases 1 to 22)
1 Lehane, M. J., Ascoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M. B., Bonaldo, M. F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse24f09_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
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                                                                                                                                                                          /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="bkPzp566E0624"
/tissue_type="kinhey"
/dev etage="fetal"
/lab host="xX1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LLS7 2UW
                                                                                                       D-85764 Neuherberg, Germany.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.7%; Score 19.4; DB 1; Length 22; Best Local Similarity 95.2%; Pred. No. 1.2e+03; Matches 20; Conservative 0; Mismatches 1; Indels
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    .22
/organism="Glossina morsitans"

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Genome Biol. 4 (10), R63 (2003)
                                                                                                    Ingolstaedter Landstr.1, D-85
Location/Qualifiers
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EST (Ansorge, et al.)
Unpublished (1999)
                                                   Contact: MIPS
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                                                                                                                                                             GSS 22-DEC-2005
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Secodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
                                                                                                                                                                                                                                                                                                                                                        Brassica rapa subsp. petinensis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Sprmatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 22)
Ansorge, W., Wirkner, U., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
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//lab host="E.coli DH10B"
//clone lib="KBrS, Brassica rapa Sau3AI BAC library"
//note="vector: pCvGIBACI; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
                                                                                                                                       DUB28988 22-DEC-2(KBrS004C07F KBrS, Brassica rapa Sau3Al BAC library Brassica rapa subsp. pekinensis genomic clone KBrS004C07, genomic survey sequence.
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End sequence of Brassica rapa Sau3AI (KBrS) BAC clone Unpublished (2005)
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/organism="Brassica rapa subsp. pekinensis"
/mol type="genomic DNA"
/culTivar="Chilfu"
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/db_xref="taxon:51351"
/clone="KBrS004C07"
                                                                                                                                                                                                                                                                                                                                             Brassica rapa subsp. pekinensis
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DU828988.1 GI:83865584
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Class: BAC ends.
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                                                                                                                                                         22 bp DNA linear GSS 10-JUL-2004 PRI0160a F09_2 - PRI0160a.BR (22) Note: Recurring String Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 23)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:54126"
/clone lib="Mixed stage fosmid library of P. pacificus
var. California"
                        Gaps
                                                                                                                                                                                                                                                                                                  Pristionchus pacificus
Pristionchus pacificus
Bukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.

(bases 1 to 22)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J
AppabB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39. Tuebingen D-72076, Germany
Tel: 0049707160139,
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
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Pred. No. 1.2e+03;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Pristionchus pacificus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq_primer: T7
Class: fosmid ends.
Location/Qualifiers
                                                   2708 TAAAAAAAAAAAAAAA 2728
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                                                                                    22 TATAAAAAAAAAAAAA 2
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Best Local Similarity 95.2%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.2%;
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Sus scrofa
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Matches 20; Conserv
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Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing, Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII (KS+) R. Site 1:
ECORI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
                                                                                                                                                                                                                                                                                                                                                                                          1. .23
/organism="Sus scrofa"
/organism="Sus scrofa"
/mol_type="many"
/mol_type="many"
/db_xref="taxon:9823"
/clone="C0000033_H19"
/clone_Tib="CSEORAN09"
/clone_Tib="CSEORAN09"
/note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised_library
constructed from pooled tissue from day 30 placentas."
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DKFZD566K213, mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.

1 (bases 1 to 23)

Koehrer, K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehrer, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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/note="Vector: pAMP1, Site_1: Not1; Site_2: Sall"
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0.7%; Score 19.4; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels
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Location/Qualifiers
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Pred. No. 1.2e+03;
0; Mismatches 1;
embryo development in pigs and cattle Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566K213"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
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Best Local Similarity 95.2
Matches 20; Conservative
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.
E l (bases 1 to 23)
S Kim,J.S., Jun,K.M., K.M., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
L Uppublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                  23 bp mRNA linear EST 18-AUG-2003 DMT--02-N11.gl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--02-N11, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCR4-TOPO, Site_1: EcoR1; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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Dillon, G. P., Feltwell, T., Skelton, J. P., Ashton, P. D., Coulson, P. S., Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C. Microarray analysis identifies genes preferentially expressed in Unpublished (2005)
Contact: Ivens AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="NackGong"
/db_xref="taxon:39947"
/clone="JMT--02-N11"
/tissue_type="lasf"
/dev stage="la farga"
/lab_host="E.coli DH10B"
/clone lib="AtJMT-overexpressing transgenic rice plasmid
/clone lib="AtJMT-overexpressing transgenic rice plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smail: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
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CF333801.1 GI:33815910
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AM043222.1 GI:75970086
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Schistosoma mansoni
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Matches 20; Conservative
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RESULT 1431
CF333801/c
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lone_lib="Mouse lokb plasmid UUGCIM library"
/note="Voctor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
// (Attrib // www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroldea; Muridae; Murinae; Mus.
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Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Niederhausern, A. and Wright, D., Weiss, R.

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                          /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                              Length 24;
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                                                                                                                                                                                                                                                                                                                0.7%; Score 19.2; DB 1;
87.5%; Pred. No. 1.3e+03;
ative 0; Mismatches 3;
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/organism="Schistosoma mansoni"
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                                                                                                                                                                                                                                            /clone_lib="Schistosoma mans
/note="country: Puerto Rico"
Microarrays Group
Trust Sanger Institute
CB10 1SA, UNITED KINGDOM.
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 24.
Location/Qualifiers
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/clone="UUGC1M0005124"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
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Best Local Similarity 87.5%
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  Pathogen Nellcome 1
                                                  Hinxton,
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AZ304870/c
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KEYWORDS
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polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gif4732114 gb[AR129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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E 1 (Dases 1 to 24)
S Dunn,D., Aoyagi,A., Barber,M., Reacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Tingey,A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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MNO16810F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0016B10 F, genomic survey sequence.
AZ309553
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Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: B column: 10
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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    .24
    /organism="Mus musculus"

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Location/Qualifiers
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Fax: 801 585 7177
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84112, US
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COMMENT
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AUTHORS
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KEYWORDS
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polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0245E16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Ren. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                          ch 0.7%; Score 19.2; DB 1; Length 24; Il Similarity 87.5%; Pred. No. 1.3e+03; 21; Conservative 0; Mismatches 3; Indels
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AZ448207
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Insert Length: 10000 Std Error: 0.00
Plate: 0245 row: E column: 16
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
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/clone="UUGC1M0245E16"
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Fax: 801 585 7177
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AZ448207
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polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gildy132114 gblAR129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-GGold (Stratagene) cells and selected for ampicillin resistance."
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone="Wector: PWD42nv; Purified genomic DNA from M.
musculus GS7BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
/http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus
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Dunni, A., Angaci, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                              0.7%; Score 19.2; DB 1; Length 24; 17.5%; Pred. No. 1.36+03;
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Fax: 801 585 7177

Email: ddundgenetics.utah.edu

linest Length: 10000 Std Error: 0.00

Plate: 0082 row: P column: 18

Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                87.5%; Pred. ...
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/strain="C57BL/6J"
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/clone="UUGC2M0082P18"
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AZ814559.1 GI:12984467
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Best Local Similarity 87.59
Warches 21; Conservative
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84112, USA
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AZ814559/c
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polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil #4732114[gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XILO-GOld (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 24)
Srinivasan, U., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. Appadb: an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: foomid ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pristionchus pacificus
Pristionchus pacificus
Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
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                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.7%; Score 19.2; DB 1; Length 24; Best Local Similarity 87.5%; Pred. No. 1.3e+03; Matches 21; Conservative 0; Mismatches 3; Indels
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0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 3; Indels
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Max-Planck-Institute for Developmental Biology
Spenannstr. 37-39, Tuebingen D-72076, Germany
Tal: 00497071601371
Fax: 00497071601498
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/mol_type="genomic DNA"
/strain="California"
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CL676551.1 GI:50182187
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CL676551/c
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DEFINITION
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RESULT 1438

AJ668179/c

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Roslin Institute
Roslin Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and triamed with phred
Single pass sequencing. Bases called and triamed with the -minscore 20
and -minmatch 12 options Vector:pBlueScriptIKS+) R. Site 1:
ECORI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institite,
Location/Qualifiers
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Genomics and Bioinformatics
Roslin Institute
Foslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
                                                                                                                                                                                                                                                              Anderson, S. I., Finlayson, H.A. and Archibald, A. L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
(Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
AJ668179 LEGRANO9 Sus scrofa cDNA clone C0000045_L19, mRNA
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol type="mkNA"
/db_xref="taxon:9823"
/clone="C0000045_L19"
/clone_Type="placenta"
/clone_Type="placenta"
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
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/organism="Sus scrofa"
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                                                                                                                                Sus scrofa (pig)
Sus scrofa
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Matches 19; Conserv
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KEYWORDS
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/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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1 (bases 1 to 19)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., and Radelof,U.
                                                                                                                                                                        /mol type="mmkha"
/db_xref="taxon:9823"
/clone="c0000048_012"
/tissue type="placenta"
/clone Tib="CSEORANO9"
/note="vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
Not1; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."
EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK. EH25 9PS, www.arkgenomics.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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S013713-024-014-B24-T7 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-014-B24 3-PRIME, mRNA sequence.
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/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 19 Std Error: 0.00
Plate: 14 row: B column: 24
Seq primer: T7; GTAATACGACTACTATAGGGC.
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/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
                                                                                                                                                                                                                                                                                                                                                                                                                Query Matcn
Best Local Similarity 100.0%; Pred. NO. 1.2
10. Conservative 0; Mismatches
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|db xref="taxon:161934"
|clone="024-014-B24"
                                                                                                                                                          /organism="Sus scrofa"
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1 (basea 1 to 19)

2 Young, J.M., Shykind, B.M., Lane, R.P., Tonnes-Priddy, L., Ross, J.A., Walker, M., Williams, E.M. and Trask, B.J.

Odorant receptor expressed sequence tags demonstrate olfactory expression of over 400 genee, extensive alternate splicing and unequal expression levels

L Genome Biol. 4 (11), R71.1-R71.15 (2003)

Contact: Young JM

Trask Lab, Division of Human Biology

Fred Hutchinson Cancer Research Center

1100 Pairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA
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/dev_stage="Adult"
/clone_lib="Adult"
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LambdaZAPII-XR; Site 1: EcoRI; Site 2: XhoI; This library
was provided by Leslie Vosshall: mRNA was prepared from
the olfactory and respiratory epithelium of an adult
mouse. Oligo-dT primed cDNA was directionally cloned into
Stratagene's lambdaZAPII-XR vector:
Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                     OR 2032F05 010529.y1 Adult mouse olfactory epithelium library Mus musculus cDNA clone 2032F05 5', mRNA sequence.
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100.0%; Pred. No. 1.2e+03;
ive 0; Mismatches 0; Indels
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Pred. No. 1.2e+03;
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Fax: 206 667 6524
Email: jayoung@fhcrc.org
Seq primer: M13 Reverse.
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CB174047.1 GI:37592676
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Matches 19; Conservative
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Expands in to 19)

Songs.1.1, Xim.,J.K., Xim.Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)

Contact: Nahm B.H.

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Yongin, XyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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14ROOT--01-G03.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-G03, mRNA
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Oryza sativa (japonica cultivar-group)
Bukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                              Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bloinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organisme="Oryza sativa (japonica cultivar-group)"
/mol_type="mgNA"
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/lab_host="E.coli DH10B"
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/lab_host="E.coli DH10B"
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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100.0%; Pred. No. 1.2e+03
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1. .19
/organism="Oryza sativa (japonica cultivar-group)"
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bloscience and Bioinformatics, MyongJi University
Vongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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100.0%; Pred. No. 1.2e+03;
ative 0; Mismatches 0; Indels
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.00.0%; Pred. No. 1.2e+03;
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Best Local Simi
Matches 19;
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CF299598
7LEAF--03-K23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-K23, mRNA
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7LEAF--07-L24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-L24, mRNA
                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Contact: Nahm B.H.
Generalcs and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongGj, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Bource

FEATURES

Query Match

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CF309801
ABF--04-C04.gl ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
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Oryza sativa (japonica cultivar-group)
Enkaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Enkaryota, Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Enrhartoideae; Oryzeae; Oryza.

I (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="leaf"
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cDNa library (ABF)"
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ABF--04-F15.bl ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--04-F15, mRNA sequence.
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100.0%; Pred. No. 1.2e+03;
vative 0; Mismatches 0;
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 19; Conservative 0; Mismatches 0;
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

1 (bases 1 to 19)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Tel: 82 31 330 6193

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/lab_host="E.col; SOLR"
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Xno1; Leaf was dried for Zhrs. cDNA was inserted into
lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
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ABF1--05-G10.g1 ABF3-overexpressing transgenic rice lambda phage cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA clone ABF1--05-G10, mRNA sequence.
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Location/Qualifiers
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  Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhrahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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nes 19; Conserv
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 1447

LOCUS CF304589/c

EST 15-AUG-2003

Query Match

source

FEATURES

TITLE JOURNAL COMMENT

REFERENCE AUTHORS ö

Gapa

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19 AAAAAAAAAAAAAAAA 1
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19 bp mRNA linear EST 15-AUG-2003

ABF-06-L18.gl ABF3-overexpressing transgenic rice plasmid cDNA

library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

ABF--06-L18, mRNA sequence.

CF311496.1 GI:33683257
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermarophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, BEP
                                                           Thurst intercolours of years; Oryzens; 
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongln, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Bhrhartoideae; Oryzeae; Oryza.
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Mod_Lype="maRNA"
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100.0%; Pred. No. 1.2e+03;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bhnahm@bio.myongji.ac.kr.
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/cultivar="Nackdong"
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Location/Qualifiers
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ABF--06-M03.gl ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--06-M03, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                          /note="Weetor: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
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cDNA library (ABF)
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Pred. No. 1.2e+03;
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100.0%; Pred. No. 1...
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Matches 19; Conserva
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Best Local Similarity
Matches 19; Conserv
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RESULT 1452 CF312403

LOCUS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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cDNA library (HD)"
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.K., and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
                       Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongli, KyeongQi, Korea
Yengli, KyeongQi, Korea
Fax: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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100.0%; Pred. No. 1.2e+03;
ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:39947"
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Best Local Similarity 100.0%;
Matches 19; Conservative 0
  Contact: Nahm B.H.
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                                  19 bp mRNA linear EST 15-AUG-2003 library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--08-C07, mRNA sequence. CF312403.1 GI:33684164
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhatroideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza, Oryzae;
(Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeongqi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="ABF3-overexpressing transgenic rice plasmid cDNA lIbrary (ABF)"
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/lab_host="E.coli DH10B"
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Local Similarity 100.0%; Pred. No. 1.2e+03;
nes 19; Conservative O; Mismatches O;
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FEATURES

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Oryza sativa (japonica cultivar-group)

SM Oryza sativa (japonica cultivar-group)

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-Grale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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19 bp mRNA linear EST 18-AUG-2003 NACL--08-G19.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--08-G19, mRNA
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cultivar-grackong"
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                                                                                Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaae; Oryza.
I (bases 1 to 19)
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Larges-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yooghu, KyeongQi, Koesa Tel: 82 31 330 6193 Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clome_lib="Rice callus plasmid cDNA library (NACL)" /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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100.0%; Pred. No. 1.2e+03;
ive 0; Mismatches 0; Indels
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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lbrary (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-A23, mRNA sequence.
CF318788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee, T.H., Shin, Y.C.,
treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
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Location/Qualifiers
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahn,B.H.
Unpublished (2003)
                                                                                                                                0.7%; Score 19; DB 1; Le
100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0;
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Best Local Similarity 100.0*; Pred. No. 1.2

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                                                                                                                                                                 Similarity
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TITLE JOURNAL COMMENT

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19 bp mRNA linear EST 18-AUG-2003 JMT--03-C09.gl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--03-C09, mRNA sequence.
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was reverse transcribed and then used for PCR. mRNA was
pepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyte; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Enthatroideae; Oryzaa.

1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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100.0%; Pred. No. 1.2e+03;
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RESULT 1459
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                             /fissue_type="callus"
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.L., Kim,Y.K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Tongli, Kyeongqi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
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/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA_library (JMT)
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/mol_type="mRNA"
/cultivar="Nackdong"
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1.2e+03;
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    Location/Qualifiers
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Vitis vinifera

Vitis vinifera

Vitis vinifera

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SM Vitis vinifera

Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicotyledons; cosids; Vitaceae; Vitis.

I (bases 1 to 19)

S Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Gentra, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

L Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pCR4-TOPO, Site_1: EcoRI; Oligo-capped mRNA was reverses transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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/note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1: Sfila; Site_1:
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
                                                                                                                                                                                                                                                                         /tissue_type="leaf"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 bp mRNA linear EST 30-APR.
EST 17546 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00KL003H10 3', mRNA sequence.
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    19 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /mol_tyne="mRNA" /mol_tyne="mRNA" /db xref="taxon:39947" /db xref="taxon:39947" /clone="JMT--03-C09"

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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de'la Recherche
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             of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Fax: 82 313 421 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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00.0%; Pred. No. 1.2e+03;
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
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EST 17912 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CSOORLOOGH10 3', mRNA sequence.
CN545964.
CN545964.1 GI:46910589
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SfilA; Site_2: SfilB; Oriented library"
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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1 (bases 1 to 19)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Handi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, Vitaceae, Vitis.
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UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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        Length 19;
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0.7%; Score 19; DB 1; Le
100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0;
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Pred. No. 1.2e+03;
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/mol_type="mRNA"
/culTivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006D07"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: 9.hamdl@bordeaux.inra.fr
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CN545922.1 GI:46910547
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Tue Nov

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (dog)
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Matches 1
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CX007355/c
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71, Avenue Edouard Bourleaux, BP 01, 33883 Villenave D'Ornon Cedex,
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Vitis vinifera
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons,
rosida, Vitaceae, Vitis.
I (Dasea I to 19)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
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                Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, B. Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
Onpublished (2002)
Contact: Hamdi S.
UNR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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Universite de Bordeaux I, Institut National de la Recherche
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1.2e+03;
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/cultivar="Cabernet Sauvignon"
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/cultivar="Cabernet Sauvignon"
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100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                           Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: 8.hamdi@bordeaux.inra.fr
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Fax: 00-33-(0)5-57-12-25-48
Email: 8.hamdl@bordeaux.inra.fr
Seg primer: 17.
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71, Avenue Edouard Bourleaux,
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CN546303.1 GI:46910928
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Best Local Similarity 100.(
Matches 19, Conservative
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                                                                                                                                                                                                                                                                                                                      Seg primer: T7.
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/clone lib-"Brain - Cerebellum Library (DOCESTB)"
/note="Organ: Brain; Vector: pBluescript II SK; Site 1:
/note="Organ: Brain; Vector: pBluescript II SK; Site 2:
KR kit from Stratagene. Cloned CDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Vecerinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                    האסט 19 bp mRNA linear EST 03-DEC-2004
iv25a12.bl Brain - Cerebellum Library (DOGESTB) Canis familiaris
cDNA, mRNA sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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/note="Organ: Fruit without seeds; Vector: Lambda
TriplEx2; Site_1: SfilA; Site_2: SfilB; Oriented library"
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0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels
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/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESTS from Canis familiaris cerebellum (dog) Unpublished (2004)
Contact: W. Richard McCombie
Contact: W. Richard McCombie
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.7%; Score 19; DB 1; Le
100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0;
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/organism="Canie familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
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Fax: 516 367 8874
Email: mccombie@cshl.org.
Location/Qualifiers
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Tue Nov

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Query Match
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Gnetum gnemon
Gnetum gnemon

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Gukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetophyta; Gnetopelda; Gnetales; Gnetum.

El (bases 1 to 19)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Ballia, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Benfey, P., Coruzzi, G. and Stevenson, D.
Contact: W. Richard McCombie
Lita Annanberg mazen Genome Sequencing Center
Cold Spring Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Fax: 516 367 8884
Email: mccombie@cshl.org
Seq primer: -21MlJUniveRev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev seque="3" month old normal canine"
/lab_host="XL10 Gold"
/lab_host="XL10 Gold"
/clone lib="Whole Heart Library (DOGSST5)"
/note="Organ: Heart; Vector: pBluescript II SK; Site_1:
ECORI; Site_2: Xhol; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, Phb, Pethology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"
                                   Canis familiaris
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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it71a04.gl Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
sequence.
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Balia, V.S., Nascimento, L.U. and McCombie, W.R.
ESTS from Canis familiaris whole heart (dog)
Unpublished (2004)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8874
Email: mccombie@cshl.org.
Location/Qualifiers
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Pred. No. 1.2e+03;
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/mol_type="mRNA"
/db_xref="taxon:9615"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Unknown"
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                                                                                                                     Canis.
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Green green discontinuous Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Ebraryophyta; Gnetopsida; Gnetales; Gnetume.

E 1 (bases 1 to 19)

S Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Gnetum female cone (NYBG)

L Unpublished (2003)

AL Unpublished (2003)

Contact: W. Richard McCombie

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Tel: 516 367 8884

Fax: 516 367 8874

Email: mccombie@cshl.org

Seq primer: -21M31UnivRev.
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                                                                                    /clone_lib="Gnetum female cone '(NYBG)" / hote="Organ: mature, unfertilized reproductive strobili; / hote="Organ: mature, unfertilized reproductive strobili; / vector: pBK-CMV; Site 1: Xhoi; Site 2: Eco Ri; Date: Completed 02/11/02, submitted for sequencing 02/12/02. Library: Stratagene ZAP Express CDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts. Sample: NYBG accession number #436/84.
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hote="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhOi; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express CDNA Synthesis Kit. The
Library was size-fractionated to enrich for large inserts.
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/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
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Matches 19; Conservative
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SOURCE ORGANISM

KEYWORDS

VERSION

REFERENCE AUTHORS

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FEATURES

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Cycas rumphii

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ENaryoptyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Cycadophyta; Cycadales; Cycadaceae; Cycas.

1 (bases 1 to 19)

Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,

O'Shaughnessy, A.L., Balija, V., Martianssen, R.A., McCombie, R.W.,

Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Cycas ovules (NYBG)

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Seq primer: -21Ml3UnivRev.
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1924h10.gl Cycas ovule (NYBG) Cycas rumphii cDNA 3', mRNA sequence.
DR063041
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/note="Organ: Ovules; Vector: pBK-CMV; Site_1: XhoI;
Site_2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
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/note="Organ: Sporophyll with ovules detached.; Vector:
DBK-CMV, Site 1: Kho 1; Site 2: Eoc RI; Date: Completed
DBK-CMV, Site 1: Kho 1; Site 2: Eoc RI; Date: Completed
DBK-CMV, Site 1: Kho 1; Site 2: Eoc RI; Date: Completed
DBK-CMV, Site 1: Kho 1; Site 2: Eoc RI; Date: Completed
DBK-CMV, Site 1: Site 2: Eoc RI; Date: Completed
DBK-CMV, Site 1: Site 2: Eoc RI; Date: Completed
DBK-CMV, Site 1: Ditary: Made using Stratagene's ZAP Express
Vector Kit. Library: was size fractionated for large
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'organism="Cycas rumphii"
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/db_xref="taxon:58031"
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Cycas rumphis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Cycadaceae; Cycas.

Spermatophyta; Cycadophyta; Cycadaceae; Cycas.

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S Brenner, E. D., Twigg, R. W., Runko, S. J., Katari, M. S., Dedhia, N. N., O'Shaughnessy, A. L., Balija, V., Martienssen, R. A., McCombie, R. W., Enfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Cycas sporophyll (w/o ovule) (NYBG)

L. Contact: W. Richard McCombie Sequencing Center

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Best Local Similarity 100.0
Matches 19; Conservative
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KEYWORDS SOURCE ORGANISM

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ISM Ginkgo biloba

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

SB Fermatophyta; Ginkgophyta; Ginkgoales; Ginkgo.

SB Brenner, E. D., Twigg, R. W., Runko, S. J., Katari, M. S., Dedhia, N. N.,

O'Shaughnessy, A. L., Balija, V., Martienssen, R. A., McCombie, R. W.,

Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo microsporophyll (NYBG)

Uppublished (2005)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

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Email: mccombie@cshl.org
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El (Massea It ol 19)

Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgo.

S. I (Massea It ol 19)

S. Brenner, E. D., Twigg R. W., Runko, S. J., Katari, M. S., Dedhia, N. N., O'Shaughnessy, A. L., Balija, V., Martienssen, R. A., McCombie, R. W., Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo megasporophyll (NYBG)

Unpublished (2005)

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Fax: 516 367 8874

Email: mccombie@eshl.org

Seq primer: -21M13UnivRev.
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/note="Organ: megasporophyll; Vector: pBK-CMV; Site_1:
/note="Organ: megasporophyll; Vector: pBK-CMV; Site_1:
/note="Site_2: Eco RI; Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts."
ip65g04.g1 Ginkgo megasporophyll (NYBG) Ginkgo biloba cDNA 3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Cinkgo biloba"
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/sex="Female"

    19
    /organism="Ginkgo biloba"

                                                                                                               Ginkgo biloba (maidenhair tree)
Ginkgo biloba
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

El (bases I to 19)

El (bases I to 10)

Shaughnessy, A. L., Balija, V., Martienssen, R. A., McCombie, R. W., O'Shaughnessy, A. L., Balija, V., Martienssen, R. A., McCombie, R. W., Dephished tag sequences from Ginkgo female leaf (NYBG)

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PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

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Fax: 516 367 8884

Fax: 516 367 8884
                                                               /clone lib="Ginkgo microsporophyll (NYBG)"
/note="Organ: microsporophyll; Vector: pBK-CMV; Site_1:
/Not], Site_2: Eco RI; Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts."
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BD774208.1 GI:67052176
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/note="Organ: leaf, Vector: :pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
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100.0%; Pred. No. 1.2e+03;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ginkgo biloba (maidenhair tree)
Ginkgo biloba
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                            Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Eutheria; Butheria; Butheria; Burarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

E 1 (Dases 1 to 19)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ralla, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R. Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R. Unpublished (2000)
L Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Ginkgo male leaf (NYBG)"
/clone lib="Ginkgo male leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI; Site_2:
Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large
inserts."
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1M0008H20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0008H20 R, genomic survey sequence.
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0008 row: H column: 20
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
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/mol_type="mRNA"
/db_xref="taxon:3311"
Ginkgo biloba (maidenhair tree)
Ginkgo biloba
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
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Fax: 801 585 7177
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Matches 19; Conserv
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Rm. 308, Bic
USA
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of puble [4732114]gb] AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                /clome_lib="Mouse 10kb plasmid UUGCIM library"
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                      /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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University of Utah Genome Center
University of Utah
Rm. 1908 Biomedical Polymers Research Bldg., 20
84112, USA
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100.0%; Pred. No. 1.2e+03;
ive 0; Mismatches 0;
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Insert Length: 10000 Std Error: 0.00
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High quality sequence stop: 19.
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Mus musculus
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                                                                                                                                                                                                                           /sex="Male
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Fax: 801 585 7177
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gil #4732114|gb|AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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84112, USA
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1M0018E21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0018E21 R, genomic survey sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Welss, R.
Niederhausern, A. and Wright, D., Welss, R.
Unpublished (2000)
Contact:
Unpublished (2000)
University of Utah Genome Center
University of Utah Genome Center
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Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: E column: 21
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0.7%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 19; Conservative 0; Mismatches
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Seg primer: CACACAGGAAACAGCTATGACC
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                                                                                     /mol_type="genomic DNA"
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  .ocation/Qualifiers
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AZ310105.1 GI:10351761
                                                                                                                                                                                                        /sex="Male"
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Fax: 801 585 7177
                                   source
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AZ310105/c
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SOURCE
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/lab host="E. Coli strain XLI0-Gold, T1-resistant, F-"
/lab host="E. Coli strain XLI0-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated earth of polynucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gf rom a derivative
of pWD42 (gil 4732114 gpl AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
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adaptored vector DNA, and transformed into
chemically-competent E. coli Xil10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (Dases 1 to 19)

2 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Unpublished (2000)

L Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0036 row: B column: 18
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Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                                                           /sex="Male"
                              source
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cocation/Qualifiers
                                                                                                                                                                                               /sex="Male
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Fax: 801 585 7177
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/clone llb="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nr; Purified genomic DNA from M.
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0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated from a fra
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inducible derivative of plasmid R1. The vector was ligated
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University of Utah Genome Center
University of Utah
Wen. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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1M0072H15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0072H15 F, genomic survey sequence.
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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Insert Length: 10000 Std Error: 0.00
Plate: 0072 row: H column: 15
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
                                                           'organism="Mus musculus"
                                                                                        mol_type="genomic_DNA"
/strain="C57BL/6J"
                                                                                                                                        xref="taxon:10090"
                                                                                                                                                                     clone="UUGC1M0036B18"
     location/Qualifiers
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                                                                                                                                                                                                    /sex="Male"
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwDAQ2 (gild)AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0088A10F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0088A10 F, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stockes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                           /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /clone lib="Mouse lokb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/63 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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100.0%; Pred. No. 1.2e+03;
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Insert Length: 10000 Std Error: 0.00
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Seg primer: CGTGTAAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
'organism="Mus musculus"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                  'mol_type="genomic DNA"
'strain="C57BL/6J"
                                                                                                 db_xref="taxon:10090"
                                                                                                                             /clone="UUGC1M0072H15"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalpd (gql 4732114 [gb] AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0110B24F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0110B24 F, genomic survey sequence.
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Murinae, Mus.
                                                                                                                                                                                                        /lab_host="B. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Twetcor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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Best Local Similarity 100.0%; Pred. No. 1.2.
Matches 19; Conservative 0; Mismatches
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0110 row: B column: 24
                                                        'organism="Mus musculus"
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Seg primer: CGTTGTAAAACGACGGCCAGT
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University of Utah Genome Center
University of Utah
                                                                                  'mol_type="genomic DNA"
'strain="C57BL/6J"
                                                                                                                                  /db_xref="taxon:10090"
/clone="UUGC1M0088A10"
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     Location/Qualifiers
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                                                                                                                                                                                     /sex="Male"
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nr; Purified genomic DNA from M.
musculus C57BL/G/ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dhares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hybut end-repaired with T4 DNA polymerase and T4
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMPA2 (gil 4/732114 gb) AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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E (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2010)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Tnsert Length: 10000 Std Error: 0.00
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                                                                                                                                                   /sex="Male
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Fax: 801 585 7177
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gol electrophoresis. Vector DNA was prepared from a derivative of pwalez (gill #1732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0127F04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0127F04 R, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
84112, USA
Fax: 801 S85 5606
Fax: 801 S85 57177
Email: ddunn@genetics.urah od...
                                                                                                                                                                                                                                                                 /clome_lib="Mouse 10kb plasmid UUGCIM library"
//note=="Wector: PWD42IV'; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Anyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Musse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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100.0%; Pred. No. 1.2e+03;
ive 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
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                                                                                                                                                                                                                                     /lab_host="E.
                                                                                                                                                                                                             /sex="Male
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AUTHORS
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1MO127D10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0127D10 F, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                               /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"/clone_lib="Mouse_10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/60 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Waiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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100.0%; Pred. No. 1.2e+03;
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Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 19.
                                                                organism="Mus musculus"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                               /mol_type="genomic DNA"
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   Location/Qualifiers
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                                                                                                                                                                                                                      /sex="Male
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Fax: 801 585 7177
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Matches 19; Conserv
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RESULT 1484 AZ374409

DEFINITION

ACCESSION

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ORGANISM

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Class: plasmid ends
High quality sequence stop: 19.
          Location/Qualifiers
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1M0144L10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0144L10 R, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                        /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
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musculus C57BL/64 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Waiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Insert Length: 10000 Std Error: 0.00
Plate: 0144 row: L column: 10
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                     /sex="Male"
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Fax: 801 585 7177
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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complamentary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli X110-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Sciurognathi; Muroidea; Muridae; Mus.

1 (Dases 1 to 19)

Sunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Rilly,M., Rose,M., Rose;R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R. Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R. Diasmid inserts

Diasmid inserts

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1M0153K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
losert Length: 10000 Std Error: 0.00
Plate: 0153 row: K column: 08
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organism="Mus musculus"
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/strain="C57BL/6J"
                                                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0144L10"
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Mus musculus
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                            /lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bylorynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1M0182P04F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0182P04 F, genomic Burvey sequence.
AZ410050
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Wouse, whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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Insert Length: 10000 Std Error: 0.00
Plate: 0182 row: P column: 04
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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                                                                               'mol_type="genomic DNA"
'strain="C57BL/6J"
                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC1M0153K08"
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Location/Qualifiers
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Mus musculus
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Fax: 801 585 7177
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Best Local Similarity
Matches 19; Conserv
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Rm. 308, Bic
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1M0188013R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0188013 R, genomic survey sequence.
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="Mouse 10kb plasmid UUGCiM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                             /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
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100.0%; Pred. No. 1.2e+03;
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Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 19.
                                                                                                       'organism="Mus musculus"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
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Fax: 801 585 7177
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse lokb plasmid UUGCIM library"
/note=="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose get
electrophoresis. Vector DNN was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Sciurognathi; Muroidea; Murinae; Mus.

1 (Joses 1 to 19)

S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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19 bp DNA linear GSS 03-OCT-2000
1M0204020F Mouse 10kb plasmid UGGIM library Mus musculus genomic
Clone UUGCIM0204020 F, genomic survey sequence.
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddundgenetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0204 row: O column: 20
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                                                                                                                                                             xref="taxon:10090"
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            Location/Qualifiers
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                                                                                                                                                                                                                        /sex="Male"
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            FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwdet (gil 47321141gbl A7122072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0201B21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Niederhausern, A. and Wright, D., Weiss, R.

Unpublished (2000)

Contact: Robert B.

University of Utah Genome Center

University of Utah
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00.0%; Pred. No. 1.2e+03;
ve 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0201 row: B column: 21
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                                                                    'organism="Mus musculus"
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      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ422604.1 GI:10546617
                                                                                                                                                                                                                  /sex="Male"
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Fax: 801 585 7177
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Best Local Similarity
Matches 19; Conserv
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                                     source
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AUTHORS
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High quality sequence stop: 19.
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Matches 19; Conserv
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AZ442365/c
                           source
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                                                                                                                                                                                               /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polyrucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pwd2 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1M0233D01F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0233D01 F, genomic survey sequence.
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1 (basea 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Walse, R.
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                                                 'organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                      clone="UUGC1M0204020"
                                                                                                                                xref="taxon:10090"
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Location/Qualifiers
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Mus musculus
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Unpublished (2000)
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Fax: 801 585 7177
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FEATURES
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muscular C.7 Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adappored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                           /sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Tingey, A., von

Niederhausern, A. and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact Robert B. Weiss

University of Utah Genome Center

University of Utah
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Insert Length: 10000 Std Error: 0.00
Plate: 0236 row: C column: 13
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tive 0; Mismatches
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Class: plasmid ends
                                                                   'organism="Mus musculus"
                                                                                                     'mol_type="genomic DNA"
'strain="C57BL/63"
                                                                                                                                                              xref="taxon:10090"
                                                                                                                                                                                                /clone="UUGC1M0233D01"
Location/Qualifiers
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Fax: 801 585 7177
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Class: plasmid ends
High quality sequence stop: 19.
             Location/Qualifiers
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|RF129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Ztokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clome_lib="Mouse_lokb_plasmid_UGCIM_library."
/note="Vector: PWB4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0248 row: K column: 13
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Seg primer: CACACAGGAAACAGCTATGACC
                                                         organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                                  'mol_type="genomic DNA"
'strain="C57BL/6J"
                                                                                                                                    /db_xref="taxon:10090"
/clone="UUGC1M0236C13"
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  cocation/Qualifiers
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Fax: 801 585 7177
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Best Local Similarity
Matches 19; Conserv
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84112, USA
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/daca="Male"
//dab host="Male"
/lab host
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E 1 (bases 1 to 19)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ralla, H., Longacre, S., Mahmoud, M., Meen, E., Pedersen, T., Really, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Unpublished (2000)
L Unpublished (2000)
L Context: Robert B. Weiss University of Utah Genome Center University of Utah
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1M0255G11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0255G11 R, genomic survey sequence.
AZ453930
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Pred. No. 1.2e+03;
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Insert Length: 10000 Std Error: 0.00
Plate: 0255 row: G column: 11
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Best Local Similarity 100.0%; Pred. No. 1.4
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organism="Mus musculus"
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Location/Qualifiers
                                                                                                                                                                                           /sex="Male"
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Fax: 801 585 7177
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Matches 19; Conserv
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AZ471494/c
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        FEATURES
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                                                                                                                                                                                                           /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (basea 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rally, M., Rose, M., Rose, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Muse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ460906
1M0266E03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0266E03 R, genomic survey sequence.
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                                                            'organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                                        'mol_type="genomic DNA"
'strain="C57BL/6J"
                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC1M0255G11"
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        ocation/Qualifiers
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Mus musculus
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GSS.
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Fax: 801 585 7177
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/done libs-mouse libb plasmid UUGCIM library.
//clone libs-mouse libb plasmid UUGCIM library.
//clone libs-mouse libb plasmid UUGCIM library.
//core="Vector: PWD4nnv; Purified genomic DNA from M.
musculus G57BL/G3 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XIIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.

1. (bases 1 to 19)
1. (bases 1 to 19)
1. (bases 1 to 19)
1. (ann,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
18lam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
18lam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
18lam,H., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von
Dlasmid inserts
1. (Dnyublished (2000)
1. Unquelished (2000)
1. Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
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                                                                                                                                                                                                                    Coli strain XL10-Gold, T1-resistant, F-"
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100.0%; Pred. No. 1.2e+03;
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Insert Length: 10000 Std Error: 0.00
Plate: 0286 row: E column: 11
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
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organism="Mus musculus"
                                  'mol type="genomic DNA"
'strain="C57BL/6J"
                                                                                                        /db xref="taxon:10090"
                                                                                                                                              /clone="UUGC1M0266E03"
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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/lone=11b="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gen
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Warshity of Utah
University of Utah
84112, USA
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1M0315D21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0315D21 F, genomic survey sequence.
AZ486786
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1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., R
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
lnesrt Length: 10000 Std Error: 0.00
Plate: 0315 row: D column: 21
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                            organism="Mus musculus"
                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                      xref="taxon:10090"
                                                                                                                                                                                                                                                        /clone="UUGC1M0295F04"
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                Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                                                                                                                                      /sex="Male"
                                                          source
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                                                                                                                                                                                                                                                                                                      /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
/http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated by series
ligated to rifica at constant velocity. The sheared DNA
was blunt ende-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Murinae; Musi

1 (bases 1 to 19)

S Dunn, D., Aoyagai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

University of Utah
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19 bp DNA linear GSS 04-OCT-200
1M0295F04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Insert Length: 10000 Std Error: 0.00
Plate: 0295 row: F column: 04
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Class: plasmid ends
High quality sequence stop: 19.
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                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                          /db_xref="taxon:10090"
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    Location/Qualifiers
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                                                                                                                                                                                                                                                                                              /sex="Male"
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Fax: 801 585 7177
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transfermed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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E 1 (bases 1 to 19)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Mesen, E., Pedersen, T., Really, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Unpublished (2000)
L Ontact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
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1M0123E17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0323E17 R, genomic survey sequence.
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0323 row: E column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
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                                                                              'mol_type="genomic DNA"
'strain="C57BL/6J"
                                                                                                                                                   clone="UUGC1M0315D21"
                                                                                                                                xref="taxon:10090"
.ocation/Qualifiers
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of public [A132114 [ph] RF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xi10-Gold (stratagene) cells and selected for ampicillin resistance."
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1 (basea I to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R., Tingey, A., von plasmid inserts
                                                                                                                                                                                                                        /gex="Male" Coli strain XL10-Gold, T1-resistant, F-" /lab host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGCIM library" /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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100.0%; Pred. No. 1.2e+03;
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Insert Length: 10000 Std Error: 0.00
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deg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
                                                         'organism="Mus musculus"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                              mol_type="genomic_DNA"
'strain="C57BL/6J"
                                                                                                                                                        /db_xref="taxon:10090"
/clone="UUGC1M0323E17"
Location/Qualifiers
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Fax: 801 585 7177
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Location/Qualifiers
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                                                                                                                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ583970
                                     source
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ORGANISM
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                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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E 1 (Dases 1 to 19)
S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Relly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R., Tingey,A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
L. Contact: Robert B. Weiss
University of Utah Genome Center
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84112, USA
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                                                                                                                                                                           /gex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Pred. No. 1.2e+03;
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                                                  organism="Mus musculus"
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Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                             /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0350B04"
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Insert Length: 10000 Std Erro
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     Location/Qualifiers
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Mus musculus
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Fax: 801 585 7177
                             source
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AZ579119
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ORGANISM
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KEYWORDS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gilfa712114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Wis musculus
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mummalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weise, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                             /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse lokb plasmid UGCIM library"
/note="Vector: PWP4Zlv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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(Unpublished (2000)
(Unpublished (2000)
(University of Utah Genome Center
University of Utah
(Rm. 108, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Fax: 801 585 7177
Eax: 801 585 7177
Eax: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0388 row: M column: 11
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
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organism≃"Mus musculus"
                          /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0363M16"
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seg primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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Fax: 801 585 7177
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Matches 19; Conserv
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AZ593210
                               source
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AUTHORS
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  FEATURES
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                                                                                                                                                                                               /lab hoste="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone lib="Wenuse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was blut cond repaired by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gf rom a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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19 bp DNA linear GSS 13-DEC-20C
1M0391D21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0391D21 F, genomic survey sequence.
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1 (Joasea 1 to 19)

1 (Joasea 1 to 19)

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1 (Joasea 1 to 10)

Niederhausern, A. and Wright, D., Walsa, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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100.0%; Pred. No. 1.2e+03;
ive 0; Mismatches 0; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0391 row: D column: 21
Seq primer: CGTTGTAAAACGACGCCAGT
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Best Local Similarity 100.(
Matches 19; Conservative
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KEYWORDS
SOURCE
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (giffa732114 gbl.RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-GGld (Stratagene) cells and selected for ampicillin resistance."
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1M0404C09R Mouse 10kb plasmid UUGCIM library Mus musculus genomic close UUGCIM0404C09 R, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                           /sex="Male"
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0404 row: C column: 09
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organism="Mus musculus"
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/lab host="E. Coli strain Xil0-Gold, Tl-resistant, F-"
/lab host="E. Coli strain Xil0-Gold, Tl-resistant, F-"
/clone lib="Woouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42iv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was blydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerses and T4
polymuclectide kinase. Adaptor olignnuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gfrom a derivative
of pWDAQ (gil 4/732114 gb) AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xil0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (bases 1 to 19)

2 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Waiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

Contact: Robert B. Weiss
University of Utah
Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1M0474705F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474J05 F, genomic survey sequence.
AZ627844
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THI: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: 0474 row: J column: 05
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High quality sequence stop: 19.
      Location/Qualifiers
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Mus musculus
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Plate: 0474 row: J c
                                                                                                                                                                                                                    /sex="Male"
                                     source
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KEYWORDS
      FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalpd (gql/4732114[gbl/A7129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-GG1d (Stratagene) cells and selected for ampicillin resistance."
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1M0445P16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0445P16 R, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                    /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Kose, R., Stokes, R.,

Niederhausern, A. and Wright, D., Weiss, R.,

Nouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah
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Insert Length: 10000 Std Brror: 0.00
Plate: 0445 row: P column: 16
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Class: plasmid ends
High quality sequence stop: 19.
                                                              'organism="Mus musculus"
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Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                                              /sex="Male"
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Tel: 801 585 5606
Fax: 801 585 7177
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murcidea; Muridae; Murinae; Mus.
1 (bases 1 to 19)
1 (bases 1
                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_llb="Mouse 10kb plasmid UUGCNM library"
/note="Voctor: PWDAny, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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100.0%; Pred. No. 1.2e+03;
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Class: plasmid ends
High quality sequence stop: 19.
                                                                              organism="Mus musculus"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                             /db xref="taxon:10090"
                                                                                                                                                                                                                                /clone="UUGC1M0486E01"
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Insert Length: 10000 Std Erro
Plate: 0489 row: H column: 15
Location/Qualifiers
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Fax: 801 585 7177
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84112, USA
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                                                                                                                                                                                                                                                            / Jean-Book Coll strain XL10-Gold, T1-resistant, F-"
/ Lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/ Clone libe-"Wouse 10kb plasmid UUGCIM library"
/ Clone libe-"Wouse 10kb plasmid UUGCIM library"
/ Note="Vector: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gql 4712114 gbl AF129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed inco
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Tel: 801 585 5606
Fax: 801 585 7177
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Diasmid inserts
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0486 row: E column: 01
Seg primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
                                                                                  'organism="Mus musculus"
                                                                                                                          mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0474J05"
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Plate: 0508 row: E column: 17
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends ends they quality sequence stop: 19.
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1M0507D18F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0507D18 F, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Niederhausern, A. and Wright, D., Weiss, R.
Unpublished (2000)

Contact: Robert B.
University of Utah Genome Center
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.7%; Score 19; DB 1; Length 19; 00.0%; Pred. No. 1.2e+03;
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Insert Length: 10000 Std Error: 0.00
Plate: 0507 row: D column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 1.2.
Marches 19; Conservative 0; Mismatches
                                                  'organism="Mus musculus"
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Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                             'mol_type="genomic DNA"
'strain="C57BL/6J"
                                                                                                                          db_xref="taxon:10090"
clone="UUGC1M0489H15"
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Location/Qualifiers
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                                                                                                                                                                               /sex="Male"
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Fax: 801 585 7177
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AZ643659
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/dex="Male" Coli strain XLID-Gold, Tl-resistant, F-"
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/clone_lib="Mouse lokb plasmid UUGCIM library"
/note="Vector: PWD4Znv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orfifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMp42 (gil 47321141gb] AF129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLLO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Siturognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 19)

Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Meiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
/mol_type="genomic_DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0507D18"
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Mus musculus
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19; Conservative
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Fax: 801 585 7177
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                                                                                                                                                                                                      /lab host="E. Coli strain Xi10-Gold, T1-resistant, F-"
/lab host="E. Coli strain Xi10-Gold, T1-resistant, F-"
/clone lib="Mouse lokb plasmid UUGCIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated for sheared DNA
was blunt end-repaired with T4 DNA polymerses and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWDAD2 (gil 4772114) gpl AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xii0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1MO517116F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse, whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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100.0%; Pred. No. 1.2e+03;
ive 0; Mismatches 0; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0517 row: L column: 16
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
                                                     'organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                                 'mol_type="genomic DNA"
'strain="C57BL/6J"
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Mus musculus
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Best Local Similarity
Matches 19; Conserv
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of publy (gilfallalghAll29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll Xil0-Gold (stratagene) cells and selected for ampicillin resistance."
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                   /clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                  /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0519 row: E column: 15
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Class: plasmid ends
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Location/Qualifiers
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                                                                                                                                                                                                                                                /sex="Male"
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High quality sequence stop: 19.
          Location/Qualifiers
                                                                                                                                                                                          /sex="Male"
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                                     source
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                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalot (gilfyla) [A132114 [B] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0560H03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560H03 R, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G79BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: H column: 03
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0.7%; Score 19; UB
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 19; Conservative 0; Mismatches
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                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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cocation/Qualifiers
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                                                                                                                                                                                  sex="Male"
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Tel: 801 585 5606
Fax: 801 585 7177
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Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus

Eukaryorat, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Butheria; Buarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Mus.

I (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                  /lab.host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab.host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/note="Vector: PWD42ry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4732114) gb |AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1M0560E16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560E16 R, genomic survey sequence.
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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High quality sequence stop: 19.
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Woetor: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
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chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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E 1 (bases 1 to 19)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ralla, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R. Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R. Unpublished (2000)
L Onbarts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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1M0560P14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Plate: 0560 row: P column: 14
Seg primer: CACACAGGAAACAGCTAATGACC
                                          organism="Mus musculus"
                                                                                       mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                       _xref="taxon:10090"
                                                                                                                                                                   clone="UUGC1M0560E16"
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High quality sequence stop: 19.
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Fax: 801 585 7177
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(http://www.nduer.DNA.nesources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of puble (4732114 [gb]AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 19)

S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Unpublished (2000)

L Unpublished (2000)

L Contact: Robert B. Weiss
University of Utah Genome Center University of Utah
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                                                                                                                                                                                                                                                 /lab host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCLM library" /note="Vector: PUP22nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jacksor Laboratory Mouse DNA Resource
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Insert Length: 10000 Std Erro
location/Qualifiers
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AZ770387.1 GI:12891520
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Fax: 801 585 7177
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWaD42 (gil 4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0014020F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0014020 F, genomic survey sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Musinae, Mus.
                                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus G73BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhäusern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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100.0%; Pred. No. 1.2e+03;
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Insert Length: 10000 Std Error: 0.00
Plate: 0014 row: O column: 20
Seg primer: CGTTCTAAAACGACGCCCAGT
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organism="Mus musculus"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                       /mol_type="genomic DNA"
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                                                                                                                       /db_xref="taxon:10090"
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Location/Qualifiers
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                                                                                                                                                                          /sex="Male"
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwDA2 (gilfa713114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent B. coli XL10.601d (Stratagene) cells and selected for ampicillin resistance."
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Sciurognathi; Muroidea; Muridae; Mus.

1 (bases 1 to 19)

Na Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rodilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Dlasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
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                                                                                                                                                                                    /sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: E column: 16
Seq primer: CACAGGAAACAGGTATGACC
Class: plasmid ends
High quality sequence stop: 19.
organism≈"Mus musculus"
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High quality sequence stop: 19.
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84112, US
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FEATURES
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                                                                                                                                                                                               /Bab.male...
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was blut-ida.corg/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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2M0021003R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0021003 R, genomic survey sequence.
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1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rally, M., Rose, M., Rose, M., Meenen, E., Pedersen, T., Niederhausern, A. and Wright, D., Waise, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0021 row: O column: 03
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                  .. .19
'organism="Mus musculus"
                                                                              mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                 xref="taxon:10090"
                                                                                                                                                         'clone="UUGC2M0016E16"
location/Qualifiers
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Mus musculus
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Best Local Similarity 100.(
Matches 19; Conservative
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pMAP2 (gil 4)91AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. ool KL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0034M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0034M12 F, genomic survey sequence.
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Plannid inserts
                                                                                                                                                                                                                                                                                                                                                         from the Jackson
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                                                                                                                                                                                                                           /sex="Male"
/lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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100.0%; Pred. No. 1.2e+03;
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Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: M column: 12
Seq primer: cGTTGTAAAACGACGCCAGT
Class: plasmid ends
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                                                               'organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                            _xref="taxon:10090"
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location/Qualifiers
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Fax: 801 585 7177
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares/). The
Nash journal.cally sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated excess and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
adaptored using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4732114 gb) [AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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2M0037G06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC2M0037G06 R, genomic survey sequence.
AZ789590
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University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rally, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von plasmid inserts

Unpublished (2000)
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Fax: 801 585 7177
Email: ddunmagenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 row: G column: 06
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Sage primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
                                                                            organism="Mus musculus"
                                                                                                        /mol_type="genomic DNA"
/strain="C578L/6J"
                                                                                                                                                                     /db_xref="taxon:10090"
/clone="UUGC2M0034124"
                   Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                                                                    /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWaPA2 (gil-f4732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0034I24R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Insert Length: 10000 Std Exror: 0.00
Plate: 0034 row: I column: 24
Seg primer: CACACAGGAAACAGCTATGACC
                                                                     'organism="Mus musculus"
                                                                                                     mol_type="genomic DNA"
strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                  db xref="taxon:10090"
                                                                                                                                                                                           clone="UUGC2M0034M12"
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         location/Qualifiers
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                                                                                                                                                                                                                           sex="Male"
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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High quality sequence stop: 19.
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Fax: 801 585 7177
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AUTHORS
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                                                                                                                                                                               / Jab hose="B. Coli strain Xil0-Gold, Tl-resistant, F."
/ Jab hose="B. Coli strain Xil0-Gold, Tl-resistant, F."
/ Clone lib="Mouse lukb plasmid UUGCIM library"
/ Note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orfifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
processing the process of the context was and process of the context was and process of the context was not and process of the context was ligated
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University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: C column: 22
Seg primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
                                                       organism="Mus musculus"
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'strain="C57BL/6J"
                                                                                                                                _xref="taxon:10090"
                                                                                                                                                           'clone="UUGC2M0037G06"
ocation/Qualifiers
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwnot (gql 4732114|gbl AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed inco chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0049C12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0049C12 R, genomic survey sequence.
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse lokb plasmid UNGCNM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                          Laboratory Mouse DNA Resource
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                               /db xref="taxon:10090"
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Insert Length: 10000 Std Erro
Plate: 0049 row: C column: 12
                                                                                                                                                                                             /clone="UUGC2M0045C22"
Location/Qualifiers
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nr; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose get a 9.5 to
10.5 kb range using preparative agarose gfrom a derivative
of pWD42 (gi | 4732114 | gb | AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Murinae; Mus.

1 (Dasas 1 to 19)

2 (Dasas 1 to 19)

2 (Dasas 1 to 19)

3 (Dasas 1 to 19)

4 (Dasas 1 to 19)

5 (Dasas 1 to 19)

6 (Dasas 1 to 19)

6 (Dasas 1 to 19)

6 (Dasas 1 to 19)

7 (Dasas 1 to 19)

8 (Dasas 10
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2M0095E17F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0095E17 F, genomic survey sequence.
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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geg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
                                                                                                               /mol_type="genomic DNA"
/strain="C578L/6J"
/db xref="taxon:10090"
                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC2M0060112"
           Location/Qualifiers
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Plate: 0095 row: E
                                                                                                                                                                                                                                                                               /sex="Male"
                                                   source
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           FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gil 47121141gb]AR12977.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
                                                                           'organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                                                                   mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="UUGC2M0049C12"
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   Location/Qualifiers
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                                                                                                                                                                                                                                                                       'sex="Male"
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Fax: 801 585 7177
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AZ801970/c
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DEFINITION
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Plate: 0139 row: A column: 16
Seg primer: CACAGAGAAACAGCTATCACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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Fax: 801 585 7177
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Matches 19; Conserv
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E Sciuropnathi; Muroidea; Muridae; Musinae; Mus.

E 1 (bases 1 to 19)

S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacres, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

D Inpublished (2000)

L Onbact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                        /lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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was hydrodynamically sheared by repeated for second polynucleotide kinase. Adaptor oligonucleotides were
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adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
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inducible derivative of plasmid R1. The vector was ligated
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and selected for ampicillin resistance."
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100.0%; Pred. No. 1.2e+03;
ive 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: G column: 08
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
                                                            'organism="Mus musculus"
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Best Local Similarity 100.
Matches 19; Conservative
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Fax: 801 585 7177
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84112, USA
                                   source
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp (19172114 [gb] AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (stratagene) cells and selected for ampicillin resistance."
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2M0139A16R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0139A16 R, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Muright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Wouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                      from the Jackson
                                                                                                                                                                             /sex="Male"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jacksor
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100.0%; Pred. No. 1.2e+03;
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Insert Length: 10000 Std Error: 0.00
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'organism="Mus musculus"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                       /db_xref="taxon:10090"
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       Location/Qualifiers
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Plate: 0193 row: L c
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                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gqi 4732114 [gb] AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0168P10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0168P10 R, genomic survey sequence.
AZ861896
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1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von. Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von. Dunce whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                 /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note=""Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0168 row: P column: 10
Seg primer: CACACAGGAAACAGCTATGACC
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                                                  organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                          mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                         /db_xref="taxon:10090"
/clone="UUGC2M0139A16"
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Location/Qualifiers
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Mus musculus
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                                                                                                                                                                              /sex="Male"
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Fax: 801 585 7177
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Best Local Similarity
Matches 19; Conserv
                             source
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AZ861896
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FEATURES
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
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ligated to the blunt ends in high molar excess. The
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of pWD42 (gi|4732114|gb|AR129072.1), a copy-number
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adaptored vector DNA, and transformed into
chemically-competent B. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidaa; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R.,
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
/lab host="B. Coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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(Dipublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Blommedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0;
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TE1: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAPA2 (gilfa732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0288121F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0288121 F, genomic survey sequence.
                                                                                                                                                                                                                                /lab_hogt="E. coli strain XL10-Gold, Tl-resistant, F-" clone lib-"Mouse lbkb plasmid UNGC2M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0288 row: I column: 21
                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
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Seg primer: CGTTGAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                       /mol_type="genomic DNA"
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                                                                                                                                                 db xref="taxon:10090"
                                                                                                                                                                            /clone="UUGC2M0267E21"
Location/Qualifiers
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Fax: 801 585 7177
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bulmanalia; Eutheria; Euarchoncoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
Sciurognathi; Muroidea; Muridae; Musinae; Mus.
I (basea 1 to 19)
S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
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2M0267E21F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0267E21 F, genomic survey sequence.
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/clome_lib="Mouse lokb plasmid UNGC2M library.
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
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tive 0; Mismatches 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0267 row: E column: 21
Seg primer: CGTGTAAAACGACGCCAGT
Class: plaamid ends
High quality sequence stop: 19.
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                                                                  organism="Mus musculus"
                                                                                             mol_type="genomic DNA"
'etrain="C57BL/6J"
                                                                                                                                                 db_xref="taxon:10090"
clone="UUGC2M0193L10"
         location/Qualifiers
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AZ985501.1 GI:13856728
                                                                                                                                                                                                                 /sex="Female
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Fax: 801 585 7177
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Length 19; 0; Indels 5

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Gaps

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GSS 09-JUL-2004

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PRIO160C_BOS_2 - PRIO160C.BR (19) Note: Recurring String Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
CL693186.1 GI:S0215094
                                                                                                                                                                                                                                                                                                                                                                                                           CL685439 19 bp DNA linear GSS 09-JUL-2004
PRI0141b_A04_2 - PRI0141b.BR (19) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
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var. California"
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Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppabB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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var. California"
/note="Vector: pEpifos-5 Fosmid vector"
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Fal: 0049707160139,
Fax: 00497071601498
Email: ralls. Sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
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Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridas; Pristionchus.
                                                                                                                                               0.7%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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                                                                                                /note="Vector: pEpifos-5 Fosmid vector"
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/mol_type="genomic DNA"
/strain="California"
       /strain="California"
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Class: fosmid ends.
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                                                                                                                                                                                    /lab host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCZM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/60 (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Srinivasan, I., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
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This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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ve 0; Mismatches 0; Indels
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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  Location/Qualifiers
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Class: fosmid ends.
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                                                                                                                                                                     /sex="Female"
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA" |
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/clone lib="Mixed stage fosmid library of P. pacificus var. California" |
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Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristinchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 19)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppabB: an AcedB database for the nematode satellite organism
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Max-Planck-Institute for Developmental Biology
Spemannstr. 379. Tuebingen D-72076, Germany
Tel: 00497071601391
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
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Email: salf.sommerated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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Max-Planck-Institute for Developmental Biology
Spemannetr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371

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/organism="Pristionchus pacificus"

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Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447

    19
/organism="Pristionchus pacificus"

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Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
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CL693191.1 GI:50215099
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20 bp mRNA linear EST 06-JUL-2004
DKRZp566F0346 rl 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKR2p566F0346, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 20)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                   P. pacificus
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1 (bases 1 to 20)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
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                                            /db_xref="taxon:54126"
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var. California"
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1 Similarity 100.0%; Pred. No. 1.2e+03;
19; Conservative 0; Mismatches 0;
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EST (Ottenwaelder, et al.)
Unpublished (1999)
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AL038576.1 GI:49682161
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Matches 19; Conservative
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DKFZp566P1746, mRNA sequence.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 20)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
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Location/Qualifiers
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Location/Qualifiers
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EST (Ottenwaelder, et al.)
Unpublished (1999)
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               EST (Ottenwaelder, et al.)
Unpublished (1999)
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Homo sapiens
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Matches 19; Conservative
                                             Contact: MIPS
MIPS
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 Wiemann,S.
                                                                                                                                                                                                                                                                                             Query Match
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AL038754
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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ALS87759 BP Chicken Brain Library Gallus gallus cDNA clone ROS061G06, mRNA sequence.
ALS87759.1 GI:13192793
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                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                             1. .20
| organism="Homo sapiens"
| organism="HOmo sapiens"
| morganism="HOmo sapiens"
| db xref="taxon:966"
| clone="DKFZp566P1746"
| clone="DKFZp56F1746"
| dev stage="fetal"
| lab_host="x1.2blue"
| clone lib="566 (synonym: hfkd2)"
| note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
                                                                                                 Hominidae; Homo.
1 (bases 1 to 20)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
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0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .20
/organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db xref="taxon:9031"
/clone="ROSG1606"
/tissue type="Brain"
/dev_stage="Unknown"
                                                                                                                                                      Wiemann, S.
EST (Ottenwaelder, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
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AL038845.1 GI:49682220
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                                    Homo sapiens (human)
Homo sapiens
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Page 610

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Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorthyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 20)
Hunter, W., Martines-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
Stern, D., Tagu, D. and Wincker, P.
An expressed sequence tags database for the pea aphid Acyrthosiphon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DN955202 20 bp mRNA linear EST 04-MAY-2005 it83f09.gl Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="Apps"
/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
Sample name: IDOAAA; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University;
Soil conditions: Soil; Sowing date: 01/06/1999;
Harvesting date: 01/06/1999; Stress date: no stress;
Description: Applids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"
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Brenner, E. D., Twigg, R. W., Runko, S. J., Katari, M. S., Dedhia, N. N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="whole insect"
/dev stage="mymphs and adults (parthenogenetic females)"
/lab_host="XLI-Blue"
  IDOAAA12AG12RM1 ApMS Acyrthosiphon pisum cDNA clone IDOAAA12AG12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.7%; Score 19; DB 1; Length 20; 35.0%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMR Bi03P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/cultivar="developmentstage"
/db_xref="taxon:7029"
/clone="ID0AAA12AG12"
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FORWARD: CAGGAAACAGCTATGACC
Plate: 12 row: G column: 12.
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                                                                               CN754148.1 GI:47519145
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                     5', mRNA sequence.
CN754148
                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2004)
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INRA Rennes
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DN955202
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fissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/dav_stage="proliferated"
/lab_nost="E.coli DH10B"
/clone_lib="OsHBAC1-overexpressing transgenic rice plasmid cDNA lbrary (HD)"
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF318278

HD--08-F13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--08-F13, mRNA sequence.
CF318278

CF318278.1 GI:33690039
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kin, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR: mRNA was derived from rice Histone Deacetylase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                             Query Match 0.7%; Score 19; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 19; Conservative 0; Mismatches 0; Indels
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    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:39947"
/clone="HD--08-F13"
                                                                                                                                                               Clonetech (*6854-1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
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Best Local Similarity
Matches 19; Conserv:
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JOURNAL COMMENT

TITLE

FEATURES

REFERENCE AUTHORS

EST

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

RESULT 1543

ઠે 원 CF318278/c DEFINITION ö

Gaps

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AUTHORS

EST 19-MAY-2004

linear

mRNA

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20

RESULT 1544 CN754148 LOCUS

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/clone_lib="Gnetum female cone (NYBG)"
/note="Organ: mature, unfertilized reproductive strobili;
/ector: pBK-CMV; Site_l: XhoI; Site_2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express CDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"
O'Shaughnessy, A. L., Balija, V., Martienssen, R. A., McCombie, R. W., Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
L. Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Hazen Genome Sequencing Center
Cold Spring Hazen Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8884
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.
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1M0073G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0073G03 R, genomic survey sequence.
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1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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100.0%; Pred. No. 1.2e+03;
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Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: G column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plaemid ends
High quality sequence stop: 20.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                          /organism="Gnetum gnemon"
/organism="Gnetum gnemon"
/mol_type="mcNA"
/db_xref="taxon:3382"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2709 AAAAAAAAAAAAAAAA 2727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
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Fax: 801 585 7177
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Matches 19; Conserv
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84112, US
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AUTHORS
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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was blydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated for sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gfrom a derivative
of pMD42 (gil 4732114 gb) AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli X110-Gold (Stratagene) cells
and selected for ampicillin resistance."
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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Pred. No. 1.2e+03;
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/db_xref="taxon:10090"
/clone="UUGC1M0073G03"
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Location/Qualifiers
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Mus musculus
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Fax: 801 585 7177
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/mol_type="genomic DNA"

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                                                                                                                                                                         Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM92 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah Genome Center
University of Utah
TRM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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1 (basel t.c. 20)

1 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarcte, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
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                                                                        /lab host="E. Coli strain XLIO-Gold, TI-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0498 cow: E column: 13
Seq primer: CACAGGGAAACAGCTATGACC
Class: plasmid ends
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100.0%; Pred. No. ...
0; Mismatches
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/mol_type="genomic DNA"
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/clone="UUGC1M0363F11"
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Location/Qualifiers
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Best Local Similarity 100.
Matches 19; Conservative
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Laboratory Mouse DNA Resources (ductor). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gilfa732114 [gb] [AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Sciurognathi; Murcidea; Muridae; Murinae; Mus.

I (basea I to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Really, M., Rose, M., Neight, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                              /lab host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UVGCLM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus G57BL/6J (male) was obtained from the Jacksor Laboratory Mouse DNA Resource
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Pred. No. 1.2e+03;
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Fax: 801 585 7177
Eax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: P column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.2
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Contact: Robert B. Weiss
Contact: Quah Genome Center
University of Utah
/db_xref="taxon:10090"
/clone="UUGC1M0498E13"
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GSS.
                                                                            /sex="Male"
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/organism="Mus musculus" /mol_type="genomic DNA"

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AZ309907
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ORGANISM
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AZ309907/c
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                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pubMed (gql 4732114[gb]AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL587702
AL587702 BP Chicken Brain Library Gallus gallus cDNA clone
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bmail: frazer.murray@bbsrc.ac.uk
GCGGCCGCTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
                                                        /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse lokb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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1.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.7%; Score 19; DB
100.0%; Pred. No. 1.2
ative 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
/db_xref="taxon:10090"
/clone="UUGC2M0150P21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="ROS060H09"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roslin, Midlothian, EH25 9PS,
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seg primer: M13F.
Location/Qualifiers
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ALS87702.1 GI:13192736
EST
Gallus gallus (chicken)
Gallus gallus
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KEYWORDS
SOURCE
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AUTHORS
TITLE
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COMMENT
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22 bp mRNA linear EST 06-JUL-2004 DKFZp566B0646 rl 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566B0646, mRNA sequence.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Sciurognathi; Muroidea; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longaore, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
unidirectionally. Primer: Oligo dr. 5' adaptor sequence: 5' TCGAGA. 3'; 3' adaptor sequence: 5' GCGGCCGTTTTTTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from clonetech (6854-1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thominidae; Homo.
1 (bases 1 to 22)
Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
                                                                                                                                                                  Gaps
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/mol_type="mRNA"
/mol_txye="mRNA"
/db_xref="taxon:9606"
/tissue_type="kidney"
/fdv_crage="fetal"
/ldb_host="X1-2blue"
/ldb_host="X1-2blue"
/clone_lib="566 (Synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: Sall"
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Location/Qualifiers
                                                                                                            Length 22;
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Pred. No. 1.3e+03;
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100.0%; Pred. No. ...
                                                                                                                                                                                                        2709 AAAAAAAAAAAAAAAAAA 2728
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EST (Ottenwaelder, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
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Best Local Similarity luv...
Local 19; Conservative
                                                                                                          Query Match
Best Local Similarity
Matches 19; Conserval
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DX032218
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       COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BI/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli Xi10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                        S. 2030 E., SLC,
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Balija,V.S., Nascimento,L.U. and McCombie,W.R.
ESTS from Canis familiaris left cardiac ventricle (dog)
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19; DB 1; Length 22;
Pred. No. 1.3e+03;
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                                                                                                                                                                Rm. 308, Blomedical Polymers Research Bldg., 20 84112, USA
Tel: 801 585 5606
Fax: 801 57 177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
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                                                                                                                                                                                                                                                                                                    Plate: 0017 row: N column: 14
Seg primer: CGTTCTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="genomic DNA"
/strain="C578L/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0017N14"
                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 22.
Location/Qualifiers
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CX002873.1 GI:56274289
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Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'sex="Male"
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Best Local Similarity 100.
Matches 19; Conservative
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/tissue_type="Cardiac muscle"
/dev stage="3 month old normal canine"
/dev stage="X110 Gold"
/lab_host="X110 Gold"
/clone lib="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site 1:
EcoRI; Site_2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned coNA was size selected
between 1-3 kb. Tissue supplied by Mark Haskins VMD, Phb,
pathology and Medical Genetics, School of Veterinary
Medicine, University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"
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Brassica rapa subsp. pekinensis
Brassica, Viridiplaintes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  υλυ32218
KBrB029E14R KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB029E14, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yang, Yang, Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Yang, T.J., Kwon, S.J., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
Contact: Beom-Seok Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 23;
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National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
PER: 516 367 8884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 0.7%; Score 19; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                             organism="Canis familiaris"
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/db_xref="taxon:51351"
/clone="KBrB029514"
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/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
                                                                                                                                                                                    Email: mccombie@cshl.org.
Location/Qualifiers
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Class: BAC ends.
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4732114 [gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
/lab_host="E.coli DH10B"
/clome_llb="KBrB, Brassica rapa BamHI BAC library"
/clome_lbector: pCUGIBAC1; Site_l: BamHI; Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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1M0234B16R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0234B16 R, genomic survey sequence.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae, Mus

1 (bases 1 to 22)
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42Ivv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                             0.7%; Score 19; DB 1; Length 23;
100.0%; Pred. No. 1.3e+03;
ive 0; Mismatches 0; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0234 row: B column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends

    .22
    organism="Mus musculus"

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/strain="C57BL/6J"
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/clone="UUGC1M0234B16"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                         Conservative
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Fax: 801 585 7177
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Best Local Similarity
Matches 19; Conserv
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Rm. 308, Bio
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with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                 22 bp DNA linear GSS 09-AUG-2005
KBrH (HindIII) BAC library Brassica rapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAC end sequences of Brassica rapa BAC clone KBrH128J11; generated as contribution to the 'Multinational Brassica rapa Sequencing Project' Seq primer: sp6B ATTTAGGTGACACTATAG Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-AUG-2005) Weisshaar B., Bielefeld University, Institute for Genome Research, Universitaetsstrasse 25, D-33594 Bielefeld, Germany Contact: Bernd Weisshaar
                                                                                                                                                                                  Gaps
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/db_xref="taxon:51351"
/clone="xBH128011"
/clone=lib="KBH", Brassica rapa HindIII BAC library
GP-SCF-1002, Vector: pCUGIBac1"
/lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bielefeld University, Institute for Genome Research
Universitaetsstrasse 25, D-33594 Bielefeld, Germany Email:
bernd.weisshaar@uni-bielefeld.de
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                                                                                                                                   0.7%; Score 18.8; DB 1; Length 22; 90.9%; Pred. No. 1.3e+03;
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BAC end sequences of Brassica rapa
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                  KBrH128J11 genomic clone, KBrH (HindIII) BA
subsp. pekinensis, genomic survey sequence.
CT017313
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Pred. No. 1.3e+03;
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/strain="Chiifu type 401-42"
/cultivar="Chiifu"
                                                                                                                                                                               0; Mismatches
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Brassica rapa subsp. pekinensis
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Li,Y. and Weisshaar,B.
Direct Submission
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Gaps

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/tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone lib="OshDACI-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="vector: pCR4-TOPO; Site 1: EcoR1; Callus was treated with ABA(20um) for lhr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
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DKF2p566B2246 rl 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKF2p566B2246, mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
/organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nackdong"
/db xftexon:3997"
/clone="HD--01-G01"
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                                                                                                                                                                                                                                                                                                                                                                                 0.7%; Score 18.8; DB 1; Length 23; 90.9%; Pred. No. 1.3e+03; tive 0; Mismatches 2; Indels
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/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
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/clone="DKF2p566B2246"
/tissue_type="kidney"
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Location/Qualifiers
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Unpublished (1999)
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1 (bases 1 to 20)
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                                                                                              Oryza sativa (japonica cultivar-group)
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Straptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

E 1 (bases 1 to 23)
S Kim,J.S., Jun,K.M., K.M., Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Lupublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin; Kyenea
Tel: 82 31 330 6193
Fax: 82 31 321 635
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Brhartoideae; Oryzea.

E 1 (bases 1 to 23)
S Kim,J.S., Jun,K.M., K.M., K.M., Y.K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Blostience and Bloinformatics, MyongJi University
Yongin; Kyenea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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//mol_type="mRNA"
/cultivar="mRNA"
/cultivar="MacMong"
/db_xref="taxon:39947"
/clone="14ROOT--01-021"
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/clone="14ROOT--01-021"
/clone="14ROOT--01-021"
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/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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HD--01-G01.g1 OsHDAC1-overexpressing transgenic rice plasmid CDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--01-G01, mRNA sequence.
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/organism="Oryza sativa (japonica cultivar-group)"

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Location/Qualifiers
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E 1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTB
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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20 bp mRNA linear EST 15-AUG-2003
ABF--03-A01.gl ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--03-A01, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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/db_xref="taxon:1994"
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/tissue type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: ECORI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCR4-TOPO; Site 1: ECORI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone lib="ABF7-overexpressing transgenic rice plasmid cDNA lTbrary (ABF)"
                                          organism="Oryza sativa (japonica cultivar-group)"
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                                                                                                                                                                                                                                                                                                                                                         0.7%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 1.3e+03;
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0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels
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/cultivar="Nackdong"
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Oryza sativa (japonica cultivar-group)

Bukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

Extim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, Y.F., and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Lupublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: Not1; Site 2: Sal1; Cloned unidirectionally. Primer: Oligo dT. 5' adaptor sequence: 5' TCGACCTCGAG 3' 1' 3' adaptor sequence: 5' GCGGCCCCTTTTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech (*6854-1)"
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                                                                           Gallus gallus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                        Email: frazer.murray@bbsrc.ac.uk
GCGGCCGCTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF299570 20 bp mRNA linear EST 15-AUG-20 7LEAF--03-K09.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-K09, mRNA
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                                                                                                                                                                                                                    BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .20
/organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059B11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH108"
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          GI:13192606
                                                         Gallus gallus (chicken)
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CF299570.1 GI:33671331
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EST.
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CF299570/c
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Gaps

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

RESULT 1563 CF316662/c DEFINITION

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AZ375620 20 bp DNA linear GSS 02-OCT-2000 1M0129A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0129A08 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: :pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus subtactos, Chordata, Craniata, Vertebrata, Euteleostomi, Baukaryota, Metazoa, Chordata, Craniata, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Bactor, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Miederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2005)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mccombie@cshl.org

Original 3 prime EST has been reverse completed to be in 5 prime direction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.7%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 1.3e+03; tive 0; Mismatches 1; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0129 row: A column: 08
Seg primer: CGTTCTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
High quality sequence
                                                                                                                                                                                                                                                                                                                                 1. .20
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
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/clone="UUGC1M0129A08"
                                                                                                                                                                                                                                                                              Seg primer: -21M13UnivRev.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="female"
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84112, US
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                                                                                                                         20 bp mRNA linear EST 15-AUG-2003
HD--06-A20.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--06-A20, mRNA sequence.
CP316662
CP316662.1 GI:33688423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:39947"
| db_xref="taxon:39947"
| Colone="HD--06-A20"
| tissue_type="callus" |
| dev_stage="proliferated callus on 2N6 media for 2 weeks"
| day_stage="proliferated callus on 2N6 media for 2 weeks"
| day_stage="coll DH10B"
| clone_lib="OsHAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
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                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sprantophyta; Ginkgoales; Ginkgoaceae; Ginkgo. 1 (Dases 1 to 20)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N., O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W., Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Pax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCR4-TOPO, Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
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/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
Location/Quallfiers
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Ginkgo biloba
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Matches 19; Conservative
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RESULT 1564 DR073483

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                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100315D23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0315D23 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
/lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: 0315 row: D column: 23
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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/clone="UUGC1M0315D23"
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Insert Length: 10000 Std Erro
Plate: 0315 row: D column: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
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84112, USA
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gb]AP129072.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 20)

RS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Reilly,M., Rose,M., Rose,R., Strokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
Wen. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
/lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/close_lib="Mouse_10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;

Sciurconathi; Muroidea; Muridae; Musinae; Mus.

1 (bases 1 to 20)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von

Niederhauserr,A. and Wright,D.,Weiss,R., Tingey,A., von

L Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah Genome Center

University of Utah Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymcleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwafe? (gil 47321141gbl AF129072.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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/lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Wetcor: PWD42nv; Purified genomic DNA from M.
musculus G78L/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: K column: 11
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/clone="UUGC1M0510K11"
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Fax: 801 585 7177
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84112, USA
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Laboracry Mouse DNA Resources (ductp://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gil-#172114|gb].RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0094D20R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0094D20 R, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGCIM library" /note="Wector: PWB42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Unpublished (2000)

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                           Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
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geg primer: CACAGAAAACAGCTATGACC
Class: plasmid ends
High quality sequence grop: 20.
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/strain="C57BL/6J"
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/clone="UUGC2M0094D20"
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Fax: 801 585 7177
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Matches 19; Conserv
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TITLE
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                                                                                                                      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 47121141gb] AF125072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XIIO-GGold (Stratagene) cells and selected for ampicillin resistance."
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2M0213D24R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0213D24 R, genomic survey sequence.
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1 (bases 1 to 20)
/lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone_lib="Mouse_10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0213 row: D column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plaamid ends
High quality sequence stop: 20.

    .20
    /organism="Mus musculus"

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University of Utah Genome Center
Wniversity of Utah
Rm. 308, Biomedical Polymers Rese
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/strain="C57BL/6J"
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Best Local Similarity 95.0
Matches 19; Conservative
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Fax: 801 585 7177
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/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse l0kb plasmid UUGC2M library"
/note="Vector: PWD42nr; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resources
(http://www.jax.org/resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4732114 gb) | AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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PRI0128C_G05_2 - PRI0128C.BR (20) Note: Recurring String Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
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Pristionchus pacificus
Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J. AppabB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannetr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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/mol_type="genomic DNA"
/strāin="California"
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Class: fosmid ends.
Location/Qualifiers
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Best Local Similarity 95.0%;
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Seq primer: T7
Class: BAC ends.
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/lab_host="E.coli DH10B"
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/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DX071075 CSS 10-JAN-2006 KBFB080L07F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBFB080L07, genomic survey
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Brassica; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 20)
Trang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
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/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cullivar="Chiffu"
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/db_xref="taxon:51351"
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llarity 95.0%; Pred. No. 1.3e+03;
Conservative 0; Mismatches 1; Indels
                  Indels
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Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
95.0%; Pred. No. 1.3e+03;
ive 0; Mismatches 1;
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Brassica rapa subsp. pekinensis
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                                                         2709 AAAAAAAAAAAAAAAAA 2728
                                                                                  20 AAAAAAAAAAGAAAAAA 1
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DX071064.1 GI:84765360
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DX071075.1 GI:84765371
Best Local Similarity 95.0
Matches 19; Conservative
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Class: BAC ends.
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hes 19; Conserv
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Best Local Si
Matches 199
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VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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/ jub apecies="pekinensis"

/db Xref="taxon:51351"

/dclone="kxBraB080L07"

/lab host="E.coli DH10B"

/clone=lib="KBrB, Brassica rapa BamHI BAC library"

/note="Yector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiffu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX558161 Blossina morsitans morsitans adult infected gut Glossina morsitans con Tse37a05_plc, mRNA sequence.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids; eurosids II; Brassicales; Brassicaceae, Brassica.
I (bases 1 to 20)
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M., Park, D.S., Hahn, J.H., and Park, B.S.
                                                                                                                                                                                                                 End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
Contact: Beom-Seck Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Fig. +82-31-299-1670
Fax: +82-31-299-1670
Email: pbeom@rda.go.kr
Email: pbeom@rda.go.kr
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.

1 (bases 1 to 21)
Lehane, M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the teetse fly Glossina morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof: M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
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Genome Biol. 4 (10), R63 (2003)
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Best Local Similarity
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DU829016/c
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KEYWORDS
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
                                                                                                                                                                                                                                               /note="country: Zimbabwe; EST from adult gut infected with
T.brucei"
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21 bp mRNA linear EST 15-AUG-2003

HD--10-D06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--10-D06, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhatroideae; Oryza.

1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.L., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
      'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, MyongJi University
Yogin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Eax: 82 31 221 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                1. .21
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/mol_species="morsitans"
/db xref="taxon:37546"
/clone="Tse37a05_plc"
/tissue type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
        at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was rreated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
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        starting
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/mol_type="mRNA"
/cultivar="Nackdong"
/db xf taxon:39947"
/clone="HD-10-D06"
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All clones with suffix qlc are reverse primer reads end of the cDNA all plc reads are from the 3' end.
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                                                             Location/Qualifiers
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CF319625.1 GI:33691386
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Best Local Similarity
Matches 19; Conserv
                                                                                    Source
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21 bp mRNA linear EST 18-AUG-2003 JMT--02-E09.bl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--02-E09, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/lab_host="B.coli DH10B"
/clone_lib="ALMT-overexpressing transgenic rice plasmid
cDNA_lib=ary (JMT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DU829016 21-DEC-20 KBFS004D04F KBFS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBFS004D04, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 21)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/mol_type="mRNA"
/mol_type="mRNA"
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/clone="JMT--02-E09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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95.0%; Pred. No. 1.3e+03;
tive 0; Mismatches 1;
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2707 CTAAAAAAAAAAAAAAA 2726
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DU829016.1 GI:83865612
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                                                      CTATAAAAAAAAAAAAAA
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AL038692
LOCUS
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Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J. H. and Park, B.S.

End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1670
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS004D04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL048750 22 bp mRNA linear EST 04-SEP-2003 DERZp55651123 r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp5661123, mRNA sequence.
AL048750 GI:4727821
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                                                                                                                                                                                                                                                                                                                                                                                                    /gub_species="pekinensis"
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/note="Vector: pUGUSBACI; Site_1: Sau3AI, Brassica rapa ssp pekinensis var. Chiifu BAC_library (KBrS BAC) is available at NIAB."
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 22)

Kochrer, K. Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Kochrer, et al.)

Unpublished (1999)
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/lab host="X1-2blus"
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                                                                                                                                                                                                                                                                                                                                           /organism="Brassica rapa subsp. pekinensis"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Homo sapiens
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                                                                                                                                                              стотивную Z3 bp DNA linear GSS 09-AUG-200!
KBrH130A15 genomic clone, KBrH (HindIII) BAC library Brassica rapa
subsp. pekinensis, genomic survey sequence.
CT019890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Belefeld University, Institute for Genome Research Universitaetestrasse 25, D-33594 Bielefeld, Germany Email: Universitaetestrasse 25, D-33594 Bielefeld, Germany Email: bernd.weisshaar@uni-bielefeld.de
BAC end sequences of Brassica rapa BAC clone KBrH130A15; generated as contribution to the 'Multinational Brassica rapa Sequencing Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                        Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
1 (Dases 1 to 18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (09-AUG-2005) Weisshaar B., Bielefeld University,
Institute for Genome Research, Universitaetsstrasse 25, D-33594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.7%; Score 18.4; DB 1;
95.0%; Pred. No. 1.4e+03;
[ve 0; Mismatches 1;
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Contact: Bernd Weisshaar
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/note="Vector: pCMVSPORT6; Site_1: Sall; Site_2: NotI;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
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Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                /dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMPl; Site_1: NotI; Site_2: SalI"
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 18 Std Error: 0.00
Plate: 7 row: P column: 18
Seq primer: SP6; CATACGATTTAGGTGACCTATAG.
Location/Qualifiers
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100.0%; Pred. No. 1.3e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                       /organism="Homo sapiens"
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/organism="Beta vulgaris"
                                   EST (Ottenwaelder, et al.)
Unpublished (1999)
Contact: MIPS
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Beta vulgaris
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18 bp mRNA linear EST 06-DEC-2002 E012844-024-019-E24-T7 MPIZ-ADIS-024-storage root Beta vulgaris E0590027
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1 (bases 1 to 18)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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/note="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
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                        orientation:
Sep6-sall-CCACGCGCTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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/cultivar="KWS2320 (double haploid, monogerm breeding
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                          0.7%; Score 18; DB 1; Le
100.0%; Pred. No. 1.3e+03;
tive 0; Mismatches 0;
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Insert Length: 18 Std Error: 0.00
Plate: 19 row: E column: 24
Seq primer: 77; GTAATACGACTCACTATAGGGC.
Location/Qualifiers
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Best Local Similarity
Matches 18; Conserv
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RESULT 1583

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LOCUS CF277873/c

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ORGANISM

REFERENCE AUTHORS JOURNAL

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FEATURES

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E 1 (bases 1 to 18)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTS

Londact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 321 6155
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                               / ...gem.sum= ..uyza gativa (japonica cultivar-group)"
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/cultivar="Nackdong"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped /no
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7LEAF--02-N14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-N14, mRNA
Song, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 313 6193
Fax: 82 31 321 6155
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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/clone lib="Rice leaf plasmid cDNA library II (7LBAF)"

/note="Vector: pCR4-TOPD; Site 1: ECORI; mRNA was capped with oligoribonucleotides and Then used as templates for
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/cultivar="Nackdong"
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Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0;
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S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Tel: 82 31 321 6135
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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30DGS--08-F02.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--08-F02, mRNA
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Cyza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

Clade; Enthartoideae; Oryzeae; Oryza.

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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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// Organism="Oryza sativa (japonica cultivar-group)"
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// Dax xxef="Laxon:39947"
// Clone="14ETL-03-J04"
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/cultivar="Nackdong"

/db xref="taxon: 3947"

/clone="77EAF-03-M14"

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/dev stage="7 days after germination"

/dab host="E.col DH10B"

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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatrophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongln, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Matches 18; Conservative 0; Mismatches 0;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Enthartoideae; Oryzeae; Oryzea.

1 (bases 1 to 18)

1 (bases 1 to 18)

1 (kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

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YongIn, Kyeonggi, Korea
Tel: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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7LEAF--06-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--06-C12, mRNA
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Min,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
TyongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/mol type="mRNA"
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/clone="71EAF-06-C12"
/tissue_type="leaf"
/dev_stage="7 days after germination"
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Location/Qualifiers
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100.0%; Pred. No. 1.3e+03;
tive 0; Mismatches 0;
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CF301325.1 GI:33673086
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LOCUS DEFINITION RESULT 1589 CF301760/c

ઠે 셤 ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo. Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo. Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo. Spermatophyta; Ginkgoales; Ginkgoaceae; Ginkgo. Spanghnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D. Expressed tag sequences from Ginkgo female leaf (NYBG) Unpublished (2005)
Lita Annenberg Hazen Genome Sequencing Center Contact: W. Richard McCombie Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8844
Fax: 516 367 8844
Fax: 516 367 8844
                         Oryza sativa (japonica cultivar-group)

ISM Oryza sativa (japonica cultivar-group)

ENKaryotca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Enkaryotca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatcphyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryzea; Oryzea; Oryzea; Oryzea; Oryzeae; Oryzea; Oryzea; Oryzea; Clade; Ehrhartoideae; Oryzeae; Oryzea; Or
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gs66c01.gl Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/dev_stage="7 days after germination"
/lab_host="E.coli DH108"
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/db_xref="taxon:3311"
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/clone="7LEAF--07-N19"
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/lab_nost="E.coli DH10B"
/lone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with Oligoribonucleotides and then used as templates for RT-PCR."
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1B bp mRNA linear EST 15-AUG-2003
7LEAF--07-N19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-N19, mRNA
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7LEAF--06-L22.bl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--06-L22, mRNA
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Sukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTE
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yougin, Yeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
/lab host="E.coli DH10B" /clone lib="Rice leaf plasmid cDNA library II (7LEAF)" /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Location/Qualifiers
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Elkaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Shekaryota; Viridiplantae; Streptophyta; Embryophyta; Ginkgo.

El (bases 1 to 18)

Sermatophyta; Ginkgophyta; Ginkgoaceae; Ginkgo.

El (bases 1 to 18)

S Brenner, B.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Banfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo male leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie

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Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mccombie@cshl.org

Seq primer: -21M13UnivRev.
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/note="Organ: leaf; Vector: :pBK-CMV; Site_1: XhOI;
/note="Organ: leaf; Vector: :pBK-CMV; Site_1: XhOI;
/note="Organ: leaf; Vector: :pBK-CMV; Site_1: XhOI;
/note="Organ: leaf; Vector: ipBK-CMV; Site_1: XhOI;
/note="Organ: leaf; Vector: leaf; V
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/note="Organ: leaf; Vector: pBK-CMV; Site_1: The_Ibrary was size-fractionated to enrich for large inserts."
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300628-02-E02.gl Rice leaf plasmid cDNA library I (300GS) Oryza sativa (japonica cultivar-group) cDNA clone 300GS--02-E02, mRNA sequence.
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100.0%; Pred. No. 1.3e+03;
iive 0; Mismatches 0; Indels
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Pred. No. 1.3e+03;
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/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="male"
                                                                                                                                                                                                                        Query Match

0.7%; Score 18; DB
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 18; Conservative 0; Mismatches
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/sex="female"
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Best Local Similarity 100.
Matches 18; Conservative
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Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Supermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoidae; Oryza.

I (bases 1 to 19)

St Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, Y.F., and Nahm, B.H.

I arge-scale Sequencing Analysis of Rice ESTS

In Upublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Pax: 82 31 331 6193

Pax: 82 31 331 6195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/cultivar="Nackdong"
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/lab host="E.coll DH10B"
/clone="Nector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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                                                                                                                     1 (bases 1 to 19)
Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Xim, Y. -K. and Nahm, B. H.
Large-scale Sequencing Analysis of Rice ESTB
Contact: Nahm B. H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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/mol_type="mRNA"
/cultivar="Nackdong"
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Location/Qualifiers
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100.0%; Pred. No. 1.3e+03;
tive 0; Mismatches 0; Indels
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/clone="7LEAF--01-M05"
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Location/Qualifiers
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RESULT 1595 CF302456/c

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

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FEATURES

AUTHORS REFERENCE

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

El (bases 1 to 19)
SKim,J.S., Jun, K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Wettor: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcribtion factor 3 overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa (japonica cultivar-group)""
/mol cype="manA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                      Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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181: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
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Pred. No. 1.3e+03;
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                                CF309821.1 GI:33681582
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Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliophyta; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

E 1 (bases 1 to 19)

SKim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Lu Unpublished (2003)

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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

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Tel: 82 31 330 6193

Fax: 82 11 221 6355
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TLEAF--07-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-P22, mRNA
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/db xref="taxx"."
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonuclectides and then used as templates for
RT-PCR."
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/mol_type="mRNA"
/cultivar="Nackdong"
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.00.0%; Pred. No. 1.3e+03;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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CF302456.1 GI:33674217
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Best Local Similarity
Matches 18; Conserv
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Best Local Similarity
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RESULT 1596

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linear

mRNA

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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons,
rosids, Vitaceae, Vitis.
1 (bases 1 to 19)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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cDNA library (JMT)"
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/mol type="mRNA"
/cultivar="Nackdong"
/db riazar:39947"
/clone="JMT--04-017"
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bluahm@gpio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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100.0%; Pred. No. 1.3e+03;
tive 0; Mismatches 0;
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   Query Match 0.77
Best Local Similarity 100.
Matches 18; Conservative
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Enrhartoideae; Oryzae; Oryzae; Oryzae; Dryza.

I (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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/dev stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                               for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, YeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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with oligoribonucleotides and then used as templates for
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/dev
                                                                                                                                                                                                                                                                                                                                                                                                           'note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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100.0%; Pred. No. 1.3e+03;
tive 0; Mismatches 0; Indels
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Location/Qualifiers
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Location/Qualifiers
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Best Local Similarity 100.0
Matches 18; Conservative
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DEFINITION CF331361/c

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VERSION KEYWORDS

ORGANISM

TITLE JOURNAL COMMENT

FEATURES

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AUTHORS REFERENCE

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Gaps

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Length 19; 0; Indels

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Query Match
Best Local Similarity
Matches 18; Conserv
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/rote="Organ: Heart; Vector: pBluescript II SK; Site_1:
/note="Organ: Heart; Vector: pBluescript II SK; Site_2:
BCORI; Site_2: XhoI; Library constructed using pBluescript
XR kit from Strattagene. Cloned cDNA was size selected
between 1-3 kb. Tissue supplied by Mark Haakins VMD, PhD,
Pathology and Medical Genetics, School of Veterinary
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Handi S.
UNR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avene Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="ripening stage"
|Colone_libe=Ripe Grape Skin Triplex2 Library"
|note="Organ: Fruit skin; Vector: Lambda TriplEx2; Site_1:
|SfilA; Site_2: SfilB; Oriented library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canis familiaris (dog)
Canis familiaris
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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S Balija, V.S., Nascimento, L.U. and McCombie, W.R.

ESTS from Canis familiaris left cardiac ventricle (dog)

L Unpublished (2004)

Unpublished (2004)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8874

Fax: 516 367 8874

Email: mccombie@cshl.org.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.7%; Score 18; DB 1; Length 19; 100.0%; Pred. No. 1.3e+03; trive 0; Mismatches 0; Indels
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dev stage="3 month old normal canine"
/lab_host="XL10 Gold"
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/mol_type="mRNA"
/culfivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006D08"
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/mol_type="mRNA"
/db_xref="taxon:9615"
                                                                                                                                                                                                                  Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: B.hamdi@bordeaux.inra.fr
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CX002732.1 GI:56274148
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Matches 18; Conserv
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COMMENT
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                    TITLE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligomucleotides were lighted to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoreais. Vector DNA was prepared from a derivative of pWD42 (gij |473214 |qb| |AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi,

Mammalia, Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Murinae; Mus.

E 1 (bases 1 to 19)

B Dun,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Dipublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah Genome Center

University of Utah Genome Center

Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Medicine, University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ345795 110 DNA linear GSS 29-SEP-200 1M0080H09R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0080H09 R, genomic survey sequence.
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/clone_lib="Mouse 10kb plasmid UUGCNM library"
/noce="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                             Gaps
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                                                                                                         Length 19;
                                                                                                                                                                         0; Indels
                                                                                                         Score 18; DB 1; Le
Pred. No. 1.3e+03;
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Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: H column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/mol_type="genomic DNA"
/drain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC1M0080H09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
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                                                                                                                                                                             Conservative
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Fax: 801 585 7177
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nt; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0520P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0520P13 R, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Nm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Kose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weises, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                    Length 19;
                                                                                                                                             0; Indels
                                                                                 0.7%; Score 18; DB 1; Le ilarity 100.0%; Pred. No. 1.3e+03; Conservative 0; Mismatches 0;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: P column: 13
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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Location/Qualifiers
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Best Local Similarity
Matches 18; Conserv
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KEYWORDS
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AUTHORS
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Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with phred
OC 020425. C. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptI(KS+) R. Site 1:
ECORI R. Site 2: NOTI Description: Normalised library constructed
from pooled tissue from day 30 placentess. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institite,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson, S. I., Finlayson, H.A. and Archibald, A.L.
Development of CDNA and EST resources for studying reproduction and embryo development in pigs and cattle
(Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata, Craniata, Vertebrata, Euteleostomi,
Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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ALS87727 BP Chicken Brain Library Gallus gallus cDNA clone
ROSO61D01, mRNA sequence.
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/clone lib="CSEQRAN09"
/note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."
chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                 Gaps
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AJ666275 CSEQRANO9 Sus scrofa cDNA clone C0000033_B07, mRNA sequence.

AJ666275. GI:49350726
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Location/Qualifiers
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                                                                   Length 19;
                                                                                                               0; Indels
                                                                Query Match 0.7%; Score 18; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_B07"
                                                                                                                                                      2708 TAAAAAAAAAAAAA 2725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2709 AAAAAAAAAAAAAA 2726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 20)
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Sus scrofa
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Matches 18; Conserv
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CF282002
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Best Local Similarity
Them 18; Conserva
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Best Local Simi
Matches 18;
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CF320843/c
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CF282002/c
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1 (bases 1 to 20)

Alkharouf, N., Khan, R. and Matthews, B.
Analyais of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode Genome 47 (2), 380-388 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 bp mRNA linear EST 01-AUG-2003
B099H12.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
B099H12 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Alkharouf, N.W.
Sybban Ganomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bidg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                          Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Exa: +44 (0)131 440 0434
Email: frazer.murrayabbsrc.ac.uk
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 20)
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                                                                                                                                                                                                                                                              1. 20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Glycine max"/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharom@ba.ars.usda.gov.
Location/Qualiffers
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           /clone="ROS061D01"
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                                                              BP Chicken Brain Library
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA853586
CA853586.1 GI:33390391
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                                                                                            Contact: Frazer Murray
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nes 18; Conservative
                                                                                                                                                                                                                                  Seq primer: M13F.
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                                                 Murray, F.
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Matches 18;
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                                                              TITLE
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Series activa (japonica cultivar-group)

1SM Oryza sativa (japonica cultivar-group)

1SM Oryza sativa (japonica cultivar-group)

1SM Oryza sativa (japonica cultivar-group)

1 Enkarycota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

2 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

2 clade; Ehrhartoideae; Oryzeae; Oryzea.

CE I (bases 1 to 20)

RS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Sorig, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

AL Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/cultivar="Peking"
/db_xref="taxon:3847"
/clone="B09H12"
/tissue_type="Roots"
/dev_gtage="Seedlings"
/clone_lib="cDNA Peking library 12hr SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
/note="Vector pBluescript SK-; cDNA clones from mRNA
infection by SCN race 3. These are cloned in pBluescript
SK- phagemid. "
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14ETL--09-F01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F01,
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/organism="Oryza sativa (japonica cultivar-group)"
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100.0%; Pred. No. 1.4e+03;
rative 0; Mismatches 0; Indels
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/tissue type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
                                                                                                                                                                                                                                                                                                                               0.7%; Score 18; DB 1; Le
100.0%; Pred. No. 1.4e+03;
vative 0; Mismatches 0;
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/cultivar="Nackdong"
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Tue Nov

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20 bp mRNA linear EST 15-AUG-2003
HDD--11-001.gl OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HDD--11-001, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH108"
/clone lib="ColhAC1-Overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EccR1; Callus was
treated with ABA[20un] for lhr. Oligo-capped mRNA was
reverse transcribed and then used for pCR. mRNA was
derived from rice Histone Deacetylase overexpression
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                                                                                                                                                                                       Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzae, Oryza.
                                                                                                                                                                                                                                                                                                                           Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6355
Fax: 82 31 321 6355
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rosse,M., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref=taxon:39947"
/clone="HD-11-001"
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0
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100.0%; Pred. No. 1.46+03;
vative 0; Mismatches 0;
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Contact: Robert B. Weiss
                                                                                                                                             CF320843.1 GI:33692604
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD4 (gilfa712114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ370699 20 bp DNA linear GSS 02-OCT-2000 1M0121N17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0121N17 R, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroldea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse lOkb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/64 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dun, D., Agraga, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Roll, M., Rose, M., Rose, R., Stokea, R., Tingey, A., von Niederhausern, A. and Wright, D. Waiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
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100.0%; Pred. No. 1.4e+03;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                               Std Error: 0.00
                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Discr Length: 10000 Std Error: 0
Plate: 0080 row: G column: 17
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="UUGC1M0080G17"
                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 20.
Location/Qualifiers
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Mus musculus
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Unpublished (2000)
Contact: Robert B. Weiss
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AZ370699.1 GI:10484399
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Gnetum gnemon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resources (documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared but of inch orifice at constant velocity. The sheared DNA was blunt enderrepaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xilo-Gold (Stratagene) cells and selected for ampicillin resistance."
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DKF2p566N143 r1 566 (8ynonym: hfkd2) Homo sapiens cDNA clone
DKF2p566N143, mRNA sequence.
                                          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"/clone_lib="Mouse_lokb_plasmid_UdColm_library."
/note="Wector: PWP42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.

1 (bases 1 to 21)

Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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Location/Qualifiers
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                                                                     84112, usn
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                          Insert Length: 10000 Std Error: 0
Plate: 0121 row: N column: 17
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/63"
University of Utah Genome Center
University of Utah
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/clone="UUGC1M0121N17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
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source

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ISM Gnetum gnamon

Eukaryochyta; Gratophyta; Embryophyta; Tracheophyta;

Eukaryoch; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryoch; Viridiplantae; Gnetophyta; Gnetopeida; Gnetales; Gnetales; Gnetum.

CE 1 (bases 1 to 21)

Brenner, E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,

O'Shaughnessy,A.L., Balija,V., Martienseen,R.A., McCombie,R.W.,

Benfey,P., Coruzzi,G. and Stevenson,D.

Expressed tag sequences from Gnetum female cone (NYBG)

AL Unpublished (2003)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8884

Email: mccombie@cshl.org

Seq primer: -21M13UnivRev.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DN955603 21 bp mRNA linear EST 04-MAY-2005 it91b09.gl Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
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                                                                                                                                                                                                                                                                                                             Gaps
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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/cloine="bkR2p566N143"
/tissue_type="kidney"
/dev stage="fetal"
/lab_host="X1-2blue"
/clone lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: Sal1"
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                                                                                                                                                                                                                                                     0.7%; Score 18; DB 1; Le
100.0%; Pred. No. 1.4e+03;
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100.0%; Pred. No. 1.4e+03;
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    .21
    /organism="Gnetum gnemon"

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/db_xref="taxon:3382"
/sex="female"
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LOCUS
DEFINITION
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5

ORGANISM

SOURCE

ACCESSION VERSION KEYWORDS REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                      plasmid inserts
(Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 108- Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                  1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weises, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: D column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: Plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 21.
Location/Qualifiers
                                                                              Mus musculus (house mouse)
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                          GI:12879511
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                       AZ764492.1
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                                                                                                         ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared bNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophorasis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasming R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                      Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rosse, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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-ive 0; Mismatches
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Insert.Length: 10000 Std Error:
Plate: 0436 row: G column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
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University of Utah Genome Center
University of Utah
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
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              AZ610868.1 GI:11733058
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Best Local Similarity 100.C
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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FEATURES

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/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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(http://www.jax.org/resources/documents/dnares/). The DNA
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polynucleotide kinase. Adaptor oilgourcleotides were
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of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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Pred. No. 1.4e+03;
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Best Local Similarity 100.0%; Fred. No. 1.4
/db_xref="taxon:10090"
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RESULT 1614 AZ764492 LOCUS DEFINITION

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rypanosoma.
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TA231E08Q
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                                                           Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.
E (bases 1 to 22)
S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/cultivar="Nackdong"
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2M0142B07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0142B07 R, genomic survey sequence.
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(Dases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Waiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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University of Utah Genome Center
University of Utah
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Mus musculus
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AZ843648.1 GI:13013556
                     CF328832.1 GI:33805905
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Unpublished (2000)
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Fax: 801 585 7177
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/gex="Male"
// Jab host="E. Coli strain XLIO-Gold, T1-resistant, F-"
// Jab host="E. Coli strain XLIO-Gold, T1-resistant, F-"
// Clone lib="Wouse 10kb plasmid UUGCIM library"
// note="Wetcr: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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10.5 kb range using preparative agarose gol
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gil #4732114|gb]AR129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
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chemically-competent E. coli XIIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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T. brucei sheared genomic DNA clone 231e08, reverse sequence,
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Constructed at the Institute for Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRED927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
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Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
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                                           Std Error: 0.00
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0142 row: B column: 07
CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/63"
                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="UUGC2M0142B07"
                                                                                                                                                                                                                   Location/Qualifiers
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Best Local Similarity 100.0
Matches 18, Conservative
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CF330439/c
                                                                                 ACCESSION
VERSION
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Whallingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

W. Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBlo ISA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTAt 10.1) was mechanically sheared to give a tight size distribution (

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TA386H07Q 22 bp DNA linear GSS 13-DEC-2000 T. brucei sheared genomic DNA clone 386h07, reverse sequence, genomic survey sequence.
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Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Banil: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
Location/Qualifiers
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                       1.46+03;
                                                                                                                         1. .22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
                                                                                                                                                                                                                                                                  0.7%; Score 18; DB 1;
100.0%; Pred. No. 1.4e+0
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/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="386h07"
                                                                                                                                                                                                                                                                            100.0%; Preα. ...
... 0; Mismatches
                                                                                                                                                                                                     /db_xref="taxon:5691"
/clone="231e08"
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Best Local Similarity 100.
Matches 18; Conservative
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1 (bases 1 to 22)
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Best Local Similarity
Matches 18; Conserv
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AUTHORS
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RESULT 1619

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BX564412 BX564412 and morsitans morsitans adult infected gut Glossina morsitans cDNA clone Tee71e10_plc, mRNA sequence.
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T.brucei"
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                                                                                                                                                          Glossina morsitans morsitans
Glossina morsitans morsitans
Glossina morsitans morsitans
Bukaryota, Metazoa, Arthropoda; Haxapoda; Insecta; Pterygota;
Bukaryota, Metazoa, Arthropoda;
Hippoboscoidea; Glossinidae; Glossina.

1 (bases 1 to 21)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M. B., Bonaldo, M. F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/sub_species="morsitans"
/db_xref="teaxon:37546"
/clone="Tea71e10 plc"
/tissue type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     All clones with suffix glc are reverse primer reads starting at end of the cDNA all plc reads are from
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NACL--06-C12.bl Rice callus plásmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--06-C12, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
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Genome Biol. 4 (10), R63 (2003)
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School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
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                                                                                 BX564412
BX564412.1 GI:33431592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Hall N
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JOURNAL
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Gaps ó

COMMENT

source

FEATURES

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/cell line="MGC3"
/tissue type="small cell carcinoma"
/cell line="MGC3"
/lab host="DilOB (phage-resistant)"
/clone lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
CoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/Glo size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using Zap-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DV751812 21-NOV-2005
ID0AAH9BD05ZM1 ID0AAH ACyrthosiphon pisum cDNA clone ID0AAH9BD05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphididae; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 21)
Stern,D.L., Wincker,P. and Tagu,D.
Large-scale gene discovery in the pea aphid Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 1.4e+03; tive 0; Mismatches 2; Indels
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Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acyrthosiphon pisum (pea aphid)
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Location/Qualifiers
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Contact: D. Tagu
INRA Rennes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5', mRNA sequence.
DV751812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Conservative
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DV751812
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Is (bases 1 to 21)

NIH-MGC http://mgc.nci.nih.gov/.

In Unpublished (1999)

Other ESTS: 2821017.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling

Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PRRED from University of Washingtion Genome Center. Vector

Trimming: cross match from University of Mashingtion Genome Center.

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Mashingtion Genome Center:

http://www genome.washington.edu Low Quality Sequence: 21

contiguous PRRED high quality bases following vector sequence. Very

Low Quality Sequence: Trace file contained 21 contiguous distinct

peaks following vector sequence. Polyadenylation: Based upon the

presence of a Xhol site followed by a run of 14 or more T residues

at the beginning of the sequence, this CDNA insert was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW248782 21 bp mRNA linear BST 07-JAN-2000 2821017.3prime NIH_MGC_7 Homo sapiens CDNA clone IMAGE:2821017 3',
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                                                                                                                                                                                                                                                                                                                                                                   /mol type="maker" | Japonica circuity group, | mol type="maker" | Mol type="maker | Mol type="maker | Mol type="maker | Mol type="maker | Mol type="callus" | Lissue_type="callus" | Lissue_type="callus" | Mol type="callus" | Mol type="callus" | Mol type="callus" | Mol type="callus | Mol type="callu
Contact: Nahm B.H.
Genomica and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Yel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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    .21
/organism="Oryza sativa (japonica cultivar-group)"

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Plate: LLCM5 row: L column: 10
High quality sequence stop: 21.
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RESULT 1621

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AW248782/c DEFINITION

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AUTHORS TITLE JOURNAL COMMENT

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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adappicred vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ralam, L. Gongacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
                                                                                                                                                                                                                                                              AZS97932 13-DEC-201 1M0412D23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0412D23 F, genomic survey sequence. AZ597932
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                                                            Gaps
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0
          Length 21;
                                                          2; Indels
     Score 17.8; DB 1;
Pred. No. 1.4e+03;
0; Mismatches 2;
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Insert Length: 10000 Std Error: 0.00
Plate: 0412 row: D column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0412D23"
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                                                                                                    2700 GITIGIACTAAAAAAAAA 2720
                                                                                                                                                    GrrrGrcaraaaaaaaa 21
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GSS.
Query Match
Best Local Similarity 90.5%;
Matches 19; Conservative
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Fax: 801 585 7177
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84112, USA
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoreass. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Niederhausern, A. and Wright, D., Weise, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R., Dinger, S., Dinger, S., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

L Unpublished (2000)

Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UP 84112, USA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
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   Length 21;
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Query Match

0.6%; Score 17.8; DB 1;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: B column: 05
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0474B05"
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AZ627840.1 GI:11750126
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1 (basea 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ralam, D., Aoyagi, A., Bamber, M., Menen, E., Pedersen, T., Reily, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Underhausern, A. and Wright, D., Weiss, R., 
                                                                                                                                                                                                                                                                                                                                                                                                AZ647578 21 Dp DNA linear GSS 14-DEC-200
1M0514117F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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/clone_lib="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                          Gaps
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Query Match 0.6%; Score 17.8; DB 1; Length 21; Best Local Similarity 90.5%; Pred. No. 1.4e+03; Matches 19; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone UUGC1M0514117 F, genomic survey sequence.
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Plate: 0514 row: I column: 17
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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/clone="UUGC1M0514117"
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Mus musculus
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LUGS4197 KBIS, Brassica rapa Sau3AI BAC library Brassica rapa saubsp. pekinensis genomic clone KBIS013K03, genomic survey
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Brassica rapa subsp. pekinensis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, amagnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                CL693188
PRIO160C_F06_2 - PRIO160C.BR (21) Note: Recurring String Mixed stage fosmid_library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
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/clone lib="Mixed stage fosmid library of P. pacificus
var. California"
                                                           Gaps
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Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppaDB: an Aceda database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pristionchus pacificus
Pristionchus pacificus
Eukaryota, Metazca; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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Max-Planck-Institute for Developmental Biology
Spemannetr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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/mol type="genomic DNA"
/strain="California"
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Class: fosmid ends
                                                           19; Conservative
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Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermacophyta; Gudicotyledons; core eudicotyledons; cosida; eurosida II; Brassicales; Brassicacea; Brassica.

I (Bases II to 22)

S Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Hahn, J. H. and Park, B.S.

Bark, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J. H. and Park, B.S.

End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

Unpublished (2005)

L Contact Beomics Team

National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1672
                                                                                                                                                                                                                  Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
125 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1670

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BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS008L22
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/db_xref="taxon:51351"
/clone="KBrS013K03"
/lab_host="E. coli DH10B"
/clone=lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
spp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
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1 (bases 1 to 21)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Yang, T.J., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
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/mol type="genomic DNA"
/cultivar="Chiifu"
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Class: BAC ends.
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Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
25 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1672
Email: pbeom@rda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukaryota, Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bopermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases I to 22)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa SaulAI (KBrS) BAC clone
                                                                                                         /db_xref="taxon:51351"
/clone="KB:50081:22"
/lab host="B. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiffu BAC_library (KBrS BAC) is
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/note="Vector: pCUGIBACI; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."
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/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
                                                                                                                                                                                                                                                                                                                            Query Match 0.6%; Score 17.8; DB 1; Length 22; Best Local Similarity 90.5%; Pred. No. 1.4e+03; Matches 19; Conservative 0; Mismatches 2; Indels
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Pred. No. 1.4e+03;
0; Mismatches 2; Indels
                                                                             /sub_species="pekinensis"
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/cultivar="Chiifu"
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Best Local Similarity 90.5%;
Matches 19; Conservative
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Class: BAC ends.
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14-AUG-2003
14ROOT--02-D01.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-D01, mRNA
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantas, Streptrophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Gontact: Nahm B.H.

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Toyngin, Kyeonggi, Korea

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Fex: 82 31 321 6355
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Unpublished (2003)
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/organism="Oryza sativa (japonica cultivar-group)"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
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RESULT 1630
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

El (bases 1 to 19)
SKim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice EST8
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF292072
14ROOT--02-M03.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-M03, mRNA
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of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 310 6133
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Pred. No. 1.4e+03;
0; Mismatches 1; Indels
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Hel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Best Local Similarity 94.7%;
Matches 18; Conservative (
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Best Local Similarity 94.7
Matches 18; Conservative
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Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Toglin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
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NACL--04-F15.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-F15, mRNA
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                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                                                                                                                          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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14.7%; Pred. No. 1.4e+03;
ve 0; Mismatches 1;
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/clone="ABF--05-H18"
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/cultivar="Nackdong"
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptrophyta; Embryophyta; Tracheophyta;
Spermarcophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
I (bases I to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/clone="14ROOT--02-N17"
/tissue_type="root"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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|mol_type="mRNA"
|cultivar="Nackdong"
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Location/Qualifiers
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AUTHORS

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COURTELES: SAILILY: STRING.

COURTELES: SAILILY: STRING.

COURTELES: Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling

Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

CONSORTIUM (LINL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/Link at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PRRED From University of Washingtion Genome Center.

Trimming: cross mach from University of Washingtion Genome Center.

Drosophila Genome Project. University of Washingtion Genome Center:

http://www.genome.washington.edu Low Quality Sequence: 7 contiguous

PHRED high quality bases following vector sequence. Very Low

Quality Sequence: Trace file contained 19 contiguous distinct peaks

following vector sequence. Polyadenylation: Based upon the presence

of a XhoI site followed by a run of 14 or more T residues at the

Plate: LLCM5 row: P column: 16

High quality sequence stop: 7.

High quality sequence stop: 7.
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//clone="Organ: lung, Vector: poTB7; Site_1: XhoI; Site_2:
//note="Organ: lung, Vector: poTB7; Site_1: XhoI; Site_2:
CorsI; CDNA made by oligo-dr priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using 2AP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                 NIH-WGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other_EST8: 2821119.5prime
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/tissue type="small cell carcinoma"
/cell line="MGC3"
/lab_nost="DH10B (phage-resistant)"
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens (human)
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1 (bases 1 to 19)
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19 bp mRNA linear EST 18-AUG-2003
JMT--03-P13.bl AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--03-P13, mRNA sequence.
CF334610
CF334610.1 GI:33817556
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Oryza sativa (japonica cultivar-group)
Cukaryota, viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Nahm B.H.
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Boinformatics, MyongJi University
Yorgin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@pio.myongji.ac.kr.
Location/Qualifiers
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/mol type="mRNA"
/cultivar="NackGong"
/clone="JMT--03-P13"
/clone="JMT--03-P13"
/tissue_type="leaf"
/dev stage="la farga after germination"
/lab_host="E.coli DH108"
/clone lib="E.coli DH108"
/clone lib="AtJMT-overexpressing transgenic rice plasmid
cona library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rallly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
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84112, USA
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                                                                                                                                                      Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1M0360E13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0360E13 F, genomic survey sequence.
AZ513919
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1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0109 Tow: I column: 13
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC1M0109113"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Male"
                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                       plasmid inserts
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored vector DNA, and transformed into adaptored vector DNA, and transformed into chemically-competent E. Coli Kilo-Gold (Stratagene) cells
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 717.
Fax: 801 585 717.
Fax: 801 585 717.
Fax: 801 587 717.
Fax: 802 Fax
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0360E13"
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Tue Nov

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Query Match
Best Local Similarity 94.7'
Matches 18; Conservative
                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                   Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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1M0520N17F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0520N17 F, genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Cires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42xv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niedesthausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: G column: 04
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of public derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (stratagene) cells and selected for ampicillin resistance."
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1M0529F08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0529F08 F, genomic survey sequence.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murcidea; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
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                                                                                                                                                                                                                                                                                                            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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Pred. No. 1.4e+03;
0; Mismatches 1; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: N column: 17
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="genomic DNA"
fatrain="C57BL/61"
/db xref="taxon:10090"
/clone="UUGCIM0520N17"
                                                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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AppaDB: an AcedB database for the nematode satellite organism
                                                                                                                                                                                                                                                                                                                                            Seq primer: T7
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                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Wen. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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PRIO160b_GG3 2 - PRIO160b.BR (19) Note: Recurring String Mixed stage fosmid_library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

CL6931771

GL693177.1 GI:50215085
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/clone_lib="Mouse_10kb_plasmid UDGCIM library"
/note="Wector: PWD42tv; Purified genomic_DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Pristionchus pacificus
Pristionchus pacificus
Bukaryota; Metazzoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 19)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse aprome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: F column: 08
Seg primer: cGTTGTAAAACGACGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
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CF319428 20 Dp mRNA linear EST 15-AUG-2003 HD--09-020.bl OsHDAC1-overexpressing transgenic rice plasmid CDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--09-020, mRNA sequence.
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/dev_stage="proliferated"
/lab_nost="E.coli DH10B"
/clone_lib="OsHbAC1-overexpressing transgenic rice plasmid cDNA llbrary (HD)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJu, XyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db xxef="taxon:54126" /db xxef="taxon:54126" /clone lib="mixed stage fosmid library of P. pacificus var. California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                    Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Mancouver, Canada.
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0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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/clone="HD--09-020"
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/cultivar="Nackdong"
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Location/Qualifiers
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RESULT 1645 CF333052/c

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

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/lab_host==r0p10"
/lab_host==r0p10"
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Sample name: ApHL3SD; Plant growth place: INRA-Rennes,
UMR BiO3P, BP 35327, 35653 Le Rheu cedex, France; Soil
conditions: peat; Sowing date: 20/03/2003; Harvesting
date: 10/04/2003; Stress date: no stress; Description:
aphids inoculated on one-week old vicia faba germinations
under non sterile conditions.; experimental condition:
short photoperiod (12-hr light/12-hr dark at 18 c)"
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E 1 (bases 1 to 21)
S Dunn, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Rallam,H., Longacre,S., Mahmoud,M., Mesen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Diamid inserts
Unpublished (2000)
L Context: Robert B. Weiss
University of Utah Genome Center University of Utah Genome Center University of Utah
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1M0012H15F Mouse 10kb plasmid UUGCIM library Mus musculus genomic COORE UUGCIM0012H15 F, genomic survey sequence.
                                               Acythosiphon plaum Acythosiphon plaum Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota; Nooptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphididae; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 20)
1 (bases 1 to 20)
1 Large-scale gene discovery in the pea aphid Acyrthosiphon pisum (Hemiptera)
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                                                                                                                                                                                                                                                                                                                                                   UMR B103P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
FORP PRIMERS GCCGCATAACTTCGTATAGCA
Plate: 5Y row: C column: 2.
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/cultivar="yr2"
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                            Acyrthosiphon pisum (pea aphid)
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Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                                                                                                 Unpublished (2005)
Contact: D. Tagu
INRA Rennes
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Matches 18; Conserv
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TITLE
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AUTHORS
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Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhattoideae; Oryza.

Extin, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.E., and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Lupublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, KyeongJi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
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5', mRNA sequence.
DY228778
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/clone="JMT-01_MM7"
/tissue type="leaf"
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cona library (JMT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                               JMT--01-M17.gl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--01-M17, mRNA sequence.
treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                 Gaps
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/mol_type="mRNA"
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                                                                                                                                   Length 20;
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Location/Qualifiers
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                                                                                                                                      Score 17.4; DB 1;
Pred. No. 1.5e+03;
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0.6*; Score 17.4; D
Best Local Similarity 94.7*; Pred. No. 1.5e
Matches 18; Conservative 0; Mismatches
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Best Local Similarity
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TITLE JOURNAL COMMENT

FEATURES

AUTHORS REFERENCE

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Gaps ; GSS 29-SEP-2000

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RESULT 1646 DY228778/c

Matches

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ACCESSION VERSION

7 10:41:28 2006

Tue Nov

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/mol_type="mRNA" /culEivar="KWS2320 (double haploid, monogerm breeding
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Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 18 row: B column: 24
Seq primer: T7; GTAATACGACTCACTATAGGGC.
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 19 row: E column: 19
Seg primer: T7; GTAATACGACTCACTATAGGGC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                    | db_xref="GAB1:189986"
| db_xref="teaxon:161934"
| clone="024-019-E19"
| Lissue type="storage root"
| lab_hogt="EMDH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                           /lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nr; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophylales; Amaranthaceae; Beta.
Caryophylales; Amaranthaceae; Beta.
I (bases I to 17)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0012 row: H column: 15
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                      'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                             /db xref="taxon:10090"
/clone="UUGC1M0012H15"
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Best Local Similarity 94.7'
Matches 18; Conservative
                     Tel: 801 585 5606
Fax: 801 585 7177
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/clone lib=MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
CDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saetzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
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1 (bases 1 to 17)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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S013717-024-018-B24-T7 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-018-B24 3-PRIME, mRNA sequence.
BQ590687
/mol_type="mRNA" /
/cultivar="KW82320 (double haploid, monogerm breeding
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100.0%; Pred. No. 1.5e+03;
ive 0; Mismatches 0; Indels
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
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2709 AAAAAAAAAAAAAA 2725
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E01271S-024-017-B22-T7 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-B22 3-PRIME, mRNA sequence.
B0591177.1 G1:26120760
                                                                                                                                                                                                                       /clone lib="MPIZ-ADIS-024-storage root" | /clone lib="WPIZ-ADIS-024-storage root" | /note="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1; /note="Vector: pcmVsPoRT6; Site 1: Sal1; Site 2: Not1; /clone sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
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/clone lib="MPL2-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: Sall; Site_2: NotI;
/note="Vector: pCMVSPORT6; Site_1: Sall; Site_2: NotI;
/note="Vector: pCMVSPORT6; Site_2: Sall; Site_2: NotI;
/note="Vector: pcmvsport6"
// Note="Vector: pcmvsport6"
// Note:"
// No
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1 (bases 1 to 17)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Not1-T7; Note: Sequencing granted in the context of the GAB1-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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|organism="Beta vulgaris"
|mol type="MRXA"
|cultiva="KWS2320 (double haploid, monogerm breeding
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg de
Insert Length: 17 Std Error: 0.00
Plate: 17 row: B column: 22
Seq primer: T7; GTAATACGACTCACTATAGGGC.
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CF294668 17-50 Rice leaf plasmid cDNA linear EST 14-AUG-2003 30DGS--04-E17.91 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--04-E17, mRNA
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Oryza sativa (japonica cultivar-group)
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Large-scale Sequencing Analysis of Rice ESTs
SP6-Sall-CCACGCGTCCG-5prime-cDNA-polyA-CC-Not1-T7; Note: Sequencing granted in the context of the GABI-Beet project, local Pi: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Yongin, KyeongJi, Korea
Yell 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/clone lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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/clone="14ROOT--01-A21"
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaea; Oryza.

(bases I to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Aim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoR1; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                   Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yonglin, Kyeonggi, Korea
Tel: 82 31 330 6193
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|mol_type="mRNA"
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ive 0; Mismatches 0; Indels
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzea; Oryza.

(bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7LEAF--02-A18 bl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A18, mRNA
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Query Match
Best Local Similarity
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CF336950/c
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streeptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

E I (bases 1 to 17)
S Kim,J.S., Jun,K.M., Cheong, D.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bloinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 21 6155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group)

Cyza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyra; Embryophyta; Tracheophyta; Spermatophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.

El (bases 1 to 17)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

L Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

YongJu, KyeongGi, Korea

Tel: 82 31 330 6193
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Pred. No. 1.5e+03;
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Location/Qualifiers
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100.0%; Pred. No. ...
0; Mismatches
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                     ABF--04-M02, mRNA sequence.
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CF334566.1 GI:33817460
                                                         CF310219.1 GI:33681980
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Best Local Similarity 100.
Matches 17; Conservative
                                     CF310219
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/dev_stage="14 days after germination"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
pepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissuc_type="leaf"
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cDNA library (JMT)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JMT--07-D04.gl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--07-D04, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                 bhnahm@bio.myongji.ac.kr
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Best Local Similarity 100.0%; Pred. No. 1.5e+03;
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                                                                                                                                                                                                                                                                        /tissue_type="leaf"
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                                                             Location/Qualifiers
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2709 AAAAAAAAAAAAAA 2725
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Matches

ò 셤 VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

PUBMED JOURNAL

COMMENT

DEFINITION CX309551/c

RESULT

ACCESSION

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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Lupublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6135
Fax: 82 31 321 6155
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol type="mRNA"
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyra, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; BEP
clade, Ehrhartoideae, Oryzeae, Oryza
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
Clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.L., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongJi.ac.kr.
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    .18
/organism="Oryza sativa (japonica cultivar-group)"

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0.6%; Score 17; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Bubydroidea; Drosophilidae; Drosophila.

Ephydroidea; Lo 17)
Yandell, M., Bailey, A.M., Misra, S., Shu, S., Wiel, C., Evans-Holm, M.,
Celniker, S. B. and Rubin, G.M.
A computational and experimental approach to validating annotations
and gene predictions in the Drosophila melanogaster genome
Proc. Natl. Acad. Sci. U.S.A. 102 (5), 1566-1571 (2005)
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7LEAF--05-M05.b1 Rice leaf plasmid cDNa library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-M05, mRNA
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// Organism="Drosophila melanogaster"
// Organism="Drosophila melanogaster"
// Organism="Colone" Apploase"
// Orlone="Apploase"
// Sex="male and female"
// Gev_stage="0 to 24 hours mixed stage embryonic, late
// Abird instar larvae, mixed stage pupae, mixed age adults"
// Clone="Inb="Am Drosophila melanogaster Embryo Larva Pupa
Adult"
                                                                                                                                                                                                                                   CX309551
AM02384.3prime AM Drosophila melanogaster Embryo Larva Pupa Adult Drosophila melanogaster cDNA clone AM02384 3, mRNA sequence.
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: AM 23 row: G column: 12
High quality sequence stop: 17.
Location/Qualifiers
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Oryza sativa (japonica cultivar-group)
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Mismatches
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Contact: Stapleton, M.
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Best Local Similarity 100.
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| Colone="Mb--11-222"
| tissue_type="callus" |
| dev_stage="proliferated callus on 2N6 media for 2 weeks" |
| day_stage="E.coli BH108" |
| clone lib="Coli BH108"
/dev_stage="proliferated callus on 2N6 media for 2 weeks" lab host="E.coli DH10B" /clone lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 18)
Xim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bloinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 313 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 bp mRNA linear EST 15-AUG-200 HD--11-E22.gl OBHDAC1-overexpressing transgenic rice plasmid CDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--11-E22, mRNA sequence.
                                                                                                                                                     /note="Vector: pCR4-TOPO; Site_1: EcoR1; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /notes "Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(10um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
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|mol_type="mRNA"
|cultivar="Nackdong"
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000.0%; Pred. No. 1.5e+03;
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Laboratory Mouse DNA Resource Ltd. Charactery Mouse DNA Resources documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coll XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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AZ853220
2M0156J15F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0156J15 F, genomic survey sequence.
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                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone_lib="Mouse lokb plasmid UUGCNM libraty."
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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84112, USA
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Nouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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100.0%; Pred. No. 1.5e+03;
iive 0; Mismatches 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0156 row: J column: 15
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Seq primer: CGTTGTAAAACGACGGCCAGT
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/mol_type="genomic DNA"
/strain="C578L/63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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/clone="UUGC2M0156J15"
                                                                                                                                                                                         Mus musculus (house mouse)
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Best Local Similarity 100.0
Matches 17; Conservative
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Fax: 801 585 7177
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RESULT 1663

RESULT 1662

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nRNA sequence.
      Rm. 308, Bi
84112, USA
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                        CF298207
7LEAF--01-H23.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
8ætiva (japonica cultivar-group) cDNA clone 7LEAF--01-H23, mRNA
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                                                                                                                                                               Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol type="mckdong"
/cultivar="Nackdong"
/db_xere="taxon:39947"
/clone="7LBAF-01-H23"
/tissue_type="lasf"
/dev_stage="7 days after germination"
/lab_nost="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, KyeongJi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ818055 20-FEB-200 2M0087B23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0087B23 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muroidea; Murinae; Murinae; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von. Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von. Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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100.0%; Pred. No. 1.5e+03;
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University of Utah Genome Center
University of Utah
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Mus musculus
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CF298207.1 GI:33669968
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of public flatalialghlAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoacea; Ginkgo.

I (bases 1 to 21)
S Brenner, B.D., Twiggo, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Ginkgo microsporophyll (NYBG)
Unpublished (2005)
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
   Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0087 row: B column: 23
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
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    .20
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="UUGC2M0087B23"
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Ginkgo biloba
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DR065210.1 GI:66988778
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                                                                  Tel: 801 585 5606
Fax: 801 585 7177
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/clone lib="Mouse 10kb plasmid UUGCZM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus GSTBL/GJ (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
/http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                     /clone_lib="Ginkgo microsporophyll (NYBG)"
/note="Organ: microsporophyll; Vector: pBK-CMV; Site_l:
/note="Organ: microsporophyll; Vector: pBK-CMV; Site_l:
/note="Organ: BKL; Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts."
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2M0203K21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                       0.6%; Score 17; DB 1; Length 21; 00.0%; Pred. No. 1.6e+03;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.0
Plate: 0203 row: K column: 21
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                    100.0%; Prec. ...
                                                                                /organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xrefe"taxon:3311"
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/mol_type="genomic DNA"
/strain="C57BL/63"
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/clone="UUGC2M0203K21"
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Location/Qualifiers
Email: mccombie@cshl.org
Seg primer: -21M13UnivRev.
Location/Qualifiers
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/lab host="E.
                                                                                                                                                   /sex="male"
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Matches 17; Conservative
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84112, USA
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was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4712114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Cryza sativa (japonica cultivar-group)

Eukaryota; Viridiplanar-group)

Eukaryota; Viridiplanar-group)

Eukaryota; Viridiplanar-group)

Spermatcphyta; Magnoliophyta; Liliopsida; Embryophyta; Tracheophyta;

Clade; Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 20)

SK Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Large-Grale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

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Email: bhrahm@ggio.com, bhnahm@bio.myongji.ac.kr.
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/wol type="mRNA"
/wol type="mRNA"
/wolfivar=mackdong"
/wol type="taxon:39947"
/db xref="taxon:39947"
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/lab host="E.coli DH108"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoR1; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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100.0%; Pred. No. 1.6e+03;
tive 0; Mismatches 0;
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Matches 18; Conserv
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Query Match
Best Local Similarity
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Matches 18; Conserv
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                                               CF300961 20 bp mRNA linear EST 15-AUG-2003 7LEAF--05-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-K03, mRNA
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Spermatophyta; Viidiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 20)
1 (bases 1 to 20)
Song, S. I., Kim, J. Kim, Y. Kim, M. J., Lee, T. H., Shin, Y. C., Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantas Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
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/db.refall_wacxon.39947"
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/dev_stage="Ty days after germination"
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/note="Wettor: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, KyeongJi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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Matches 18; Conserv
                                                                                                                  sequence.
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                          CF300961/c
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/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6, sacrificed on 3/17/9) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard conditions described by vendor, Stratagene. Further details see www.uky.edu/Project/Pneumocystis/"
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/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="%lice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,
Edman, J.C., Kovacs, J. and Cushion, M.
Expressed sequence tags from Pneumocystis carinii
Unpublished (2000)
                                                                                                                              /organism="Oryza sativa (japonica cultivar-group)"
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School of Blological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40566-0225, USA
Tel: 606 257 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW333777 20 bp mRNA linear EST 3:
S25H10 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
AW333777
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Pneumocystis carinii
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 0.6%; Score 16.8; DB 1; Length 2
1 Similarity 90.0%; Pred. No. 1.6e+03;
18; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                 /mol_type="mRNA"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /GDICHARE="1720"
/ GDICHARE="1720"
/ Clone="1D0AAI10YJ1"
/ Lisbuc type="antennae"
/ dev_stage="1.2"
/ lab_host="XL1-Blue"
/ clone lib="ID0ABE"
/ clone lib="ID0ABE"
/ lote="Wetcor: pBS-SKminus; Site I: EcoRI; Site 2: XhoI;
Sample name: D0ABE; Plant growth place: INRA Rennes, UMR BiOJP, 35327, 35653 Le Rheu Cedex France; Soil conditions: Soil; Sowing date: 15/04/2004; Harvesting date: 15/04/2004; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. A. pisum YR2 is holocyclic, i.e. able to change its reproductive mode under short photoperiods (sexual) versus long photoperiods (clonal). experimental condition: long photoperiod (16-hr light/8-hr dark at 18 degc)"
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                                          DY223532 20 bp mRNA linear EST 03-FEB-2006
IDOAAI10YJ11RM1 IDOAEE ACYTCHOSiphon pisum cDNA clone IDOAAI10YJ11
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1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 20)
Stern, D.L., Wincker, P. and Tagu, D.
Large-scale gene discovery in the pea aphid Acyrthosiphon pisum (Hemiptera)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Contact: D. Tagu
INRA Rennes
UMR BiO3P, B9 5327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="yr2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y row: J column: 11.
Location/Qualifiers
                                                                                                                                                                             Acyrthosiphon pisum (pea aphid)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGGAAACAGCTATGACC
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                                                                                                                                   DY223532.1 GI:86457660
                                                                                                                                                                                                       Acyrthosiphon pisum
                                                                                  5', mRNA sequence.
DY223532
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RESULT 1671
DY223532
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                                                               DEFINITION
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AUTHORS
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/Bab. "Maile"
/ Jab. hoste="E. Coli strain XL10-Gold, T1-resistant, F-"
/ clone lib="wouse 10kb plasmid UUGCIM library"
/ note="Westor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically shaared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerses and T4
polynuclecide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose get
adaptoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptores complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chamically-competent E. coll XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1M0118G09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0118G09 R, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
1 (bases 1 to 20)
                                                                                                                                                                                                                                                                                                   Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0077 row: E column: 20
Seg primer: CGTTGTAAAACGACGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/64"
/db xref="taxon:10090"
/clone="UUGCIM0077E20"
                                                                                                                                                                                                  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 20.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: plasmid ends
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Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
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CF319122/c
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Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Waiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Elomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1M0489G12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0489G12 F, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone_lib="Mouse l0kb plasmid UGCIM library"
/note="Vector: PWB4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
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                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0118 row: G column: 09
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 20.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                    Rm. 308, Bi
84112, USA
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                                                                              TITLE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Voctor DNA was prepared from a derivative of pwapto (gill #1732114 [$A] hR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                 plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 1008, blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab host="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackso
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0489 row: G column: 12
Seg primer: CGTTCTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="UUGC1M0489G12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2709 AAAAAAAAAAAAAAAA 2728
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source

FEATURES

TITLE JOURNAL COMMENT

AUTHORS

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Gaps

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18 bp mRNA linear EST 04-SEP-2003
DKRZp5661173 rl 566 (gynonym: h£kd2) Homo gapieng cDNA clone
DKRZp5661173, mRNA gequence.
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&W University,
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mewes, H.W., Gassenhuber, J. and Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 bp mRNA linear EST 27-1
LZV602768363.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: Sall"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16.4; DB 1; Length 18;
Pred. No. 1.6e+03;
0; Mismatches 1; Indels
                                  Indels
            Pred. No. 1.6e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l. .18
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKF2p566L173"
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Adelson, D.L. and Gill, C.A.
Porcine ESTs
                                                                                  2708 TAAAAAAAAAAAAA 2725
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                                                                                                                  1 TCAAAAAAAAAAAAAA 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae, Homo.

1 (baes 1 to 18)
Koehrer, K., Beyer, A., M.
EST (Koehrer, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                  AL048754.1 GI:4727825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.6%;
Best Local Similarity 94.4%;
Matches 17; Conservative 0
         Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (pig)
Sus scrofa
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Tel: 9798452616
Fax: 9798456970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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BM658677/c
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KEYWORDS
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AUTHORS
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TITLE
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
L Unpublished (2013)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University YongJi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab host="E.coli DH10B"
/clone_lib="08HDACI-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPQ; Site_1: EcoRI; Callus was rereated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AJ725584 rikenl Gallus gallus cDNA clone 2c16r4, mRNA sequence.
AJ725584 rikenl Gallus gallus cDNA clone 2c16r4, mRNA sequence.
AJ725584.1 GI:53890998
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GSF - Forsechungszentrum, Institut fuer Molekulare Strahlenbiologie
Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria, Aves, Neognathae, Galliformes; Phasianidae; Phasianines, Gallus.

1 (Basea 1 to 18)
Caldwell, R.B., Kierzek, A.M., Arakawa, H., Bezzubov, Y., Zaim, J., Fiedler, P., Kutter, S., Blagodatski, A., Kostovska, D., Koter, M., Fiedler, P., Carninci, P., Hayashizaki, Y. and Buerstedde, J.M. Full-length CDNAs from chicken bursal lymphocytes to facilitate gene function analysis (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:39947"
/clone="HD--09-107"
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/dev_stage="2-3 weeks old"
/clone_lib="riken!"
/note="CB inbred strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Gallus gallus"
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EST

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL PUBMED

COMMENT

TITLE

FEATURES

RESULT 1676 AJ725584

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Query Match

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Gaps

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EST 27-FEB-2002

FEATURES

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18 bp mRNA linear EST 15-AUG-2003 library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF-03-119, mRNA sequence.
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NACL--04-I22.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-I22, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCR4-TOPO; Site 1: EcoR1; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:39947"
/clone="ABF"-03-119"
/tissue_type="last"
/dev_stage="lat days after germination"
/lab_host="B.coli DH108"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA_library (ABF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 18)
Kim, J. S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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    Location/Qualifiers
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CF329285
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Best Local Similarity 94.4%;
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Organ sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liptophyta; L
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94.4%; Pred. No. 1.6e+03;
ative 0; Mismatches 1;
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Email: david.adelson@tamu.edu
                         Location/Qualifiers
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RESULT 1679 CF300456/c

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza,
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm B.H.
Large-scale Sequencing Analysis of Rice ESTs
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/lab_host="E.coli DH10B"
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University YongJi, Kveongqi, Korea Tel: 82 31 330 6193
Pax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongjin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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    70 Caganism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nackdong"

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/mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                                                                                                 /db_xref="taxon:39947"
/clone="NACL--04-122"
/tissue_type="callus"
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/organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nackdong"
/cultivar="Nackdong"
/cultivar="13947"
/clone="NaCL--04-N06"
/tissue type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH108"
/lab_host="E.coli DH108"
/lone lib="Rice callus plasmid cDNA library (NACL)"
/nore="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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DKFZp468J2331_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone
DKFZp468J2331_5', mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Pongo.

I (bases 1 to 18)

Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,

Fobo, G., Han, M. and Wiemann, S.
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Fax: 82 31 321 6355
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1 (Dassa 1 to 18)
Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice EST8
Unpublished (2003)
Contact: Nahm B.H.
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4.4%; Pred. No. 1.6e+03;
ve 0; Mismatches 1; Indels
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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CF298472.1 GI:33670233
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Best Local Similarity
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Roslin Midlothian, EH25 9PS, UNITED KINGDOW
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called by cross match with the -minscore 20.
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
EGORI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institite,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
                                                                            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKRZ);
Email s.wiemann@dkfz-heidelberg.de; mforschung GmbH in Berlin,
Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi.bin/products/cl.cgi?CloneID=DKFZp468JZ331
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson, S. I., Finlayson, H. A. and Archibald, A. L. Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AJ666205 CSEQRANO9 Sus scrofa cDNA clone C0000033_E15, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="468 (synonym: phrtl)"
/note="Vector: pSportl_Sfi; Site_l: SfilA; Site_2: SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2: NoLI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."
    Pongo pygmaeus mRNA (Koehrer, K., Beyer, A., Mewes, H.W., et al.)
Unpublished (2004)
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4.4%; Pred. No. 1.6e+03;
ve 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mrNA"
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/organism="Sus scrofa"
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Genomics and Bioinformatics
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AJ666205.1 GI:49350656
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Best Local Similarity 94.4%;
Marches 17; Conservative
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                                                Contact: MIPS
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/wol_type="mRNA"
/wol_type="mRNA"
/wol_type="mRNA"
/wol_type="mRXACKdong"
/wol_type="leat"
/wol_type="leat"
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/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
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Oryza sativa (japonica cultivar-group)
Cukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplance; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
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                                                                  Indels
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Score 16.4; DB 1;
Pred. No. 1.6e+03;
0; Mismatches 1;
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Bohlmann, J.
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NACL--02-C04.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-C04, mRNA
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="callus"
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//dev stage="prolliterated callus on 2N6 media for 30 days"
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//clone_lib="Rice callus plasmid cDNA library (NACL)"
//clone_lib="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and Then used as templates for RT-PCR."
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/lab_host="B.coli DH108"
                                                                                                                                        Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bioinformatics, MyongJi University
YongJi, Kyeonggi, Korea
Tel: 82 31 310 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                    1 (bases 1 to 19)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Pred. No. 1.6e+03;
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clade, Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="NACL--01-B12"
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Best Local Similarity 94.4%;
Matches 17; Conservative
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/lab_hoste=a.

/lab_hoste=a.

/lab_hoste=a.

/clone lib="gr-P-FL-A-2"

/clone lib="gr-P-FL-A-2"

/note="Vector: pBluescript II SK (+) XR; Site i: SstI (5')
end of cDNA); Site_2: XhoI (3' end of cDNA); Fhloem and
cambium from 8 year old trees harvested within the Boise
Cascade region of Washington state on May 15th, 2001. cDNA
was prepared from 20 micrograms of mRNA according to the
full-length cDNA library construction method described by
Carninci P. et al. (2000), Genome Research
10(10):1617-1630 and directionally ligated into the
pBluescript II SK (+) XR vector digested with SstI (5')
end) and XhoI (3'). Plasmid DNA was then transformed by
electroporation into DH10B cells (Invitrogen) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 19)
Ralph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y.,
Kirkpatrick, R., Liu, J., Palaquist, D., Stott, J., Barber, S., Yang, G.,
Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A.,
Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A.,
Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          WSO113.BR A21 PT-P-FL-A-2 Populus trichocarpa cDNA clone WSO113_A21 DT497638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Malpighiales, Salicaceae, Saliceae, Populus.
/clone_lib="Rice callus plasmid cDNA library (NACL)" /note="Vector: pCR4-TOPO; Site_l: EcoRI; mRNA was capped with_oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contract: Joseph Bolhmann
Genome BC ferest genomics program
Genome BC ferest genomics program
Genome BC ferest genomics program
University of British Columbia 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Plate: WS0113 row: A column: 21
High quality sequence stop: 129.
Location/Qualifiers
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Pred. No. 1.6e+03;
0; Mismatches 1; Indels
                                                                                                                                                         Length 19;
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                                                                                                                                                            Score 16.4; DB 1;
Pred. No. 1.6e+03;
                                                                                                                                                                                                                        0; Mismatches
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/clone="WS0113_A21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.68;
                                                                                                                                                                   0.68;
                                                                                                                                                                                            94.48;
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                                                                                                                                Query Match
Best Local Similarity 94.1.
Best Local 17; Conservative
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Best Local Similarity 94.4
Matches 17; Conservative
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source
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KEYWORDS
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/ Jab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/ Clone lib="Mouse 10kb plasmid UUGCIM library."
// Intoe="Vector: PWASINY; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi| 47321141gb] AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                  AZ360314 linear GSS 02-OCT-2000 1M0103G03R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0103G03 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Murinae, Mus.

1 (basea 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 19.
Location/Qualifiers
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/clone="UUGC1M0103G03"
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                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
2708 TAAAAAAAAAAAAA 2725
                                                           1 TCAAAAAAAAAAAAAA 18
                                                                                                                                                                                                                                                                                                                   AZ360314.1 GI:10474014
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                             DEFINITION
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AUTHORS
                                                                                                                                                                     AZ360314
LOCUS
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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA, was prepared from a derivative
of pWD42 (gi|4732114|gb|AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed inco
                                                                                                                                                                                                                                                                                                                                                                                                  AZ447251 19 bp DNA linear GSS 04-0CT-2000 1M0244J19F Mouse 10kb plasmid UUGCIM library Mus musculus genomic close UUGCIM0244J19 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Pred. No. 1.6e+03;
0; Mismatches 1;
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Fax: 801 585 7177.
Fax: 801 585 7177.
Fax: 801 585 7177.
Fax: 804 

    .19
    /organism="Mus musculus"

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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0244J19"
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Location/Qualifiers
2709 AAAAAAAAAAAAAAA 2726
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Best Local Similarity 94.4%;
Matches 17; Conservative
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0.6%; Score 16.4; DB 1; Length 19; 94.4%; Pred. No. 1.6e+03; tive 0; Mismatches 1; Indels

Query Match
Best Local Similarity 94.4*
Matches 17; Conservative

Tue Nov

RESULT 1692

ठ 셤 BQ590166/c

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

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Beta vulgaris

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons;

Caryophyllales, Amaranthaceae, Beta.

(bases 1 to 16)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,

Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.,

and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCMVSFORT6; Site 1: Sal1; Site 2: Not1; cDNA library from sugar beet, lTbrary provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caryophyllales, Amaranthaceae; Beta.
1 (bases 1 to 16)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Herwig,R., Sthulz,B., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               orientation:
SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/culTivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DQJ9J2bUU 16 bp mRNA linear EST 06-I S013686-024-028-F08-SPER MPIZ-ADIS-024-developing root Beta Wulgaris CDNA clone 024-028-F08 5-PRIME, mRNA sequence. BQ592600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
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.00.0%; Pred. No. 1.6e+03;
.ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 19 row: M column: 04
Seq primer: T7; GTAATACGACTCACTATAGGGC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Beta vulgaris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:161934"
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CDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae, Streptophyta;

Caryophylaies, Magnoliophyta; eudicotyledons;

Caryophyllaies, Amaranthaceae; Beta.

1 (bases 1 to 16)

1 (bases 1 to 16)

Perwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,

Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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/cultivar="KWS2320 (double haploid, monogerm breeding
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
MAX-Planck-Institute for Plant Breeding Research
Fax: 00492215062851
Email: Weisshaa@mpiz-koeln.mpg.de
Insert Length: 16 Std Brror: 0.00
Plate: 19 row: K column: 18
Seg primer: T7; GTAATACGACTCACTATAGGGC.
Location/Qualifiers
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/organism≈"Beta vulgaris"
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RESULT 1693 BQ590507/c

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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Not1, primer sites and
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 16)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
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Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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                                                                                                 Contact: Weisshaar B
ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: Weissha@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 28 row: F column: 08
Seq primer: SP6r; ATTTAGGTGACACTATAGAAGA.
Location/Qualifiers
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
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| /clone="lyector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1; Once="taxory from sugar beet, library provided by KWS |
| Kleinwanzlebener Saazzucht AG Einbeck, Germany, contact: b. schulz@kws.de; cloning sites Sal1-Not1, primer sites and
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( aryophyllales; Amaranthaceae; Beta.

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
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S013317-024-022-P02-T7 MPIZ-ADIS-024-developing root Beta vulgaris
CDNA clone 024-022-P02 3-PRIME, mRNA sequence.
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                    Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
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Insert Length: 16
Plate: 28 row: A
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CF296130 16 bp mRNA linear EST 14-AUG-2003 30DGS--06-F22.bl Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--06-F22, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 14-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF279325
14 bp mRNA linear EST 14-AUG-20
14ETL--05-J09.gl Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-J09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                       Gaps
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                                                                                                                                 0.6%; Score 16; DB 1; Length 16;
100.0%; Pred. No. 1.6e+03;
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100.0%; Pred. No. 1.6e+03;
ative 0; Mismatches 0; Indels
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/dev_stage="14 days after_germination"
/lab_host="E.coli_DH10B"
                                                                                                                                           Similarity 100.0%; Pred. No. ...
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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--05-J09"
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Location/Qualifiers
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BQ595717.1 GI:26125300
                                                                                                 /dlone lib="MRIZ-ADIS-024-developing root"
/clone TVector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
/note="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
/clone TVector: pcMVSPORT6; Site 2: Not1;
/clone Subary from sugar beet, library provided by KWS
/clone Saatsucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="developing root"
/tish host="EMDH10B"
/clone lib="MPIZ-ADIS-024-developing root"
/note="vector: pCMVSPORT6; Site_1: Sal1; Site_2: Not1;
/note="vector: pCMVSPORT6; Site_1: Sal1; Site_2: Not1;
/note="vector: pCMVSPORT6; Site_1: Sal1; Site_2: Not1;
/note="vector: pCMVSPORT6; Site_2: Sal1; Site_2: Not1;
/note="vector: pcm, site_2: Not2;
/note: pcm, site_2: Not2;
/not2: pcm, site_2: Not2: pcm, site_
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 16)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,

and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

Eingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                             orientation:
SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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/organism="Beta vulgaris"
/mol type="mRNA"
/cultivar="KWS2120 (double haploid, monogerm breeding
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 16 Std Exror: 0.00
Plate: 22 row: H column: 07
Seg primer: SP6; CATACGATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16; DB 1; Length 16;
Pred. No. 1.6e+03;
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                                         /tissue_type="developing root"
/lab_host="EMDH10B"
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0.6*; Score 10; DB. Best Local Similarity 100.0%; Pred. No. 1.6

Matches 16; Conservative 0; Mismatches
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/clone="024-022-H07"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                I (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.-K. and Nahm,B.H.
Large-Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Generics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
YongJin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fex: 82 31 321 6555
Fex: 82 31 321 6555
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantaa, Streptophyta; Embryophyta; Tracheophyta;
Spermarcophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:3994"

/clone="30DG2-06-F22"

/tissue type="leaf"

/dev_stage="30 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bloscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                        organism="Oryza sativa (japonica cultivar-group)"
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| mol type="mRNA"
| cultivar="Mackdong"
| db_xref="taxon:39947"
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0
                                                                                                                                                                                                                                                                                                                                           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .6%; Score 16; DB 1; Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
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CF311057/c
LOCUS
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JOURNAL
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AUTHORS
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JOURNAL
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SOURCE
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HD--02-G01.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--02-G01, mRNA sequence.
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/dav_stage="proliferated"
/lab_nost="E.coli DH10B"
/clone_lib="collablaCl-overexpressing transgenic rice plasmid cDNA library (HD)"
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida, Poales, Poaceae; BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                        /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
TyongJn, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                        /clone lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
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    16. 16
/organism="Oryza sativa (japonica cultivar-group)"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
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100.0%; Pred. No. 1.6e+03;
/ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="Nackdong"
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CF314013.1 GI:33685774
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/dev_stage="proliferated"
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/clone lib="collabACI-overexpressing transgenic rice plasmid
cDNA llbrary (HD)"
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/dev_stage="proliferated"
/lab_nost="E.coli DH10B"
/clone lib="collabAC1-overexpressing transgenic rice plasmid cDNa llbrary (HD)"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscine and Bioinformatics, MyongJi University
Yongin, Kyeonegal, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 855
Exar: 82 31 321 625
Email: bhnahm@pio.myongji.ac.kr.
Location/Qualifiers
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Contact: Nahm B.H.
Genotics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
of Sioscience and Bioinformatics, MyongJi University
frogin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
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VERSION
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HD---04-N10.g1 OBHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--04-N10, mRNA sequence.
CF315789.1 GI:33687550
EST.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantas Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopaida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaee; Oryza.

1 (bases 1 to 16)
1 (kim.J.K., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nahm B.H.

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Biosience and Bioinformatics, MyongJi University
YongJin, Kyeonegl, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@pio.myongji.ac.kr.

Location/Qualifiers
                                                                                      CF314377

HD--02-001.b1 OsHDAC1-overexpressing transgenic rice plasmid CDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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100.0%; Pred. No. 1.6e+03;
ive 0; Mismatches 0; Indels
                                                                                                                                                                       HD--02-001, mRNA sequence.
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CF314377.1 GI:33686138
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CF314377/c
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TITLE JOURNAL

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS ö

Gaps

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EST 15-AUG-2003

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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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CF320356.1
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Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eneptophyta; Energe-scale Sequencing Analysis of Rice EsTs

Unpublished (2003)

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Tel: 82 31 313 06 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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HD--07-105.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--07-105, mRNA sequence.
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cDNA library (HD)"
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HD--11-D14.bl OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--11-D14, mRNA sequence.
treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
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100.0%; Pred. No. 1.6e+03;
ive 0; Mismatches 0; Indels
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ve 0; Mismatches 0; Indels
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

(bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                 Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bloscience and Bioinformatics, MyongJi University
Yorgin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Torgin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/mol_type="mRNA"
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaa.

E 1 (bases 1 to 16)

S Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Context: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6355
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NACL--04-J17.bl Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-J17, mRNA
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/organism="Oryza sativa (japonica cultivar-group)"
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100.0%; Pred. No. 1.6e+03;
ive 0; Mismatches 0; Indels
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Location/Qualifiers
                                                  /mol_type="mRNA"
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location/Qualifiers
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Best Local Similarity 100.
Matches 16; Conservative
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KEYWORDS
SOURCE
ORGANISM
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Oryza sativa (japonica cultivar-group)

ISM Oryza sativa (japonica cultivar-group)

Eukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryzea

CE I (bases 1 to 16)

RS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
CF333386

16 bp mRNA linear EST 18-AUG-2003

JMT--02-E05.gl AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reversee transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKF20652231 r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone DKF2p468E2231 s', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini;

Hominidae; Pongo.

1 (bases 1 to 16)

Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,

Fobo, G., Han, M. and Wiemann, S.

Pongo pygmaeus mRNA (Koehrer, K., Beyer, A., Mewes, H.W., et al.)

Contact: MIPS

MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone lib="ktUMT-overexpressing transgenic rice plasmid cDNa lTbrary (JMT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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/organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar-drong"
/db xref="taxon:39947"
/clone="JMT--02-E05"
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100.0%; Pred. No. 1.6e+03;
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                                                                                          JMT--02-E05, mRNA sequence.
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Populus trichocarpa
Populus trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Salicace; Populus.

Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y.,
Rirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G.,
Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,
Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Bmail s. wiemann@dkfz-heidelberg.de; mforschung GmbH in Berlin,
Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi.bin/products/cl.cgi?CloneID=DKFZp468EZ231
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
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Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="468 (synonym: phrt1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA, Site_2: SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/clone_lib="PT-P-FL-A-2"
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/cultivar="383-2499 (Niequally-1)"
/clone="W80115_M08"
/elone="W80115_M08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16; DB 1; Le
Pred. No. 1.6e+03;

    .16
    /organism="Populus trichocarpa"

                                                                                                                                                                                                                                                       /organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
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                                                                                                                                                                                                                                                                                                                             /clone="DKFZp468E2231"
/tissue_type="heart"
/dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Plate: WS0115 row: M column: (High quality sequence stop: 122
POLYN=Yes.
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100.0%; Pred
0; F
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Best Local Similarity 100.
Matches 16; Conservative
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KEYWORDS
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/note="Vector: pBluescript II SK (+) XR; Site_I: SstI (5, end of cDNA); File_2: XhoI (3' end of cDNA); Filoem and cambium from 8 year old trees harvested within the Boise Cascade region of Washington state on May 15th, 2001. cDNA was prepared from 20 micrograms of mRNA according to the full-length cDNA library construction method described by Carninci P. et al. (2000), Genome Research 10(10):1617-1630 and directionally ligated into the pBluescript II SK (+) XR vector diagested with SstI (5' end) and XhoI (3'). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E012715-024-017-H16-T7 MPIZ-ADIS-024-8torage root Beta vulgaris CDNA clone 024-017-H16 3-PRIME, mRNA sequence.
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/lab_host="EMDH10B"
/clone lib="MPIZ-ADIS-024-storage root"
/note="Vector: pGWVSPORT6; Site_1: Sal1; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saarzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 17)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     orientation:
SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KW82320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 16; DB 1; Length 16; 00.0%; Pred. No. 1.6e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 17 row: H column: 16
Seg primer: T7; GTAATACGACTCACTATAGGGC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              100.0%; Prec. ...
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/db_xref="taxon:161934"
/clone="024-017-H16"
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KEYWORDS
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Query Match

Matches

ઠે 엄 ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 1713 CF295807/c

DEFINITION

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Oryza sativa (japonica cultivar-group)

ENKaryota, (indiplantae, Streptophyta; Embryophyta; Tracheophyta; Enkaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Enkaryota, Viridiplantae, Streptophyta; Embryophyta; Magnoliophyta; Liliopsida; Embryophyta; Magnoliophyta; Liliopsida; Embryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryzea; Oryzea; Clade; Ehrhartoideae; Oryzeae; Oryzea; Clade; Ehrhartoideae; Oryzeae; Oryzea; Clade; Ehrhartoideae; Oryzeae; Oryzea; Clade; Elim, W.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-escale Sequencing Analysis of Rice ESTS
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 320 6193
Location/Qualifiers
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae, Oryza.

CE I (bases 1 to 17)

RS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyconggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CF302447
7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-P11, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:39947"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: ECORI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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/mol type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
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/cultivar="Nackdong"
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/mol type="mRNA"
/cultivar="Nackdong"
/cultivar="Nackdong"
/db xref="taxon:39947"
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with oligoribonucleotides and then used as templates for
RT-PCR."
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7LEAP--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
8ativa (japonica cultivar-group) cDNA clone 7LEAF--03-L20, mRNA
8equence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
I (bases I to I).
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                    Gaps
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                                                                       0.6%; Score 16; DB 1; Length 17; 100.0%; Pred. No. 1.7e+03; ative 0; Mismatches 0; Indels
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Location/Qualifiers
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CF295807.1 GI:33664840
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ABF--08-P19, mRNA sequence.
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ABF--06-L20.bl ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-L20, mRNA sequence.
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/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for RT-PCR."
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Genomics and Genetics Institute, Greendene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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/lab_host="B.coli DH10B"
/clone_lib="ABF2-overexpressing transgenic rice plasmid
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ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
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/mol_type="mRNA"
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100.0%; Pred. No. 1.7e+03;
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Matches 16; Conservative 0; Mismatches
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/clone="ABF--06-L20"
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Orgas sativa (japonica cultivar-group)
Orgas sativa (japonica cultivar-group)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzea.

El (bases 1 to 17)
SK Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Lu Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-Gcale Sequencing Analysis of Rice ESTs
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                                                                                                                                                                                                                                                                                                                                                                                            Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/clone_lib="ABF--overexpressing transgenic rice plasmid on Ibrary (ABF).
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CF313013.1 GI:33684774
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CF319075.1 GI:33690836
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/dev stage="proliferated callus on 2N6 media for 2 weeks"
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzae, Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTB
Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6555
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                 /note="Vector: pCR4-TOPO, Site_1: EcoR1; Callus was treated with ABA(10um) for Ihr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression
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100.0%; Pred. No. 1.7e+03;
tive 0; Mismatches 0; Indels
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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
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Best Local Similarity 100.
Matches 16; Conservative
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CF298591/c
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Oryza sativa (japonica cultivar-group)

ISM Oryza sativa (japonica cultivar-group)

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryzea

I (bases I to 19)

RS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

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Tel: 82 31 320 6193

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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                  CF278272 14-AUG-2003 14ETL--04-C01.b1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-C01,
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Oryza sativa (japonica cultivar-group)
Dukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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[00.0%; Pred. No. 1.7e+03;
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16 TAAAAAAAAAAAA 1
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/ Corganism="Oryza sativa (japonica cultivar-group)"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

(bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Exar: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Contact: Nahm B.H.

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@pio.myongji.ac.kr.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCR4-TOPO, Site_1: EcoRI, Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
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.00.0%; Pred. No. 1.7e+03;
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     Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
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Best Local Similarity 100.
Matches 16; Conservative
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/clone lib="Wouse 10kb plasmid UUGCIM library"
/note="Westor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/documents/
(http://www.jax.org/resources/documents/dhares/). The
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 19)

5 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (200)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ764517 19 bp DNA linear GSS 16-FEB-2001 1M0560L07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0560L07 R, genomic survey sequence.
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                     /note="Vector: pCR4-TOPO, Site_1: EcoRI; Leaf was dried for Zhrs. Oligo-Capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
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100.0%; Pred. No. 1.7e+03;
iive 0; Mismatches 0;
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Fax: 801 585 7177
Fmail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGCIM0560L07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 0560 row: L column: 07
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Location/Qualifiers
CDNA library (ABF)"
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                                                                                                                                                                                                                                   Similarity
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CF300236
7LEAF--04-124.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-124, mRNA
                                        Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhatroideae; Oryzeae; Oryza
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Cryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Magnoliophyta; Lilopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzeae; Oryza
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
Genomics and Bioinformatics, MyongJi University
Yonglin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6195
Eax: 82 31 321 6195
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                               Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongGi, Korea
Yongin, KyeongGi, Korea
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db.ref="tack20:39947"
/db.ref="tack20:39947"
/clone="71EAF--01-G09"
/tissue_type="leds after germination"
/dev_stage="7" days after germination"
/lab_host="E.coli DH10B"
/clone_11b="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOP0', Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 15.8; DB 1;
19.5%; Pred. No. 1.8e+03;
.ve 0; Mismatches 2;
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CF300236.1 GI:33671997
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                                                                                                                                                                                                                                                                                                            Contact: Nahm B.H.
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Roslin Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
ECORT R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institite,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli KL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF298134 11609.gl Rice leaf plasmid cDNA linear EST 15-AUG-2003 7LEAF--01-G09.gl Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-G09, mRNA
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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/mol type="mRNA"
/mol type="mRNA"
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/clone="C0000024 H21"
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/clone lib="CSEQRNN09"
/note="voctor: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."
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100.0%; Pred. No. 1.7e+03;
ive 0; Mismatches 0; Indels
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Genomics and Bioinformatics
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Matches 17; Conservative
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Best Local Similarity 100.09
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (pig)
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EST.
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FEATURES

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tisue type="14 days after germination"
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/clone lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/clone lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/clone lib="ABF3-overexpressing transgenic and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 bp mRNA linear EST 15-AUG-2003 library (ABF) Oryza sativa (japonica cultivar-group) cDNA ABF-03-008, mRNA sequence. CF309636.1 GI:33681397
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
            /db.rival. wat.xon:39947"
/clone="7LEAF--04-124"
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/dev stage="7 days after germination"
/lab_host="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonuclectides and Then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Genetics Institute, Myongji University
Yongji, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Pred. No. 1.8e+03;
0; Mismatches 2; Indels
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cultivar="Nackdong"
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19 ATTCAAAAAAAAAAAA 1

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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryza.

El (bases 1 to 19)

Kim, J.S., Jun, K.M., Cheong, D.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Lupublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bloinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 21 6355
                        19 bp mRNA linear EST 15-AUG-2003 ABF--04-D16.gl ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--04-D16, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="leaf"
/dev_stage="14 days after germination"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for library (ABF) was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
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Oryza sativa (japonica cultivar-group)
Coryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.
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Location/Qualifiers
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Best Local Similarity 89.5%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 2;
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/clone="ABF--04-D16"
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/cultivar="Nackdong"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                            /dev stage="proliferated callus on 2N6 media for 30 days" /lab_host="E.coli DH10B" /clone lib="Rice callus plasmid cDNA library (NACL)" /clone lib="Rice callus plasmid cDNA library (NACL)" with ce"Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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E 1 (basea 1 to 19)
S Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Roses, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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1M0080F06F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                        /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="txxon:39947"
/clone="NACL--04-F15"
/tissue_type="callus"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: F column: 06
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends

    .19
/organism="Mus musculus"

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/strain="C57BL/6J"
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Location/Qualifiers
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84112, USA
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Imboratory Mouse DNA Resource
[Laboratory Mouse DNA Resource
[Laboratory Mouse DNA Resource (Attp://www.jax.org/resources/documents/daraes/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 k range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb22 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0354A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
/clone_lib="Mouse 10kb plasmid_UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Pred. No. 1.8e+03;
0; Mismatches 2; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0354 row: A column: 07
Seg primer: CGTYCTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/strain="C57BL/6J"
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/sex="Male"
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AZ509929.1 GI:10691245
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Best Local Similarity 89.5
Matches 17; Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gb]AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Niederhausern, A. and Wright, D., Weiss, R.

Unpublished (2000)

Contact: Robert B.

University of Utah Genome Center

University of Utah
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/db_xref="taxon:10090"
/clone="UUGCIM0438G03"
/sex="Male"
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Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/organism="Mus musculus"
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Fax: 801 585 7177
Email: ddunm@enetics.utah.edu
Insert Length: 10000 Std Error
Plate: 0438 row: G column: 03
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Best Local Similarity
Matches 17; Conserv
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84112, US
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AUTHORS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwapt (gilfy132114[pl]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
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[S Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Dubmid inserts

[D Dlasmid inserts

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2M0031H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0031H17 R, genomic survey sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Mus.
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                         Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
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Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
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Fax: 801 585 7177
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Matches 17; Conserva
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus GS7BL/6J (male) was obtained from the Jackson
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(http://www.jax.org/resources/documents/dnares/). The DNA
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and selected for ampicillin resistance."
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 Query Match
 0.6%; Score 15.8; DB 1; Length 19;

 Best Local Similarity
 89.5%; Pred. No. 1.8e+03;

 Matches 17; Conservative
 0; Mismatches
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Search completed: November 7, 2006, 10:40:22 Job time : 108 secs